Changes in Fv/Fm in elevated nutrients and heat stress

Ana Palacio

2020-12-20

Contents

General project set-up **1**

Data exploration **2**
1. Get the files with all the YII by species 2
2. Exploratory graphs 5

Figure 3: Treatment differences by species and dominant symbiont **7**
Figure 3b (No smooth) 9
Figure 3c (Symbiont based) 11

YII GLMs **13**
All spp pooled (does not consider domminant symbiont) 13
A.cer model 15
Ofav and Ssid 22
Baseline: effect of different Symbiodiniaceae taxa before treatments 23
C: Effect of nutrient treatments at control temperature 28
H: Effect of pre-exposure to nutrient treatments during heat challenge 50

Packages used **72**

General project set-up

```
# Load libraries and sources required to run the script
    library(tidyverse)
    library(ggthemes)
    library(lmerTest)
    library(emmeans)
    library(multcomp)
    library(effects)
    library(gridExtra)
    library(rstatix)

# Default ggplot settings

    Fill.colour<-scale_colour_manual(values = c("black", "gray70", "gray35"))

    ggthe_bw<-theme(plot.background=element_blank(),
          panel.grid.major.y = element_blank(),
          panel.grid.major.x = element_blank(),
          panel.grid.minor.x = element_blank(),
          panel.grid.minor.y = element_blank(),
          legend.box.background = element_rect(),
          panel.background =element_rect(fill = NA, color = "black")
```

```
          )+
    theme_bw()
```

Data exploration

1. Get the files with all the YII by species

```
  YII.data<-read.csv("YII_Data/All_YII_data.csv", header = T)
  summary(YII.data)
```

```
##         Sample             Date      Spp          Fragment    Treatment
##  Ac_288_T21:   2   2017-11-16: 354   Ac:2281   Ac_108 :  24   A  :2096
##  Ac_101_T0 :   1   2017-11-23: 354   Of:1051   Ac_116 :  24   N  :1974
##  Ac_101_T1 :   1   2017-11-29: 354   Ss:2687   Ac_119 :  24   N+P:1949
##  Ac_101_T10:   1   2017-12-06: 354             Ac_122 :  24
##  Ac_101_T11:   1   2017-12-13: 354             Ac_143 :  24
##  Ac_101_T12:   1   2018-01-03: 354             Ac_152 :  24
##  (Other)   :6012   (Other)   :3895             (Other):5875
##  Replicate      YII            Genotype         Days
##  R1:3061   Min.   :0.0000   G_62   : 577   Min.   :-112.00
##  R2:2958   1st Qu.:0.4420   G_48   : 570   1st Qu.:  14.00
##            Median :0.5030   G_07   : 462   Median :  65.00
##            Mean   :0.4988   Ss_20  : 402   Mean   :  52.42
##            3rd Qu.:0.5720   Ss_23  : 402   3rd Qu.:  92.00
##            Max.   :0.6870   Ss_27  : 400   Max.   : 156.00
##                             (Other):3206
##    Time_Point         Phase         TotalSH          logSH
##  T10    : 354   Baseline : 954   Min.   :0.000   Min.   :-5.473
##  T5     : 354   Heat     :1520   1st Qu.:0.020   1st Qu.:-1.709
##  T6     : 354   Nutrients:2818   Median :0.057   Median :-1.243
##  T7     : 354   Ramping  : 514   Mean   :0.116   Mean   :-1.317
##  T8     : 354   Recovery : 213   3rd Qu.:0.158   3rd Qu.:-0.802
##  T9     : 354                    Max.   :1.394   Max.   : 0.144
##  (Other):3895                    NA's   :4657    NA's   :4657
##      D.Prp        Community InitialCommunity
##  Min.   :0.0000   A :2281   A :2281
##  1st Qu.:0.0000   B : 195   B : 186
##  Median :0.0000   C1: 538   C1: 468
##  Mean   :0.1705   C3: 727   C3: 762
##  3rd Qu.:0.0000   D :2278   D :2322
##  Max.   :1.0000
##  NA's   :2836
```

Merge/Transform

```
# Organize data type
      YII.data$Date<-as.Date(YII.data$Date, "%Y-%m-%d")
      YII.data$Days<-(as.numeric(YII.data$Date) -17485)
      #Time as a factor, not as int
      str(YII.data)
```

```
## 'data.frame':    6019 obs. of  16 variables:
##  $ Sample          : Factor w/ 6018 levels "Ac_101_T0","Ac_101_T1",..: 1 2 10 11 12 13 14 15 16 17 .
```

```
##  $ Date            : Date, format: "2017-07-26" "2017-08-30" ...
##  $ Spp             : Factor w/ 3 levels "Ac","Of","Ss": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Fragment        : Factor w/ 354 levels "Ac_101","Ac_102",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Treatment       : Factor w/ 3 levels "A","N","N+P": 3 3 3 3 3 3 3 3 3 3 ...
##  $ Replicate       : Factor w/ 2 levels "R1","R2": 1 1 1 1 1 1 1 1 1 1 ...
##  $ YII             : num  0.644 0.576 0.563 0.568 0.645 0.589 0.595 0.606 0.605 0.606 ...
##  $ Genotype        : Factor w/ 17 levels "G_07","G_08",..: 5 5 5 5 5 5 5 5 5 5 ...
##  $ Days            : num  -112 -77 -36 -27 -9 1 8 14 21 28 ...
##  $ Time_Point      : Factor w/ 25 levels "T0","T1","T10",..: 1 2 12 19 20 21 22 23 24 25 ...
##  $ Phase           : Factor w/ 5 levels "Baseline","Heat",..: 1 1 1 1 1 1 3 3 3 3 ...
##  $ TotalSH         : num  NA NA NA NA NA ...
##  $ logSH           : num  NA NA NA NA NA ...
##  $ D.Prp           : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Community       : Factor w/ 5 levels "A","B","C1","C3",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ InitialCommunity: Factor w/ 5 levels "A","B","C1","C3",..: 1 1 1 1 1 1 1 1 1 1 ...
```

```
      YII.data$DaysF<-as.factor(YII.data$Days)


      YII.data$Spp <- as.factor(YII.data$Spp)

      YII.data$Treatment <- as.factor(YII.data$Treatment)

      YII.data$Genotype<-factor(as.character(YII.data$Genotype),
                              levels=c("G_48", "G_62","G_31",
                                       "G_08","G_07", "G_50",
                              "Of_34","Of_20","Of_6", "Of_31",
                              "Ss_22","Ss_23","Ss_27", "Ss_28",
                              "Ss_20", "Ss_24","Ss_30"
                               ))  # D dominance order
      YII.data$Community <- factor(YII.data$Community,
                                   levels = c("A", "B", "C3", "C1", "D"))

# Check the data
      str(YII.data)
```

```
## 'data.frame':    6019 obs. of  17 variables:
##  $ Sample          : Factor w/ 6018 levels "Ac_101_T0","Ac_101_T1",..: 1 2 10 11 12 13 14 15 16 17 .
##  $ Date            : Date, format: "2017-07-26" "2017-08-30" ...
##  $ Spp             : Factor w/ 3 levels "Ac","Of","Ss": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Fragment        : Factor w/ 354 levels "Ac_101","Ac_102",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Treatment       : Factor w/ 3 levels "A","N","N+P": 3 3 3 3 3 3 3 3 3 3 ...
##  $ Replicate       : Factor w/ 2 levels "R1","R2": 1 1 1 1 1 1 1 1 1 1 ...
##  $ YII             : num  0.644 0.576 0.563 0.568 0.645 0.589 0.595 0.606 0.605 0.606 ...
##  $ Genotype        : Factor w/ 17 levels "G_48","G_62",..: 6 6 6 6 6 6 6 6 6 6 ...
##  $ Days            : num  -112 -77 -36 -27 -9 1 8 14 21 28 ...
##  $ Time_Point      : Factor w/ 25 levels "T0","T1","T10",..: 1 2 12 19 20 21 22 23 24 25 ...
##  $ Phase           : Factor w/ 5 levels "Baseline","Heat",..: 1 1 1 1 1 1 3 3 3 3 ...
##  $ TotalSH         : num  NA NA NA NA NA ...
##  $ logSH           : num  NA NA NA NA NA ...
##  $ D.Prp           : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Community       : Factor w/ 5 levels "A","B","C3","C1",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ InitialCommunity: Factor w/ 5 levels "A","B","C1","C3",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ DaysF           : Factor w/ 26 levels "-112","-77","-36",..: 1 2 3 4 5 6 7 8 9 10 ...
```

```
summary(YII.data)
```

```
##         Sample          Date            Spp          Fragment
##  Ac_288_T21:   2   Min.   :2017-07-26   Ac:2281   Ac_108 :  24
##  Ac_101_T0 :   1   1st Qu.:2017-11-29   Of:1051   Ac_116 :  24
##  Ac_101_T1 :   1   Median :2018-01-19   Ss:2687   Ac_119 :  24
##  Ac_101_T10:   1   Mean   :2018-01-06             Ac_122 :  24
##  Ac_101_T11:   1   3rd Qu.:2018-02-15             Ac_143 :  24
##  Ac_101_T12:   1   Max.   :2018-04-20             Ac_152 :  24
##  (Other)   :6012                                  (Other):5875
##  Treatment  Replicate      YII            Genotype         Days
##  A  :2096   R1:3061   Min.   :0.0000   G_62   : 577   Min.   :-112.00
##  N  :1974   R2:2958   1st Qu.:0.4420   G_48   : 570   1st Qu.:  14.00
##  N+P:1949             Median :0.5030   G_07   : 462   Median :  65.00
##                       Mean   :0.4988   Ss_23  : 402   Mean   :  52.42
##                       3rd Qu.:0.5720   Ss_20  : 402   3rd Qu.:  92.00
##                       Max.   :0.6870   Ss_27  : 400   Max.   : 156.00
##                                        (Other):3206
##    Time_Point         Phase         TotalSH          logSH
##  T10    : 354   Baseline : 954   Min.   :0.000   Min.   :-5.473
##  T5     : 354   Heat     :1520   1st Qu.:0.020   1st Qu.:-1.709
##  T6     : 354   Nutrients:2818   Median :0.057   Median :-1.243
##  T7     : 354   Ramping  : 514   Mean   :0.116   Mean   :-1.317
##  T8     : 354   Recovery : 213   3rd Qu.:0.158   3rd Qu.:-0.802
##  T9     : 354                    Max.   :1.394   Max.   : 0.144
##  (Other):3895                    NA's   :4657    NA's   :4657
##      D.Prp        Community InitialCommunity     DaysF
##  Min.   :0.0000   A :2281   A :2281          1      : 354
##  1st Qu.:0.0000   B : 195   B : 186          8      : 354
##  Median :0.0000   C3: 727   C1: 468          14     : 354
##  Mean   :0.1705   C1: 538   C3: 762          21     : 354
##  3rd Qu.:0.0000   D :2278   D :2322          28     : 354
##  Max.   :1.0000                             49     : 354
##  NA's   :2836                               (Other):3895
```

Remove / subset timepoints

```
# Remove baseline values
    YII.data<-subset(YII.data, Days>-1)
  # Remove recovery values
    YII.data<-subset(YII.data, Days<112)
    # write.csv(YII.data, "Outputs/Experiment_YII_data.csv", row.names = F)
  # YII.Wide<- reshape(YII.data, idvar = "Fragment", timevar = "Days", direction = "wide")

    Spp.fragments<-YII.data %>%
      group_by(Spp, Genotype, Treatment, Replicate) %>% count(Fragment)
    Spp.fragments
```

```
## # A tibble: 354 x 6
## # Groups:   Spp, Genotype, Treatment, Replicate [102]
##    Spp   Genotype Treatment Replicate Fragment     n
##    <fct> <fct>    <fct>     <fct>     <fct>    <int>
##  1 Ac    G_48     A         R1        Ac_176      17
##  2 Ac    G_48     A         R1        Ac_182      17
##  3 Ac    G_48     A         R1        Ac_189       9
```

```
##  4 Ac    G_48     A         R1        Ac_281      17
##  5 Ac    G_48     A         R1        Ac_287      17
##  6 Ac    G_48     A         R2        Ac_179      17
##  7 Ac    G_48     A         R2        Ac_186      17
##  8 Ac    G_48     A         R2        Ac_277      17
##  9 Ac    G_48     A         R2        Ac_284      17
## 10 Ac    G_48     A         R2        Ac_290       9
## # ... with 344 more rows
```

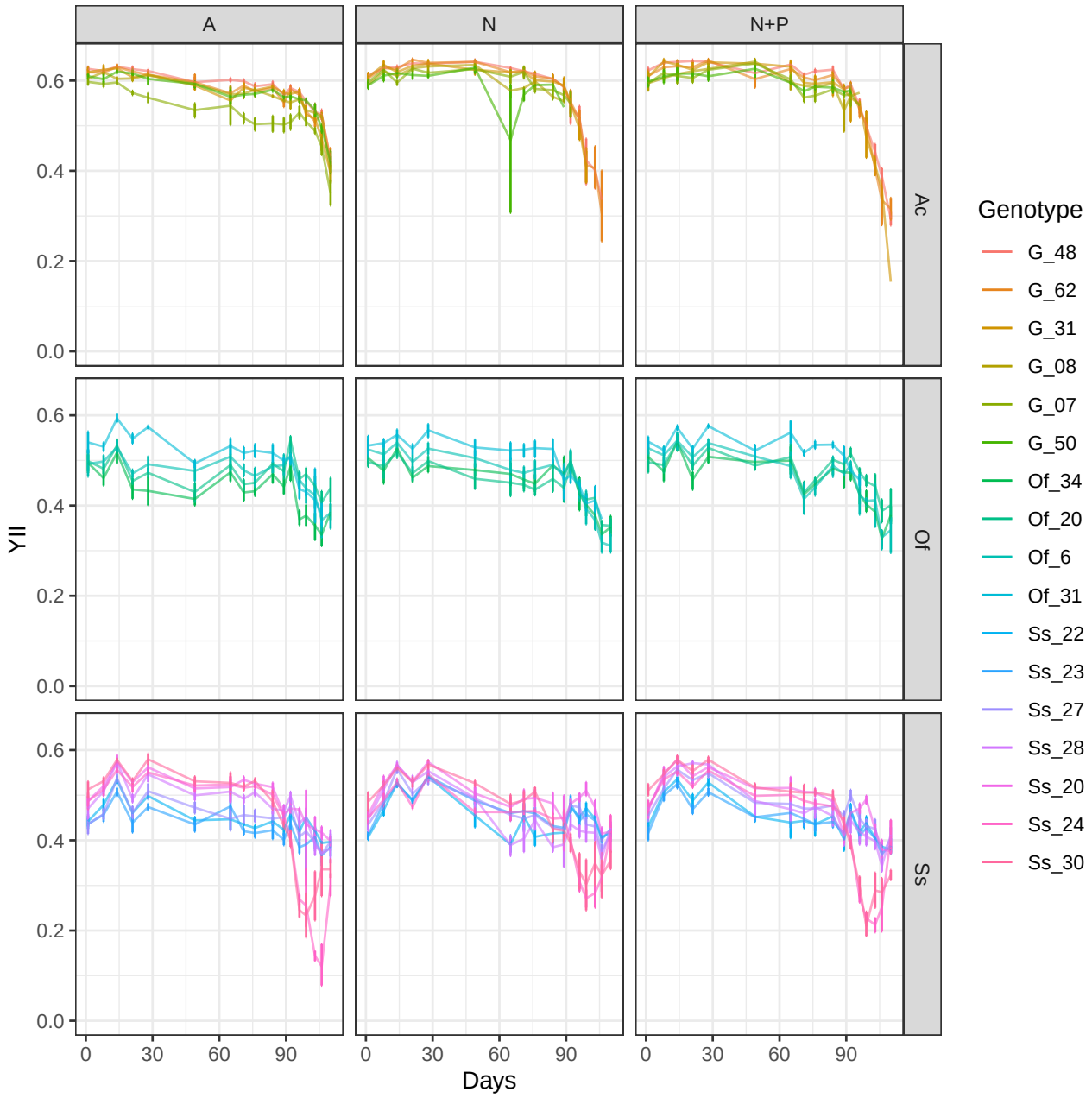
```
      #write.csv(Spp.fragments, "Outputs/Meassurments_perFragments.csv", row.names = F)

# Subset data
      YII.nutrients<-subset(YII.data, Days<80)
      YII.heat<-subset(YII.data, Days>75)
```

2. Exploratory graphs

All time points (nutrients + heat stress)

- Colony (Genotype) differences

```
YII_Colony<- ggplot(YII.data, aes (Days, YII, colour=Genotype)) +
        stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 0.5)+
        stat_summary(fun.y=mean, geom="line", alpha=0.6) +   theme_bw()
      YII_Colony + ylim(0.0, 0.65) + facet_grid (Spp~Treatment)
```




```
YII_Frag_Gen<- ggplot(YII.data, aes (Days, YII, colour=Genotype, group=Fragment)) +
        stat_summary(fun.y=mean, geom="line", alpha=0.5) +
        theme_bw() + theme(legend.position = "bottom",
                           legend.title = element_blank())
      YII_Frag_Gen + ylim(0.0, 0.65) + facet_grid (Spp~Treatment)
```

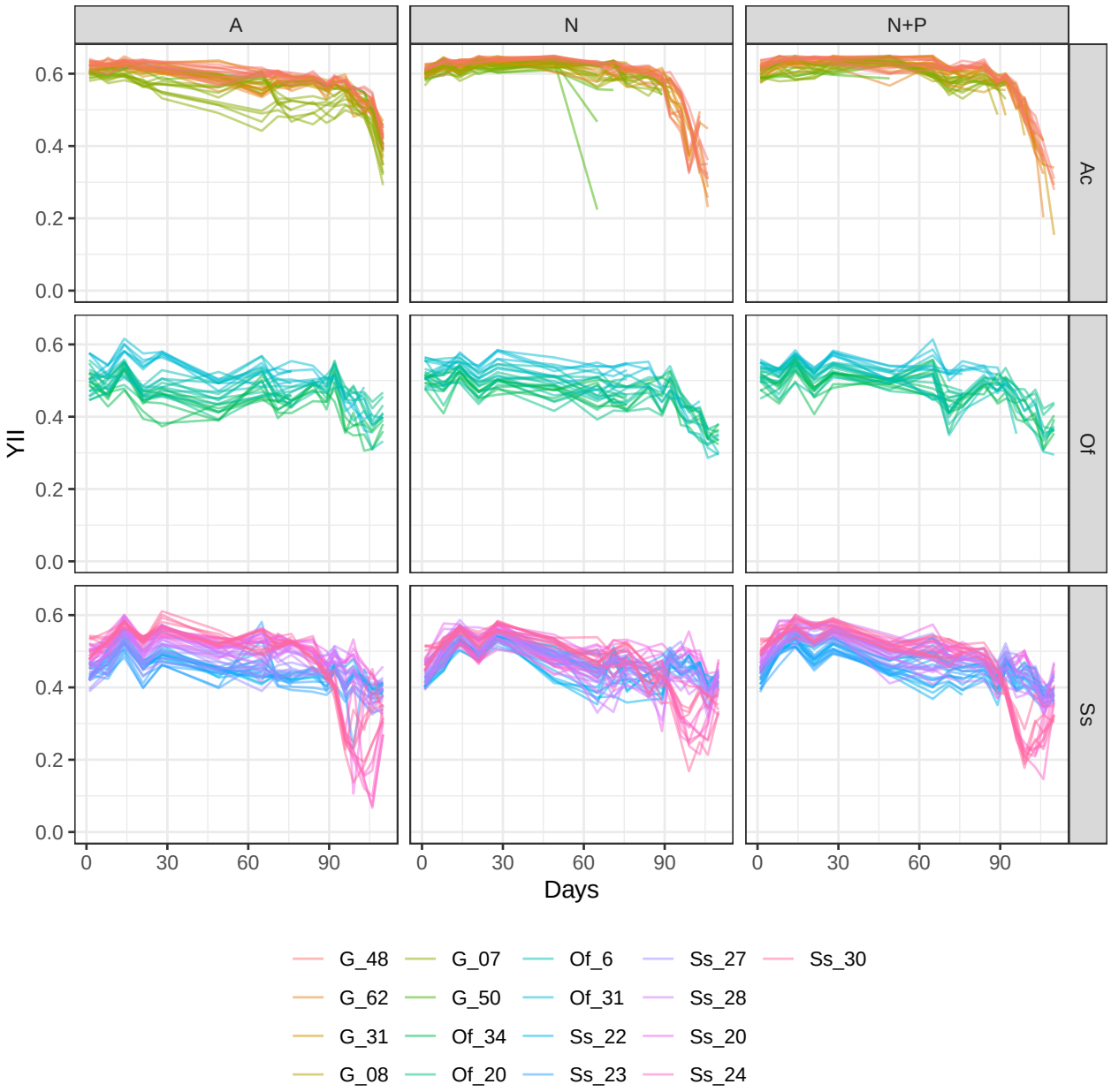
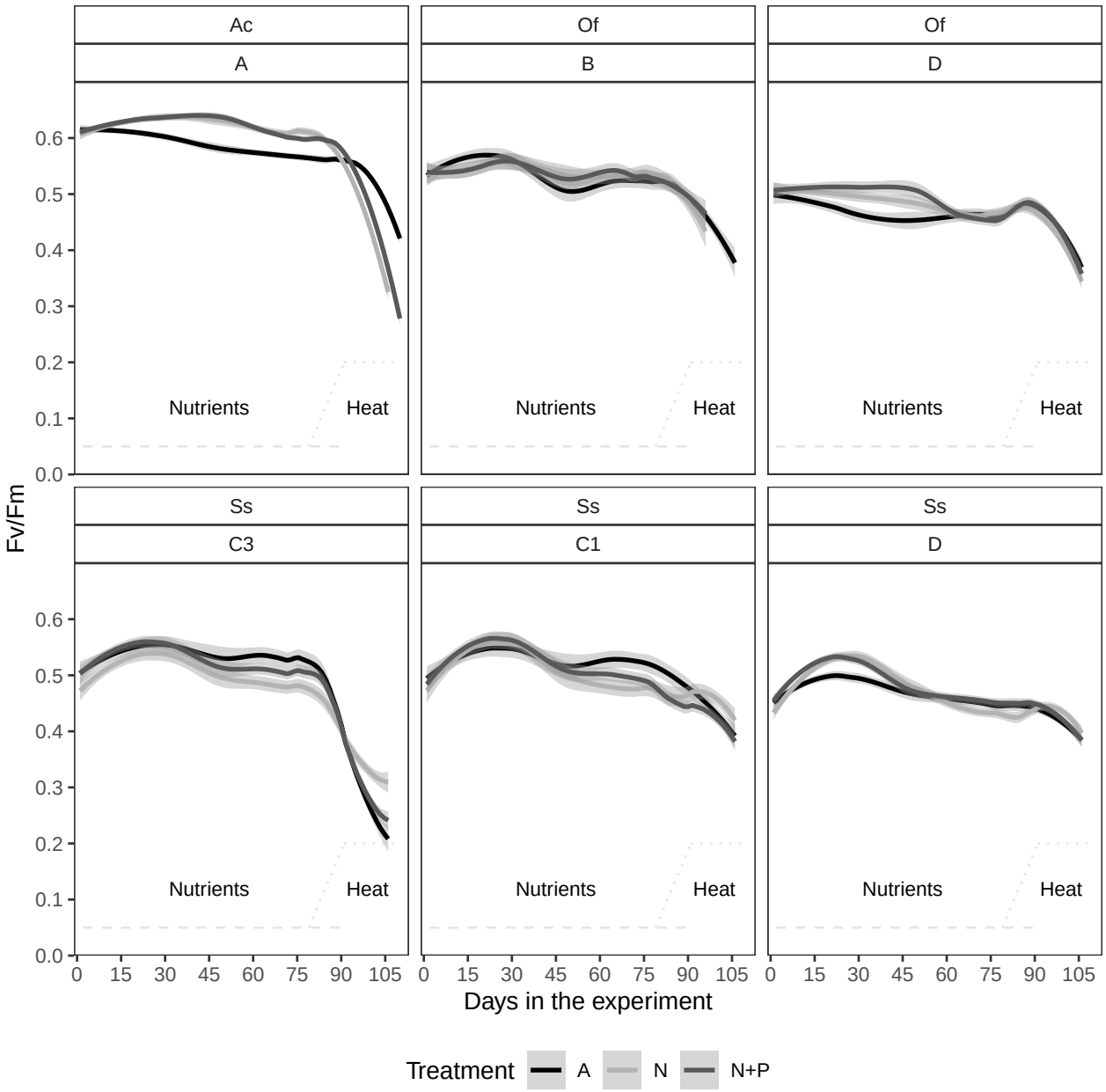


Figure 3: Treatment differences by species and dominant symbiont

```
DropPlot<-YII.data[which(YII.data$Spp !="Ac" &
                         YII.data$DaysF==110),]

YII.datab<-YII.data[!(YII.data$Sample) %in% (DropPlot$Sample),]

YII_Treat<- ggplot(YII.datab, aes (Days, YII, colour=Treatment)) +
        #stat_summary(fun.data = "mean_cl_boot",geom = "errorbar",
        #             width = 0.2, position = position_dodge(1) ) +
        ggthe_bw+ Fill.colour +
        # stat_summary(fun.y=mean, geom="point")  +
```

```
        theme(legend.position="bottom",
              strip.background = element_rect(fill="white"))+
        scale_y_continuous(limits = c(0, 0.7),
                           breaks = seq(0, 0.6, 0.1),
                           expand = c(0, 0),
                           name=("Fv/Fm")) +
        scale_x_continuous(name="Days in the experiment",
                           limits = c(-1,113),
                           breaks = seq(0, 113, 15),
                           expand = c(0, 0))+
        annotate("segment", x = 2, xend = 91, y = 0.05, yend = 0.05,
                 colour = "gray90", linetype=2)+
        annotate("segment", x = 79, xend = 91, y = 0.05, yend = 0.20,
                 colour = "gray90", linetype=3)+
        annotate("segment", x = 91, xend = 110, y = 0.20, yend = 0.20,
                 colour = "gray90", linetype=3)+
        annotate("text", x = 45, y = 0.12, label = "Nutrients", size=3)+
        annotate("text", x = 99, y = 0.12, label = "Heat", size=3)
#YII_Treat + facet_grid (~Spp) + geom_smooth(span=0.5)

All_SppFif<-YII_Treat + facet_wrap (Spp~Community) + geom_smooth(span=0.5)
All_SppFif
```

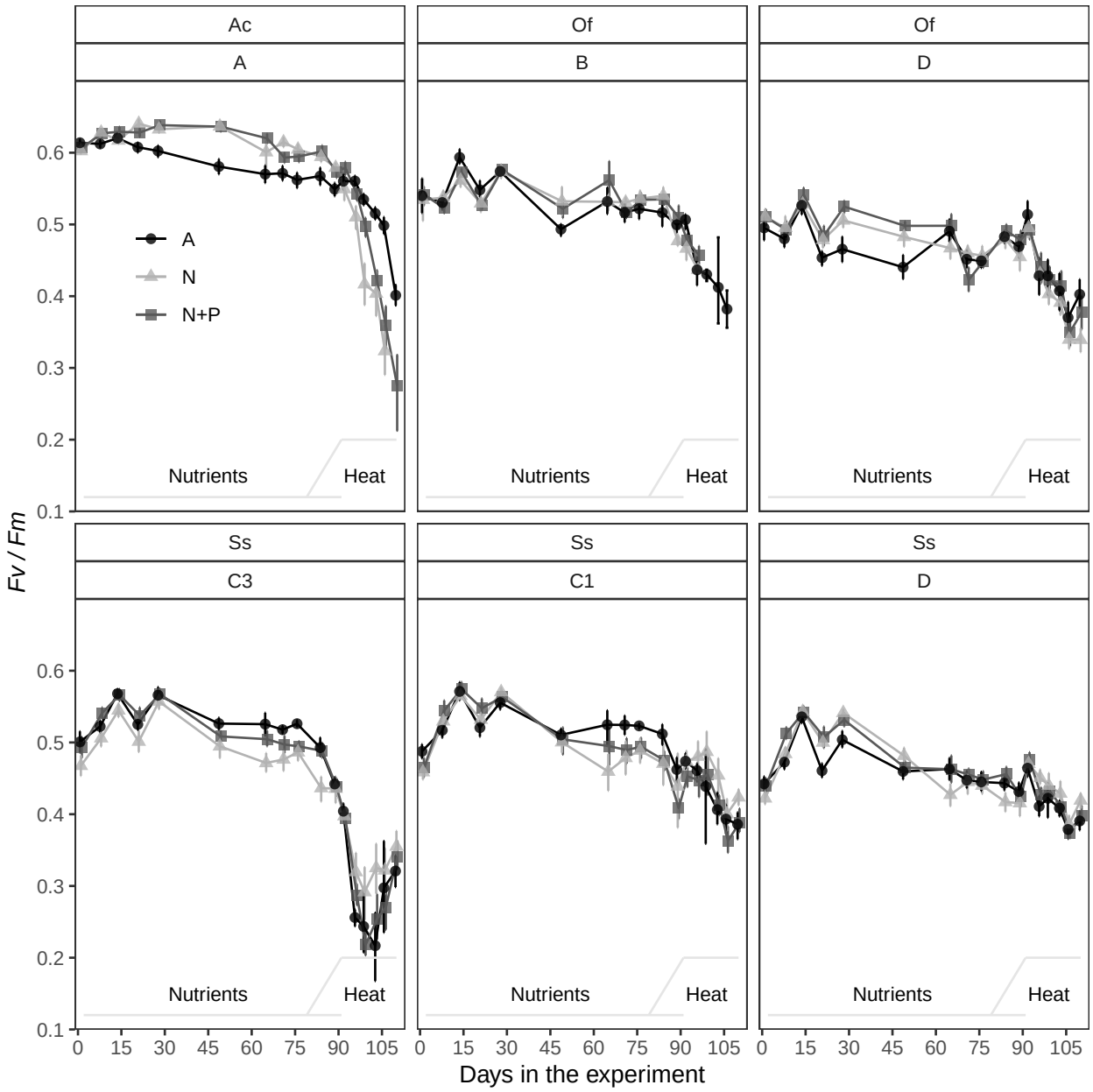



```
#ggsave(file="Outputs/All_spp_YII_Treatb.svg", plot=All_SppFif, width=7, height=6)
```

Figure 3b (No smooth)

```
YII_Treat_BW<- ggplot(data=YII.data, aes (Days, YII, colour=factor(Treatment), shape=factor(Treatment))
        ggthe_bw + Fill.colour+
        stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                     position = position_dodge(1) )+
        stat_summary(fun.y=mean, geom="line", position = position_dodge(1),
                     linetype=1, alpha=1) +
         stat_summary(fun.y=mean, geom="point", size = 2,
                    position=position_dodge(width=1), alpha=0.8)  +
        theme(legend.position=c(0.1, 0.8),
```

```
      legend.title = element_blank(),
      strip.background =element_rect(fill=NA)) + # geom_smooth()+

  scale_y_continuous(limits = c(0.1, 0.7),
                         breaks = seq(0.1, 0.6, 0.1),
                         expand = c(0, 0),
                         name=expression(~italic("Fv / Fm"))) +
      scale_x_continuous(name="Days in the experiment",
                         limits = c(-1,113),
                         breaks = seq(0, 113, 15),
                         expand = c(0, 0))+
      annotate("segment", x = 2, xend = 91, y = 0.12, yend = 0.12,
                colour = "gray90", linetype=1)+
      annotate("segment", x = 79, xend = 91, y = 0.12, yend = 0.20,
                colour = "gray90", linetype=1)+
      annotate("segment", x = 91, xend = 110, y = 0.20, yend = 0.20,
                colour = "gray90", linetype=1)


Figure3b<-YII_Treat_BW + #facet_grid (Spp~.)+
      annotate("text", x = 45, y = 0.15, label = "Nutrients", size=3)+
      annotate("text", x = 99, y = 0.15, label = "Heat", size=3)+
      facet_wrap(Spp~Community)
Figure3b
```

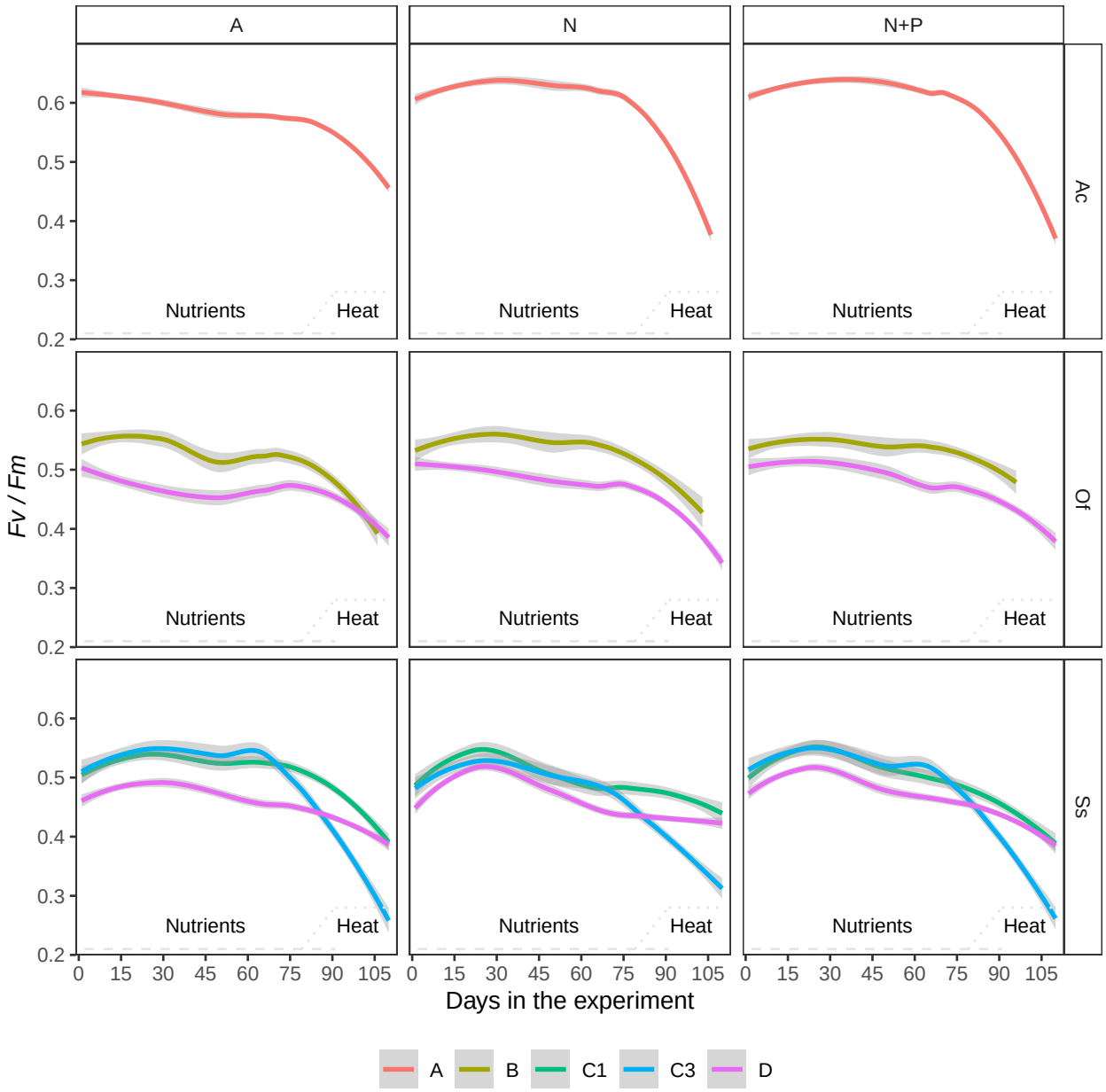



```
#ggsave(file="Outputs/Fig_3b_Acer_YII_Treat.svg", plot=Figure3, width=3.5, height=3)
```

Figure 3c (Symbiont based)

```
YII_Treat_Sym_Spp<- ggplot(data=subset(YII.data), aes (Days, YII, colour=factor(InitialCommunity))) +
        ggthe_bw + geom_smooth()+
  theme(legend.position="bottom",
            legend.title = element_blank(),
            strip.background = element_rect(fill="white"))+
  scale_y_continuous(limits = c(0.2, 0.7),
                         breaks = seq(0.1, 0.65, 0.1),
                         expand = c(0, 0),
                         name=expression(~italic("Fv / Fm"))) +
```

```
  scale_x_continuous(name="Days in the experiment",
                           limits = c(-1,113),
                           breaks = seq(0, 113, 15),
                           expand = c(0, 0))+
  annotate("segment", x = 2, xend = 91, y = 0.21, yend = 0.21,
                  colour = "gray90", linetype=2)+
  annotate("segment", x = 79, xend = 91, y = 0.21, yend = 0.28,
                  colour = "gray90", linetype=3)+
  annotate("segment", x = 91, xend = 110, y = 0.28, yend = 0.28,
                  colour = "gray90", linetype=3)


Figure3c<-YII_Treat_Sym_Spp + facet_grid (Spp~Treatment)+
        annotate("text", x = 45, y = 0.25, label = "Nutrients", size=3)+
        annotate("text", x = 99, y = 0.25, label = "Heat", size=3)
Figure3c
```



YII GLMs

All spp pooled (does not consider domminant symbiont)

```
# All spp together
      LME1<-lmer(YII ~ Treatment * DaysF * Spp + (1|Genotype),
                 REML=TRUE, data=YII.data, na.action=na.omit)
       lmerTest::step (LME1)
```

```
## Backward reduced random-effect table:
##
##                Eliminated npar logLik    AIC    LRT Df Pr(>Chisq)
```

```
## <none>                     154 8708.5 -17109
## (1 | Genotype)          0  153 8299.7 -16293 817.54  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                     Eliminated Sum Sq  Mean Sq NumDF  DenDF F value
## Treatment:DaysF:Spp          0 1.2893 0.020466    63 4851.1   14.11
##                         Pr(>F)
## Treatment:DaysF:Spp < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment * DaysF * Spp + (1 | Genotype)
```

```
drop1(LME1, test = "Chisq")
```

```
## Single term deletions using Satterthwaite's method:
##
## Model:
## YII ~ Treatment * DaysF * Spp + (1 | Genotype)
##                     Sum Sq  Mean Sq NumDF  DenDF F value    Pr(>F)
## Treatment:DaysF:Spp 1.2893 0.020466    63 4851.1   14.11 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

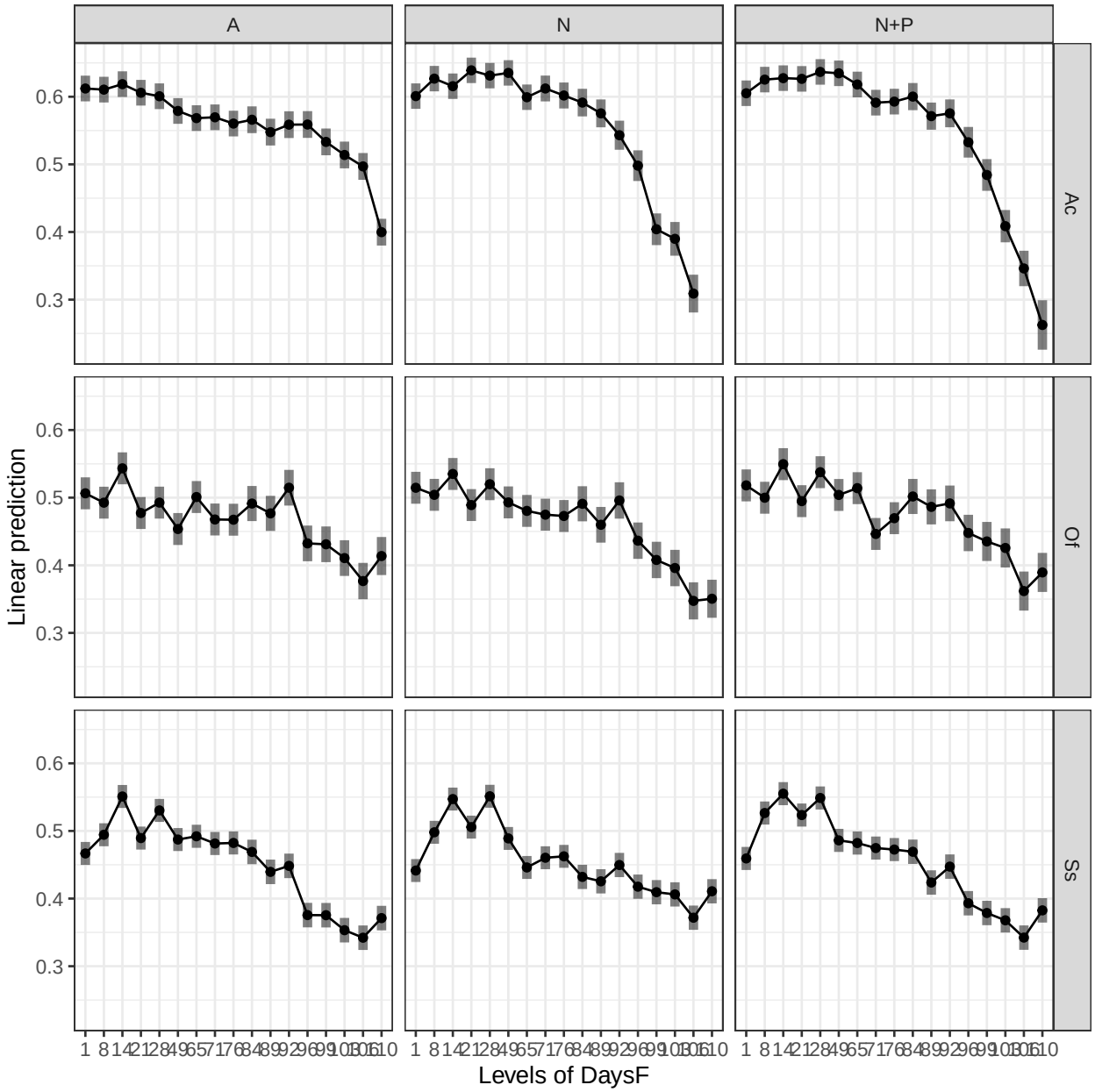
```
#summary(LME1)
anova(LME1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                      Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Treatment            0.0390 0.01948     2 4851.6  13.429 1.527e-06 ***
## DaysF               11.3115 0.70697    16 4851.3 487.419 < 2.2e-16 ***
## Spp                  0.1398 0.06991     2   14.1  48.202 4.907e-07 ***
## Treatment:DaysF      0.5202 0.01626    32 4851.1  11.209 < 2.2e-16 ***
## Treatment:Spp        0.0884 0.02210     4 4851.6  15.234 2.203e-12 ***
## DaysF:Spp            1.5705 0.04908    32 4851.3  33.837 < 2.2e-16 ***
## Treatment:DaysF:Spp  1.2894 0.02047    63 4851.1  14.110 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ranova(LME1)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + DaysF + Spp + (1 | Genotype) + Treatment:DaysF +
##     Treatment:Spp + DaysF:Spp + Treatment:DaysF:Spp
##                 npar logLik    AIC    LRT Df Pr(>Chisq)
## <none>           154 8708.5 -17109
## (1 | Genotype)   153 8299.7 -16293 817.54  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# EMMs
All.YII.emm<-emmeans(LME1, ~Treatment * DaysF* Spp)
emmip(LME1, ~DaysF|Treatment|Spp, CIs = TRUE) + theme_bw() + facet_grid(Spp~Treatment)
```




```
# Spp responded differently, do separate analysis for each one
```

A.cer model

Nutrient treatment

Subset Acervicornis data

```
YII.Acer<-subset(YII.data, Spp=="Ac")
YII.Acer$Nutrients<-"Nutrients"
```

```
YII.Acer$Nutrients[YII.Acer$Treatment=="A"]<-"Ambient"
```

Find best model

```
# 1. Find the best model
YII.Acer$DaysF<-as.factor(YII.Acer$Days)

LME_Acer<-lmerTest::lmer(YII ~ Treatment * DaysF +
                           (1|Genotype) + (1|Replicate) +  (1|Fragment),
                            data=YII.Acer, na.action=na.omit)
      #summary(LME_Acer)

      Step.LME_Acer<-step (LME_Acer) # Replicate is not significant
      anova(LME_Acer)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                 Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## Treatment       0.0201 0.01006     2  120.52  19.557 4.407e-08 ***
## DaysF           5.2135 0.32584    16 1460.52 633.674 < 2.2e-16 ***
## Treatment:DaysF 1.1053 0.03566    31 1460.62  69.340 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
      ranova(LME_Acer)# Replicate is not significant
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + DaysF + (1 | Genotype) + (1 | Replicate) +
##     (1 | Fragment) + Treatment:DaysF
##                 npar logLik     AIC     LRT Df Pr(>Chisq)
## <none>            54 3541.1 -6974.2
## (1 | Genotype)    53 3502.6 -6899.2  77.046  1     <2e-16 ***
## (1 | Replicate)   53 3540.4 -6974.8   1.395  1     0.2375
## (1 | Fragment)    53 3465.9 -6825.8 150.393  1     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
      # Drop (1|Replicate)
      final_fm <- get_model(Step.LME_Acer)
      #summary(final_fm)

  LME_Acer1<-lmerTest::lmer(YII ~ Treatment * DaysF +
                           (1|Genotype/Fragment),
                            data=subset(YII.data, Spp=="Ac"), na.action=na.omit)

  ranova(LME_Acer1)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + DaysF + (1 | Fragment:Genotype) + (1 | Genotype) +
##     Treatment:DaysF
##                         npar logLik     AIC     LRT Df Pr(>Chisq)
## <none>                    53 3540.4 -6974.8
## (1 | Fragment:Genotype)   52 3461.1 -6818.2 158.628  1  < 2.2e-16 ***
```

```
## (1 | Genotype)            52 3502.5 -6901.0  75.851  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
  LME_Acer2<-lmerTest::lmer(YII ~ Treatment * DaysF +
                              (1|Genotype) +  (1|Fragment),
                               data=subset(YII.data, Spp=="Ac"), na.action=na.omit)
  ranova(LME_Acer2)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + DaysF + (1 | Genotype) + (1 | Fragment) + Treatment:DaysF
##                 npar logLik     AIC     LRT Df Pr(>Chisq)
## <none>            53 3540.4 -6974.8
## (1 | Genotype)    52 3502.5 -6901.0  75.851  1  < 2.2e-16 ***
## (1 | Fragment)    52 3461.1 -6818.2 158.628  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
  anova(LME_Acer1, LME_Acer2) # LME_Acer1 and LME_Acer2 are the same
```

```
## Data: subset(YII.data, Spp == "Ac")
## Models:
## LME_Acer1: YII ~ Treatment * DaysF + (1 | Genotype/Fragment)
## LME_Acer2: YII ~ Treatment * DaysF + (1 | Genotype) + (1 | Fragment)
##           Df     AIC     BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## LME_Acer1 53 -7424.6 -7138.9 3765.3  -7530.6
## LME_Acer2 53 -7424.6 -7138.9 3765.3  -7530.6     0      0          1
```

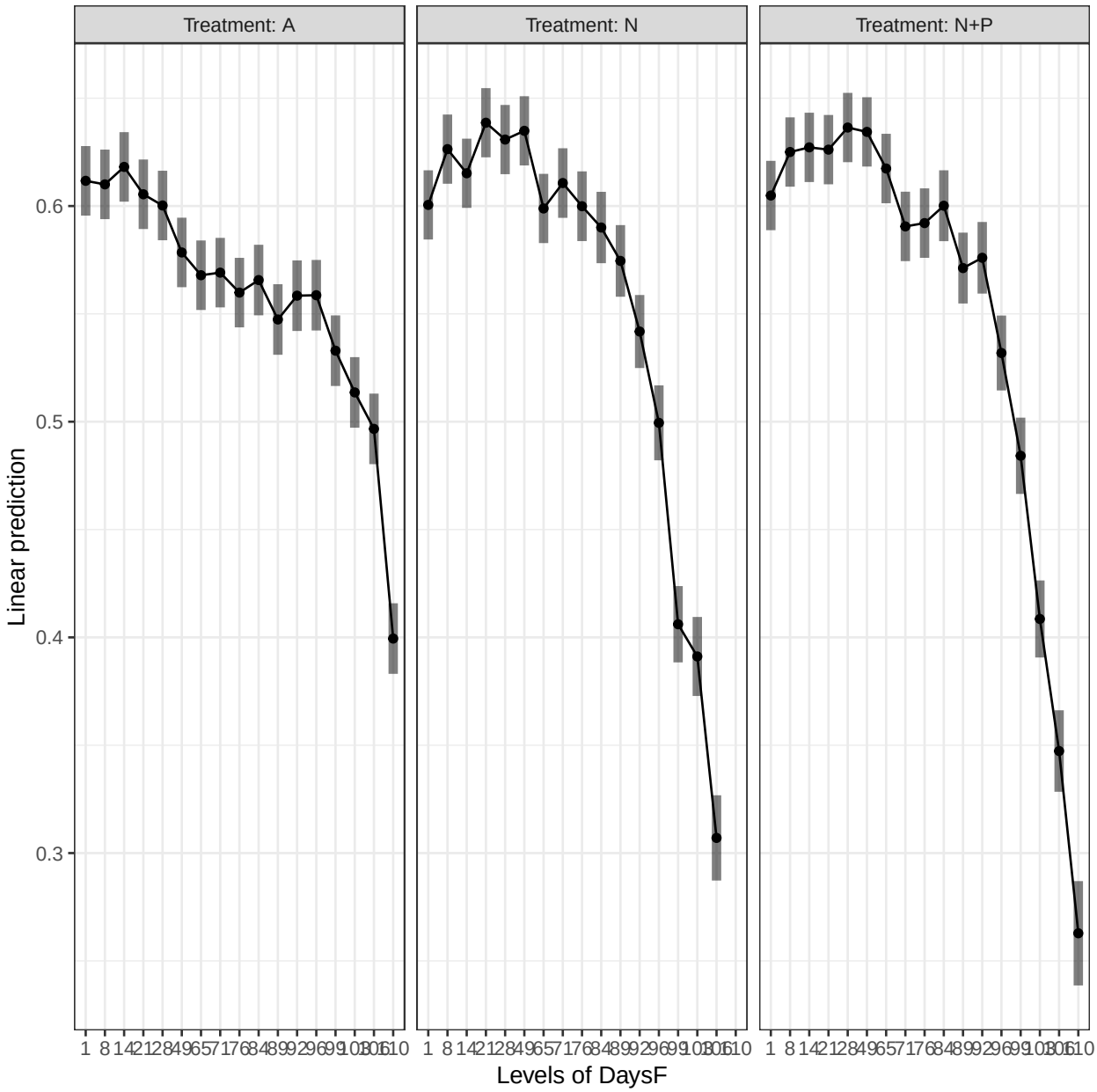
```
#2. Extract EMMs
      Acer.YII.emm<-emmeans(LME_Acer1, ~Treatment | DaysF)
      contrast(Acer.YII.emm, "tukey")
```

```
## DaysF = 1:
##  contrast estimate      SE   df t.ratio p.value
##  A - N     0.01123 0.00566 1023  1.985  0.1164
##  A - N+P   0.00684 0.00569 1022  1.202  0.4524
##  N - N+P  -0.00439 0.00562 1023 -0.781  0.7147
##
## DaysF = 8:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.01626 0.00566 1023 -2.874  0.0115
##  A - N+P  -0.01497 0.00569 1022 -2.630  0.0235
##  N - N+P   0.00129 0.00562 1023  0.229  0.9715
##
## DaysF = 14:
##  contrast estimate      SE   df t.ratio p.value
##  A - N     0.00304 0.00566 1023  0.537  0.8533
##  A - N+P  -0.00902 0.00569 1022 -1.584  0.2528
##  N - N+P  -0.01206 0.00562 1023 -2.145  0.0815
##
## DaysF = 21:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.03309 0.00566 1023 -5.849  <.0001
##  A - N+P  -0.02066 0.00569 1022 -3.629  0.0009
```

```
##  N - N+P   0.01243 0.00562 1023  2.211  0.0698
##
## DaysF = 28:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.03049 0.00566 1023 -5.389  <.0001
##  A - N+P  -0.03612 0.00569 1022 -6.344  <.0001
##  N - N+P  -0.00562 0.00562 1023 -1.000  0.5768
##
## DaysF = 49:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.05631 0.00566 1023 -9.952  <.0001
##  A - N+P  -0.05586 0.00569 1022 -9.811  <.0001
##  N - N+P   0.00045 0.00562 1023  0.080  0.9965
##
## DaysF = 65:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.03088 0.00566 1023 -5.457  <.0001
##  A - N+P  -0.04943 0.00573 1031 -8.633  <.0001
##  N - N+P  -0.01855 0.00565 1032 -3.281  0.0031
##
## DaysF = 71:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.04150 0.00575 1050 -7.212  <.0001
##  A - N+P  -0.02138 0.00573 1031 -3.734  0.0006
##  N - N+P   0.02012 0.00575 1059  3.500  0.0014
##
## DaysF = 76:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.03999 0.00579 1061 -6.909  <.0001
##  A - N+P  -0.03217 0.00573 1031 -5.619  <.0001
##  N - N+P   0.00782 0.00578 1070  1.353  0.3664
##
## DaysF = 84:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.02435 0.00644 1226 -3.784  0.0005
##  A - N+P  -0.03444 0.00634 1194 -5.436  <.0001
##  N - N+P  -0.01009 0.00652 1252 -1.547  0.2692
##
## DaysF = 89:
##  contrast estimate      SE   df t.ratio p.value
##  A - N    -0.02714 0.00649 1238 -4.179  0.0001
##  A - N+P  -0.02383 0.00634 1194 -3.760  0.0005
##  N - N+P   0.00331 0.00658 1263  0.503  0.8698
##
## DaysF = 92:
##  contrast estimate      SE   df t.ratio p.value
##  A - N     0.01667 0.00676 1295  2.466  0.0367
##  A - N+P  -0.01762 0.00649 1230 -2.713  0.0186
##  N - N+P  -0.03429 0.00699 1340 -4.906  <.0001
##
## DaysF = 96:
##  contrast estimate      SE   df t.ratio p.value
##  A - N     0.05921 0.00712 1360  8.311  <.0001
##  A - N+P   0.02681 0.00712 1352  3.764  0.0005
```

```
##  N - N+P  -0.03240 0.00790 1452 -4.103  0.0001
##
## DaysF = 99:
##  contrast estimate      SE   df t.ratio p.value
##  A - N     0.12685 0.00736 1393 17.243  <.0001
##  A - N+P   0.04875 0.00736 1388  6.627  <.0001
##  N - N+P  -0.07810 0.00831 1485 -9.397  <.0001
##
## DaysF = 103:
##  contrast estimate      SE   df t.ratio p.value
##  A - N     0.12243 0.00781 1447 15.678  <.0001
##  A - N+P   0.10504 0.00749 1406 14.022  <.0001
##  N - N+P  -0.01739 0.00883 1516 -1.970  0.1200
##
## DaysF = 106:
##  contrast estimate      SE   df t.ratio p.value
##  A - N     0.18950 0.00877 1513 21.601  <.0001
##  A - N+P   0.14946 0.00821 1478 18.205  <.0001
##  N - N+P  -0.04004 0.01026 1555 -3.904  0.0003
##
## DaysF = 110:
##  contrast estimate      SE   df t.ratio p.value
##  A - N      nonEst      NA   NA     NA      NA
##  A - N+P   0.13704 0.01142 1565 12.001  <.0001
##  N - N+P    nonEst      NA   NA     NA      NA
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

```r
Acer.YII.emm<-emmeans(LME_Acer1, ~Treatment * DaysF)

# Effect plot options
emmip(LME_Acer, ~DaysF|Treatment, CIs = TRUE) + theme_bw() # interaction plot of predictions
```




```
Acer.YII_groups<-cld(Acer.YII.emm, by=NULL) # compact-letter display
Acer.YII_groups<-Acer.YII_groups[order(Acer.YII_groups$Treatment, Acer.YII_groups$Day),]
Acer.YII_groups
```

```
##    Treatment DaysF    emmean          SE        df  lower.CL  upper.CL
## 1          A     1 0.6117568 0.007054864 10.283592 0.5960961 0.6274174
## 4          A     8 0.6101158 0.007054864 10.283592 0.5944551 0.6257764
## 7          A    14 0.6182183 0.007054864 10.283592 0.6025577 0.6338790
## 10         A    21 0.6055260 0.007054864 10.283592 0.5898654 0.6211867
## 13         A    28 0.6003209 0.007054864 10.283592 0.5846602 0.6159815
## 16         A    49 0.5785516 0.007054864 10.283592 0.5628910 0.5942123
## 19         A    65 0.5679875 0.007054864 10.283592 0.5523269 0.5836482
## 22         A    71 0.5691927 0.007054864 10.283592 0.5535320 0.5848533
## 25         A    76 0.5599363 0.007054864 10.283592 0.5442756 0.5755969
## 28         A    84 0.5657452 0.007269359 11.591023 0.5498444 0.5816459
```

```
## 31         A    89 0.5474639 0.007269359 11.591023 0.5315631 0.5633647
## 34         A    92 0.5584952 0.007269359 11.591023 0.5425944 0.5743959
## 37         A    96 0.5587139 0.007269359 11.591023 0.5428131 0.5746147
## 40         A    99 0.5329952 0.007269359 11.591023 0.5170944 0.5488959
## 43         A   103 0.5136514 0.007269359 11.591023 0.4977506 0.5295522
## 46         A   106 0.4967452 0.007269359 11.591023 0.4808444 0.5126459
## 49         A   110 0.3995264 0.007269359 11.591023 0.3836256 0.4154272
## 2          N     1 0.6005232 0.006988991  9.913563 0.5849323 0.6161140
## 5          N     8 0.6263768 0.006988991  9.913563 0.6107860 0.6419677
## 8          N    14 0.6151817 0.006988991  9.913563 0.5995908 0.6307726
## 11         N    21 0.6386207 0.006988991  9.913563 0.6230299 0.6542116
## 14         N    28 0.6308159 0.006988991  9.913563 0.6152250 0.6464067
## 17         N    49 0.6348646 0.006988991  9.913563 0.6192738 0.6504555
## 20         N    65 0.5988646 0.006988991  9.913563 0.5832738 0.6144555
## 23         N    71 0.6106897 0.007068224 10.368240 0.5950162 0.6263632
## 26         N    76 0.5999310 0.007097808 10.541474 0.5842255 0.6156365
## 29         N    84 0.5900986 0.007429981 12.649912 0.5740018 0.6061953
## 32         N    89 0.5745990 0.007478592 12.983474 0.5584404 0.5907576
## 35         N    92 0.5418235 0.007719892 14.724051 0.5253420 0.5583049
## 38         N    96 0.4995076 0.008039197 17.302248 0.4825690 0.5164463
## 41         N    99 0.4061424 0.008248461 19.163384 0.3888881 0.4233967
## 44         N   103 0.3912231 0.008656690 23.214815 0.3733245 0.4091217
## 47         N   106 0.3072467 0.009535789 34.038508 0.2878685 0.3266250
## 50         N   110        NA          NA        NA        NA        NA
## 3        N+P     1 0.6049147 0.007014286 10.059729 0.5892985 0.6205309
## 6        N+P     8 0.6250897 0.007014286 10.059729 0.6094735 0.6407059
## 9        N+P    14 0.6272397 0.007014286 10.059729 0.6116235 0.6428559
## 12       N+P    21 0.6261897 0.007014286 10.059729 0.6105735 0.6418059
## 15       N+P    28 0.6364397 0.007014286 10.059729 0.6208235 0.6520559
## 18       N+P    49 0.6344147 0.007014286 10.059729 0.6187985 0.6500309
## 21       N+P    65 0.6174145 0.007040973 10.212840 0.6017704 0.6330586
## 24       N+P    71 0.5905683 0.007040973 10.212840 0.5749243 0.6062124
## 27       N+P    76 0.5921068 0.007040973 10.212840 0.5764627 0.6077509
## 30       N+P    84 0.6001901 0.007335098 12.026136 0.5842122 0.6161681
## 33       N+P    89 0.5712901 0.007335098 12.026136 0.5553122 0.5872681
## 36       N+P    92 0.5761114 0.007474032 12.958152 0.5599595 0.5922634
## 39       N+P    96 0.5319028 0.008031533 17.250448 0.5149765 0.5488292
## 42       N+P    99 0.4842434 0.008243522 19.126555 0.4669972 0.5014895
## 45       N+P   103 0.4086133 0.008365132 20.271982 0.3911789 0.4260476
## 48       N+P   106 0.3472847 0.009015404 27.281386 0.3287956 0.3657739
## 51       N+P   110 0.2624899 0.012009589 83.700946 0.2386063 0.2863736
##                    .group
## 1                  GHIJKL
## 4                  GHIJK
## 7                   HIJKLMN
## 10                 GHIJ
## 13                FGH
## 16           0ABCDE
## 19          890AB
## 22           90ABC
## 25          890
## 28          890A
## 31        6789
## 34         7890
```

```
## 37        7890
## 40      56
## 43     45
## 46     4
## 49    3
## 2                EFGH
## 5                    IJKLMN
## 8                   HIJKLM
## 11                        N
## 14                     KLMN
## 17                       MN
## 20               EFGH
## 23                 GHIJK
## 26               EFGH
## 29            ABCDEFG
## 32           0ABCD
## 35       678
## 38     4
## 41    3
## 44    3
## 47  12
## 50
## 3                  GHI
## 6                    IJKLMN
## 9                    JKLMN
## 12                   JKLMN
## 15                      MN
## 18                     LMN
## 21                  HIJKLMN
## 24             BCDEFG
## 27              CDEFG
## 30               DEFGH
## 33          90ABC
## 36           0ABCDEF
## 39      567
## 42     4
## 45    3
## 48   2
## 51  1
```

```
      #write.csv(Acer.YII_groups, "Outputs/Multicomp_AcerYII.csv", row.names = F)
```

Ofav and Ssid

Prepare data sets:

- Time as discrete

```
#Time as a factor, not as int
      str(YII.data)
```

```
## 'data.frame':    5017 obs. of  17 variables:
##  $ Sample          : Factor w/ 6018 levels "Ac_101_T0","Ac_101_T1",..: 13 14 15 16 17 3 4 5 6 7 ...
##  $ Date            : Date, format: "2017-11-16" "2017-11-23" ...
##  $ Spp             : Factor w/ 3 levels "Ac","Of","Ss": 1 1 1 1 1 1 1 1 1 1 ...
```

```
##  $ Fragment        : Factor w/ 354 levels "Ac_101","Ac_102",..: 1 1 1 1 1 1 1 1 1 ...
##  $ Treatment       : Factor w/ 3 levels "A","N","N+P": 3 3 3 3 3 3 3 3 3 ...
##  $ Replicate       : Factor w/ 2 levels "R1","R2": 1 1 1 1 1 1 1 1 1 ...
##  $ YII             : num  0.589 0.595 0.606 0.605 0.606 0.625 0.593 0.567 0.593 0.573 ...
##  $ Genotype        : Factor w/ 17 levels "G_48","G_62",..: 6 6 6 6 6 6 6 6 6 6 ...
##  $ Days            : num  1 8 14 21 28 49 65 71 76 84 ...
##  $ Time_Point      : Factor w/ 25 levels "T0","T1","T10",..: 21 22 23 24 25 3 4 5 6 7 ...
##  $ Phase           : Factor w/ 5 levels "Baseline","Heat",..: 1 3 3 3 3 3 3 3 3 4 ...
##  $ TotalSH         : num  0.1262 NA NA NA 0.0401 ...
##  $ logSH           : num  -0.899 NA NA NA -1.397 ...
##  $ D.Prp           : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Community       : Factor w/ 5 levels "A","B","C3","C1",..: 1 1 1 1 1 1 1 1 1 ...
##  $ InitialCommunity: Factor w/ 5 levels "A","B","C1","C3",..: 1 1 1 1 1 1 1 1 1 ...
##  $ DaysF           : Factor w/ 26 levels "-112","-77","-36",..: 6 7 8 9 10 11 12 13 14 15 ...
```

```
YII.data$DaysF<-as.factor(YII.data$Days)
```

- Separate coral species
- Separate phases:
  - BaseLine
  - C (nutrients only)
  - H (Heat challenge)

Ofav:

```
YII.Ofav<-subset(YII.data, Spp=="Of")

YII.Ofav.0<-subset(YII.Ofav, Days<2)
YII.Ofav.C<-subset(YII.Ofav, Days<77)
YII.Ofav.C.1<-subset(YII.Ofav.C, Days>2)
YII.Ofav.H<-subset(YII.Ofav, Days>75)
```

Ssid

```
YII.Ssid<-subset(YII.data, Spp=="Ss")

YII.Ssid.0<-subset(YII.Ssid, Days<2)
YII.Ssid.C<-subset(YII.Ssid, Days<77)
YII.Ssid.C.1<-subset(YII.Ssid.C, Days>2)
YII.Ssid.H<-subset(YII.Ssid, Days>75)
```

Baseline: effect of different Symbiodiniaceae taxa before treatments

Ofav (day 0)

```
LME_Ofav0<-lmer(YII ~ Treatment + InitialCommunity + (1|Replicate),
                    data=YII.Ofav.0)
     #step (LME_Ofav0)
     anova(LME_Ofav0) # Treatment not significant
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                     Sum Sq   Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment        0.0020761 0.0010381     2    68  1.2626    0.2895
## InitialCommunity 0.0145249 0.0145249     1    68 17.6667 7.858e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
    ranova(LME_Ofav0) #  Replicate is not significant
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + InitialCommunity + (1 | Replicate)
##                 npar logLik     AIC        LRT Df Pr(>Chisq)
## <none>             6 139.01 -266.02
## (1 | Replicate)    5 139.01 -268.02 5.6843e-14  1          1
```

```
LME_Ofav0<-lm(YII ~ InitialCommunity, data=YII.Ofav.0)
    step (LME_Ofav0)
```

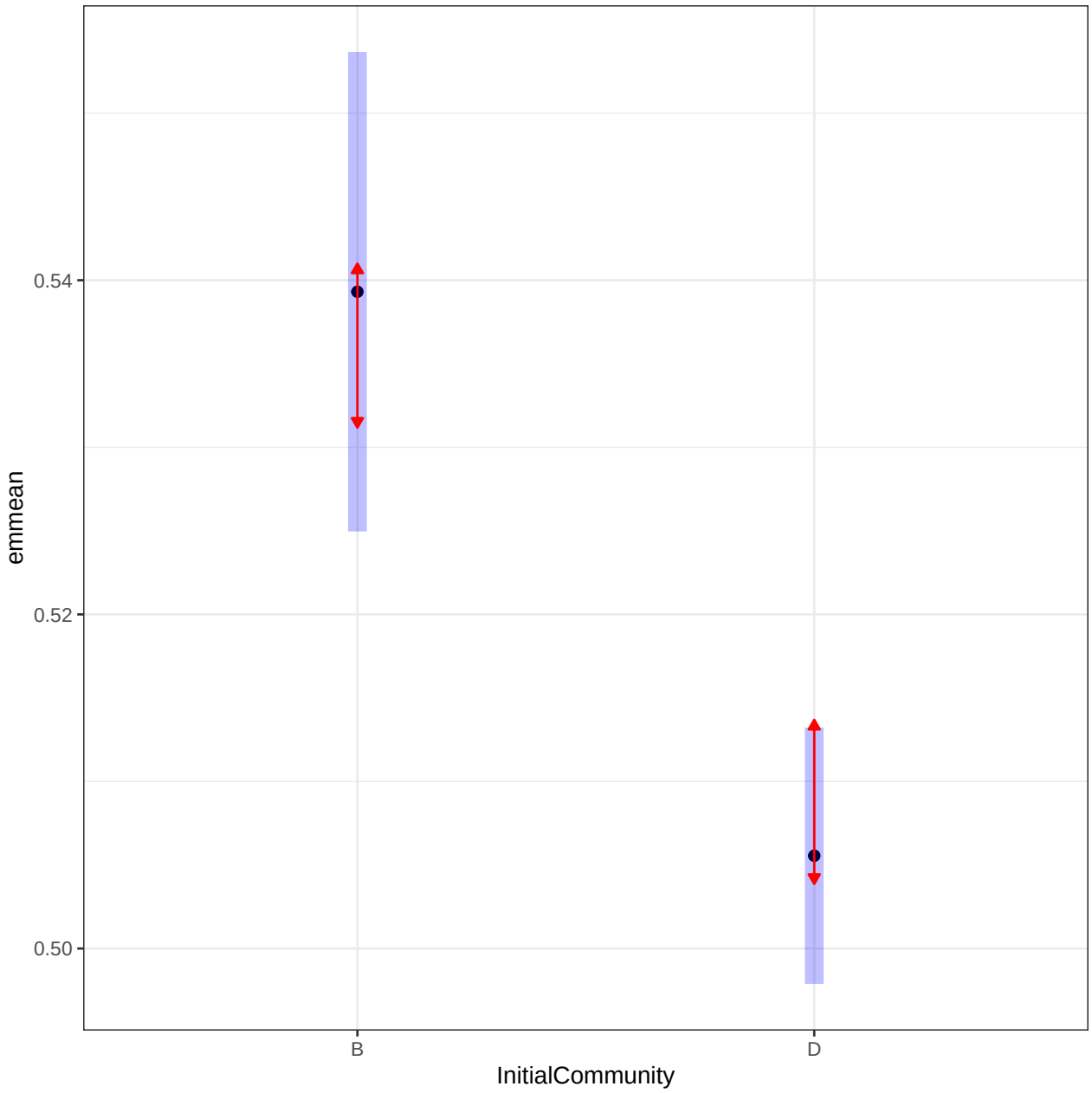
```
## Start:  AIC=-508.95
## YII ~ InitialCommunity
##
##                    Df Sum of Sq      RSS     AIC
## <none>                           0.057983 -508.95
## - InitialCommunity  1  0.014183 0.072166 -495.19
```

```
##
## Call:
## lm(formula = YII ~ InitialCommunity, data = YII.Ofav.0)
##
## Coefficients:
##       (Intercept)  InitialCommunityD
##           0.53931           -0.03376
```

```
    anova(LME_Ofav0)
```

```
## Analysis of Variance Table
##
## Response: YII
##                  Df   Sum Sq   Mean Sq F value   Pr(>F)
## InitialCommunity  1 0.014183 0.0141825  17.122 9.62e-05 ***
## Residuals        70 0.057983 0.0008283
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# EMMs
   Ofav.YII.emm0<-emmeans(LME_Ofav0, ~ InitialCommunity)
     # contrast(Ssid.YII.emm, "tukey")

     # Tukey comparison (do not trust CI to compare EMMs)
     plot(emmeans(LME_Ofav0, ~InitialCommunity), comparisons = TRUE) +
       coord_flip(xlim = NULL, ylim = NULL, expand = TRUE) +
       theme_bw()
```




```
      Ofav.YII_groups0<-cld(Ofav.YII.emm0, by=NULL) # compact-letter display
      Ofav.YII_groups0
```

```
##  InitialCommunity emmean      SE df lower.CL upper.CL .group
##  D                 0.506 0.00385 70    0.498    0.513  1
##  B                 0.539 0.00720 70    0.525    0.554   2
##
## Confidence level used: 0.95
## significance level used: alpha = 0.05
```

```
      # write.csv(Ofav.YII_groups0, "Outputs/Multicomp_OfavYII0.csv", row.names = F)
```

Ssid (day 0)

```
LME_Ssid0<-lmer(YII ~ Treatment + InitialCommunity + (1|Replicate),
                    data=YII.Ssid.0)
     step (LME_Ssid0) #  Treatemnt and replicate are significant :/
```

```
## Backward reduced random-effect table:
##
##                 Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                       7 369.23 -724.46
## (1 | Replicate)          0    6 338.52 -665.03 61.431  1  4.586e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                   Eliminated   Sum Sq  Mean Sq NumDF DenDF F value
## Treatment                  0 0.019079 0.009540     2   156  20.809
## InitialCommunity           0 0.087511 0.043756     2   156  95.445
##                      Pr(>F)
## Treatment        9.754e-09 ***
## InitialCommunity < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + InitialCommunity + (1 | Replicate)
```

```
     anova(LME_Ssid0)
```

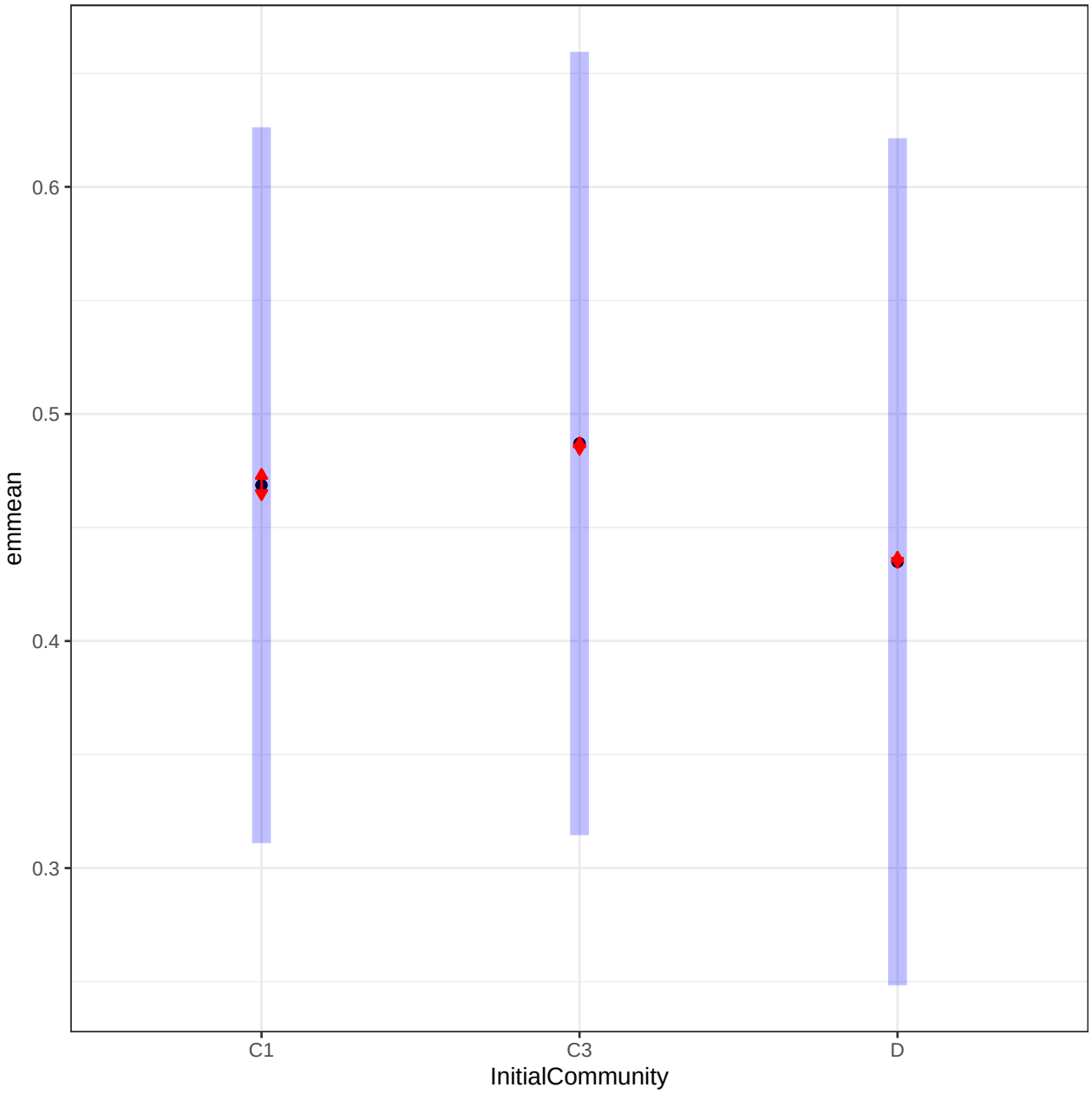
```
## Type III Analysis of Variance Table with Satterthwaite's method
##                    Sum Sq  Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment        0.019079 0.009540     2   156  20.809 9.754e-09 ***
## InitialCommunity 0.087511 0.043756     2   156  95.445 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
     ranova(LME_Ssid0)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + InitialCommunity + (1 | Replicate)
##                  npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>              7 369.23 -724.46
## (1 | Replicate)     6 338.52 -665.03 61.431  1  4.586e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# EMMs
      Ssid.YII.emm0<-emmeans(LME_Ssid0, ~ InitialCommunity)
      # contrast(Ssid.YII.emm, "tukey")

      # Tukey comparison (do not trust CI to compare EMMs)
      plot(emmeans(LME_Ssid0, ~InitialCommunity), comparisons = TRUE) +
```

```
        coord_flip(xlim = NULL, ylim = NULL, expand = TRUE) +
        theme_bw()
```




```
      Ssid.YII_groups0<-cld(Ssid.YII.emm0, by=NULL) # compact-letter display
      Ssid.YII_groups0
```

```
##  InitialCommunity emmean     SE   df lower.CL upper.CL .group
##  D                 0.435 0.0154 1.02    0.248    0.621  1
##  C1                0.469 0.0157 1.11    0.311    0.626   2
##  C3                0.487 0.0156 1.06    0.315    0.659    3
##
## Results are averaged over the levels of: Treatment
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

```
## P value adjustment: tukey method for comparing a family of 3 estimates
## significance level used: alpha = 0.05
```

```
      # write.csv(Ssid.YII_groups0, "Outputs/Multicomp_SsidYII0.csv", row.names = F)
```

C: Effect of nutrient treatments at control temperature

Ofav

- C Days pooled (days 8-76)

```
LME_Ofav1.1<-lmer(YII ~ Treatment * InitialCommunity + (1|Fragment),
                  data=YII.Ofav.C.1)
    step (LME_Ofav1.1) #  Replicate is significant
```

```
## Backward reduced random-effect table:
##
##                Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                      8 1046.0 -2075.9
## (1 | Fragment)          0   7 1036.4 -2058.8 19.116  1   1.23e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                            Eliminated   Sum Sq  Mean Sq NumDF DenDF
## Treatment:InitialCommunity          1 0.002297 0.001148     2    66
## Treatment                           0 0.013198 0.006599     2    68
## InitialCommunity                    0 0.173819 0.173819     1    68
##                             F value    Pr(>F)
## Treatment:InitialCommunity   0.8780  0.420421
## Treatment                    5.0455  0.009055 **
## InitialCommunity           132.8935 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + InitialCommunity + (1 | Fragment)
```

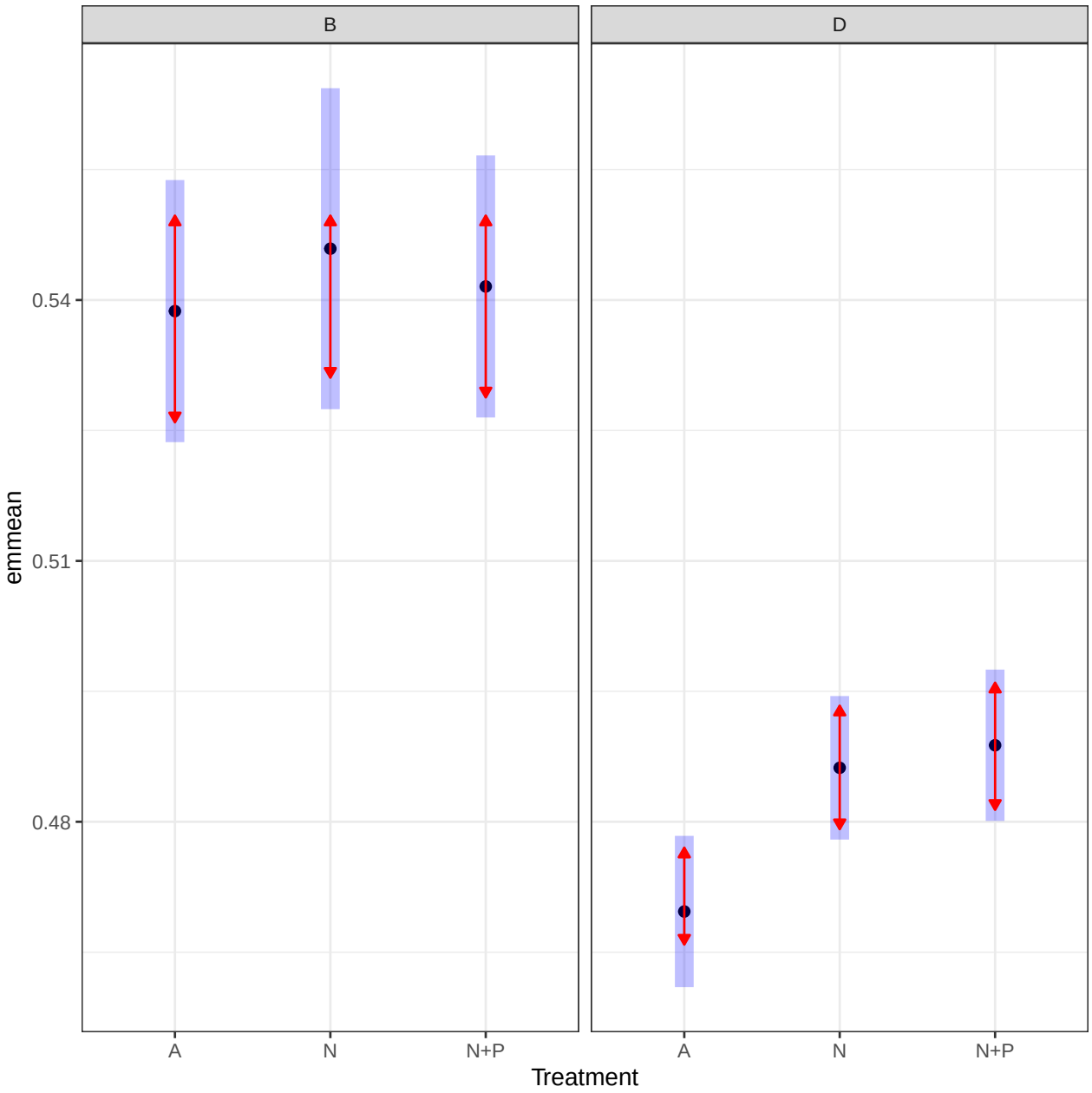
```
    anova(LME_Ofav1.1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                              Sum Sq  Mean Sq NumDF DenDF  F value Pr(>F)
## Treatment                  0.005656 0.002828     2    66   2.1622 0.1232
## InitialCommunity           0.169345 0.169345     1    66 129.4735 <2e-16
## Treatment:InitialCommunity 0.002297 0.001148     2    66   0.8780 0.4204
##
## Treatment
## InitialCommunity           ***
## Treatment:InitialCommunity
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
    ranova(LME_Ofav1.1)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + InitialCommunity + (1 | Fragment) + Treatment:InitialCommunity
##                 npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>             8 1046.0 -2075.9
## (1 | Fragment)     7 1036.4 -2058.8 19.116  1   1.23e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# EMMs
    Ofav.YII.emm1.1<-emmeans(LME_Ofav1.1, ~ InitialCommunity|Treatment)
    # contrast(Ssid.YII.emm, "tukey")

    # Tukey comparison (do not trust CI to compare EMMs)
      plot(emmeans(LME_Ofav1.1, ~Treatment|InitialCommunity), comparisons = TRUE) +
      coord_flip(xlim = NULL, ylim = NULL, expand = TRUE) + facet_grid(~InitialCommunity) +
        theme_bw()
```




```
      Ofav.YII.emm1.1<-cld(Ofav.YII.emm1.1, by=NULL) # compact-letter display
      Ofav.YII.emm1.1
```

```
##  InitialCommunity Treatment emmean      SE df lower.CL upper.CL .group
##  D                A          0.470 0.00436 66    0.461    0.478  1
##  D                N          0.486 0.00413 66    0.478    0.494  12
##  D                N+P        0.489 0.00436 66    0.480    0.497   2
##  B                A          0.539 0.00755 66    0.524    0.554    3
##  B                N+P        0.542 0.00755 66    0.526    0.557    3
##  B                N          0.546 0.00924 66    0.527    0.564    3
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 6 estimates
```

```
## significance level used: alpha = 0.05
```

```
      #write.csv(Ofav.YII.emm1.1, "Outputs/Multicomp_OfavYII1.csv", row.names = F)
```

- Model for "Days" as continous variable (days 1-76)

```
# 1. Ofav- Days
      LME_Ofav<-lmer(YII ~ Treatment * Days * InitialCommunity +
                       (1|Genotype) + (1|Fragment) +(1|Replicate),
                        data=YII.Ofav.C, na.action=na.omit)
      lmerTest::step (LME_Ofav) # Replicate is not significant
```

```
## Backward reduced random-effect table:
##
##                 Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                          16 1243.0 -2454.1
## (1 | Replicate)          1      15 1243.0 -2456.1  0.000  1          1
## (1 | Genotype)           0      14 1233.7 -2439.4 18.642  1  1.577e-05 ***
## (1 | Fragment)           0      14 1233.5 -2438.9 19.149  1  1.209e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                  Eliminated    Sum Sq   Mean Sq NumDF DenDF
## Treatment:Days:InitialCommunity          0 0.0095086 0.0047543     2   570
##                                  F value   Pr(>F)
## Treatment:Days:InitialCommunity   5.128 0.006205 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + Days + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + Treatment:Days + Treatment:InitialCommunity +
##     Days:InitialCommunity + Treatment:Days:InitialCommunity
```

```
      ranova(LME_Ofav)
```

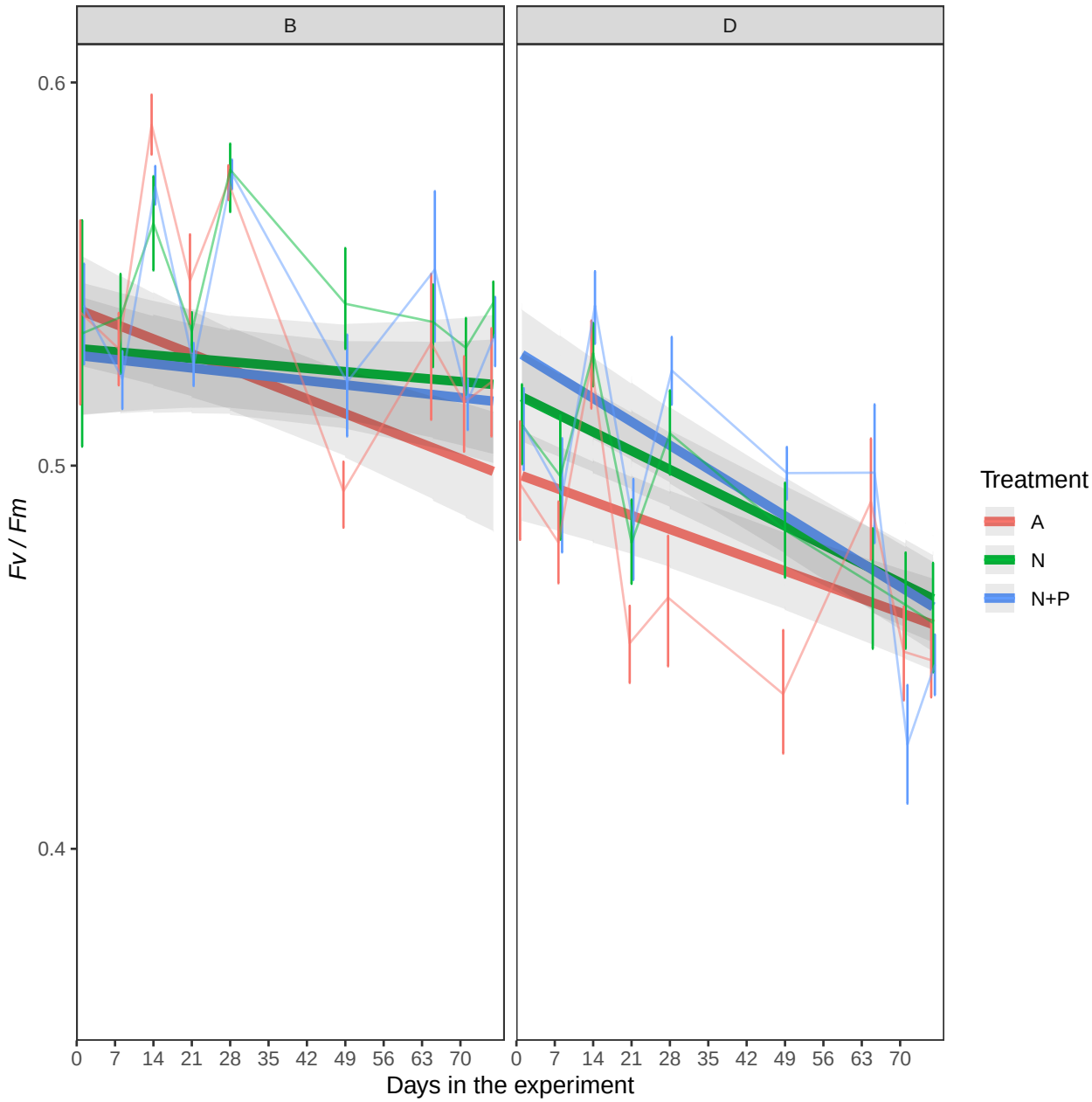
```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + Days + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + (1 | Replicate) + Treatment:Days + Treatment:InitialCommunity +
##     Days:InitialCommunity + Treatment:Days:InitialCommunity
##                 npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>            16 1243.0 -2454.1
## (1 | Genotype)    15 1233.7 -2437.4 18.649  1  1.572e-05 ***
## (1 | Fragment)    15 1233.5 -2436.9 19.149  1  1.209e-05 ***
## (1 | Replicate)   15 1243.0 -2456.1  0.000  1          1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
      LME_Ofav1<-lmer(YII ~ Treatment * Days * InitialCommunity +
                        (1 | Genotype/Fragment),
                      data=YII.Ofav.C, na.action=na.omit)
      lmerTest::step (LME_Ofav1)
```

```
## Backward reduced random-effect table:
##
##                          Eliminated npar logLik     AIC    LRT Df
## <none>                                15 1243.0 -2456.1
## (1 | Fragment:Genotype)          0   14 1233.5 -2438.9 19.149  1
## (1 | Genotype)                   0   14 1233.7 -2439.4 18.642  1
##                          Pr(>Chisq)
## <none>
## (1 | Fragment:Genotype)  1.209e-05 ***
## (1 | Genotype)           1.577e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                  Eliminated    Sum Sq   Mean Sq NumDF DenDF
## Treatment:Days:InitialCommunity          0 0.0095086 0.0047543     2   570
##                                  F value   Pr(>F)
## Treatment:Days:InitialCommunity   5.128 0.006205 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment * Days * InitialCommunity + (1 | Genotype/Fragment)
```

```
# 2. Predict values:
    pred_Ofav1 <- predict(LME_Ofav1,re.form = NA)

  #3. Bootstrap CI:
    OF.boot1 <- bootMer(LME_Ofav1, predict, nsim = 1000, re.form = NULL) # include random effects, redu
    std.err <- apply(OF.boot1$t, 2, sd)
    CI.lo_1 <- pred_Ofav1 - std.err*1.96
    CI.hi_1 <- pred_Ofav1 + std.err*1.96

  #Plot
  Model_of_1b_plot<- ggplot(
    YII.Ofav.C, aes(x = Days, y = YII, colour = Treatment)) +
    geom_line(aes(y = pred_Ofav1),size=2) +
    #geom_point(aes(fill=factor(Treatment)),
    #         shape = 21, colour = "black", size = 2, stroke = 0.3, alpha=0.3) +
    geom_ribbon(aes(ymin = CI.lo_1, ymax = CI.hi_1),
                size=2, alpha = 0.1, linetype = 0) +
    #scale_color_manual(values=my_colours) +
    #scale_fill_manual(values=my_colours) +
    scale_y_continuous(name=expression(~italic("Fv / Fm")),
                       limits = c(0.35, 0.61),
                       breaks = seq(0.4, 0.6, by=0.1), expand = c(0,0))+
    scale_x_continuous("Days in the experiment", limits = c(0, 78),
                      breaks = seq(0, 76, by=7), expand = c(0,0))+

     stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                  position = position_dodge(1) )+
```

```
    stat_summary(fun.y=mean, geom="line", position = position_dodge(1),
                 linetype=1, alpha=0.5) +

    # stat_summary(fun.y=mean, geom="point", size =1,
    #              position=position_dodge(width=1), alpha=0.8)  +
    ggthe_bw

Model_of_1b_plot + facet_grid(~InitialCommunity)
```



- Model for "Days" as factor

```
# 1. Ofav- Days
      LME_Ofav<-lmer(YII ~ Treatment * DaysF * InitialCommunity +
                       (1|Genotype) + (1|Fragment) +(1|Replicate),
```

```
                      data=YII.Ofav.C, na.action=na.omit)
     lmerTest::step (LME_Ofav) # Replicate is not significant
```

```
## Backward reduced random-effect table:
##
##                 Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                      58 1311.5 -2507.1
## (1 | Replicate)          1   57 1311.5 -2509.1  0.000  1          1
## (1 | Genotype)           0   56 1302.2 -2492.5 18.642  1  1.577e-05 ***
## (1 | Fragment)           0   56 1273.0 -2434.0 77.139  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                  Eliminated   Sum Sq   Mean Sq NumDF DenDF
## Treatment:DaysF:InitialCommunity          0 0.021644 0.0013528    16   528
##                                  F value    Pr(>F)
## Treatment:DaysF:InitialCommunity  2.7855 0.0002475 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + DaysF + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + Treatment:DaysF + Treatment:InitialCommunity +
##     DaysF:InitialCommunity + Treatment:DaysF:InitialCommunity
```

```
     ranova(LME_Ofav)
```

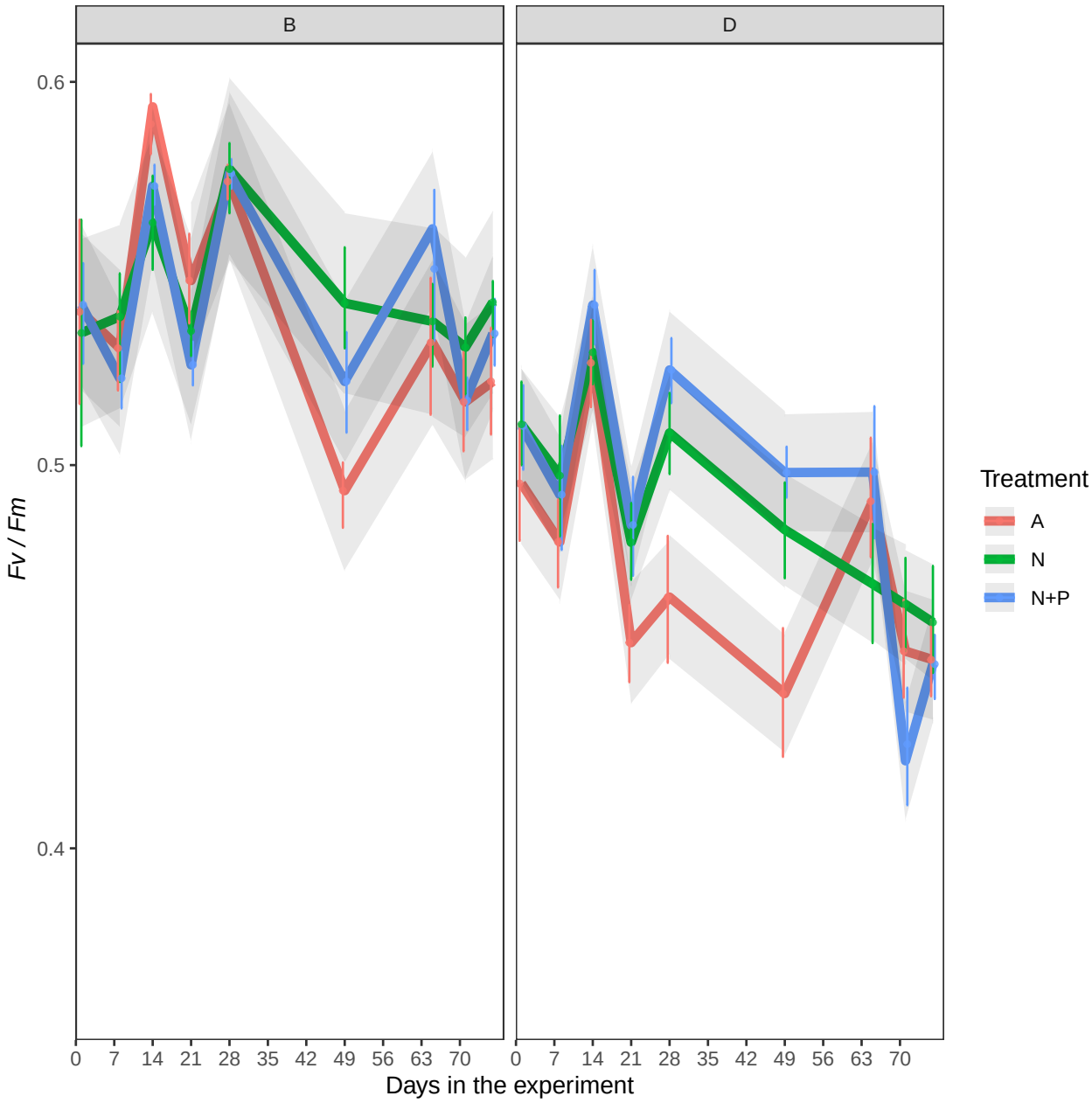
```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + DaysF + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + (1 | Replicate) + Treatment:DaysF + Treatment:InitialCommunity +
##     DaysF:InitialCommunity + Treatment:DaysF:InitialCommunity
##                 npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>            58 1311.5 -2507.1
## (1 | Genotype)    57 1302.2 -2490.5 18.642  1  1.577e-05 ***
## (1 | Fragment)    57 1273.0 -2432.0 77.139  1  < 2.2e-16 ***
## (1 | Replicate)   57 1311.5 -2509.1  0.000  1          1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
     LME_Ofav1.2<-lmer(YII ~ Treatment * DaysF * InitialCommunity +
                         (1|Fragment),
                       data=YII.Ofav.C, na.action=na.omit)
     lmerTest::step (LME_Ofav1.2)
```

```
## Backward reduced random-effect table:
##
##                Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                     56 1302.2 -2492.5
## (1 | Fragment)          0   55 1230.0 -2349.9 144.55  1  < 2.2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                 Eliminated   Sum Sq   Mean Sq NumDF DenDF
## Treatment:DaysF:InitialCommunity          0 0.021644 0.0013528    16   528
##                                 F value    Pr(>F)
## Treatment:DaysF:InitialCommunity  2.7856 0.0002475 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment * DaysF * InitialCommunity + (1 | Fragment)
```

```
  # 2. Predict values:
    pred_Ofav1.2 <- predict(LME_Ofav1.2,re.form = NA)

  #3. Bootstrap CI:
    OF.boot1.2 <- bootMer(LME_Ofav1.2, predict, nsim = 1000, re.form = NULL) # include random effects,
    std.err <- apply(OF.boot1.2$t, 2, sd)
    CI.lo_1 <- pred_Ofav1.2 - std.err*1.96
    CI.hi_1 <- pred_Ofav1.2 + std.err*1.96

  #Plot
  Model_of_1.2_plot<- ggplot(
    YII.Ofav.C, aes(x = Days, y = YII, colour = Treatment)) +
    geom_line(aes(y = pred_Ofav1.2),size=2) +
    #geom_point(aes(fill=factor(Treatment)),
    #          shape = 21, colour = "black", size = 2, stroke = 0.3, alpha=0.3) +
    geom_ribbon(aes(ymin = CI.lo_1, ymax = CI.hi_1),
                size=2, alpha = 0.1, linetype = 0) +
    #scale_color_manual(values=my_colours) +
    #scale_fill_manual(values=my_colours) +
    scale_y_continuous(name=expression(~italic("Fv / Fm")),
                       limits = c(0.35, 0.61),
                       breaks = seq(0.4, 0.6, by=0.1), expand = c(0,0))+
    scale_x_continuous("Days in the experiment", limits = c(0, 78),
                       breaks = seq(0, 76, by=7), expand = c(0,0))+

     stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                  position = position_dodge(1) )+
      stat_summary(fun.y=mean, geom="point", size =1,
                   position=position_dodge(width=1), alpha=0.8)  +
    ggthe_bw

  Model_of_1.2_plot + facet_grid(~InitialCommunity)
```




```
# EMMs
  Ofav.YII.emmC<-emmeans(LME_Ofav1.2, ~Treatment * DaysF * InitialCommunity)
  #contrast(Ofav.YII.emm, "tukey")


    # Ofav.YII_groupsC<-cld(Ofav.YII.emmC, by=NULL) # compact-letter display
    # Ofav.YII_groupsC<-Ofav.YII_groupsC[order(
    #   Ofav.YII_groupsC$Days,
    #   Ofav.YII_groupsC$Treatment,
    #   Ofav.YII_groupsC$InitialCommunity),]
    # Ofav.YII_groupsC
    # write.csv(Ofav.YII_groupsC, "Outputs/Multicomp_OfavYIIC.csv", row.names = F)
```

Ssid

- Days pooled (8-76 Days)

```
LME_Ssid1.1<-lmer(YII ~ Treatment * InitialCommunity + (1|Fragment),
                  data=YII.Ssid.C.1)
    step (LME_Ssid1.1) #  Replicate is significant
```

```
## Backward reduced random-effect table:
##
##                Eliminated npar logLik     AIC   LRT Df Pr(>Chisq)
## <none>                      11 2224.0 -4425.9
## (1 | Fragment)          0   10 2211.5 -4403.1 24.84  1  6.229e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                            Eliminated   Sum Sq   Mean Sq NumDF  DenDF
## Treatment:InitialCommunity          0 0.039046 0.0097615     4 153.16
##                            F value   Pr(>F)
## Treatment:InitialCommunity  5.9109 0.000189 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment * InitialCommunity + (1 | Fragment)
```

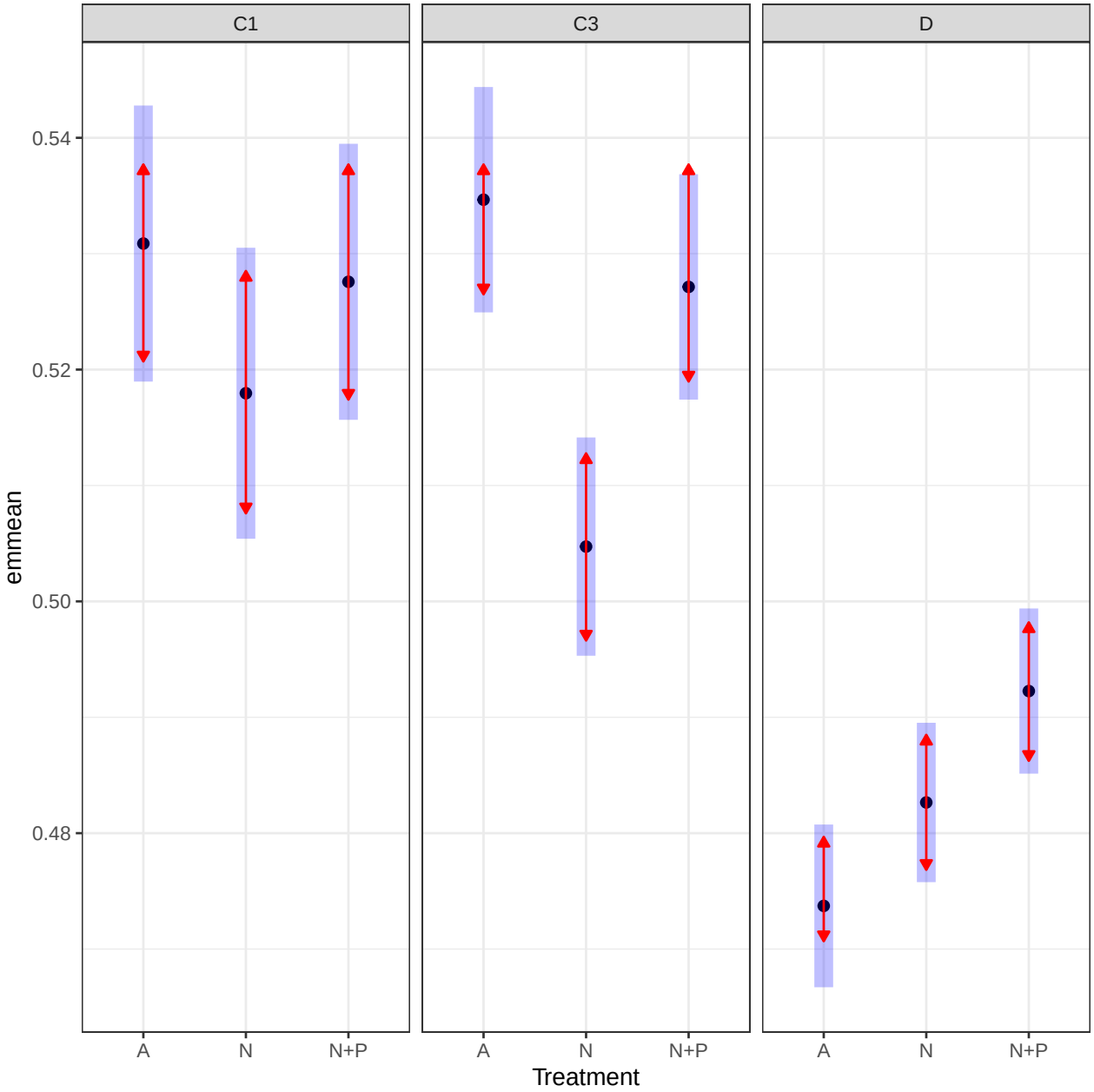
```
    anova(LME_Ssid1.1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                              Sum Sq  Mean Sq NumDF  DenDF F value
## Treatment                  0.021721 0.010861     2 153.09  6.5763
## InitialCommunity           0.301239 0.150620     2 153.16 91.2039
## Treatment:InitialCommunity 0.039046 0.009762     4 153.16  5.9109
##                               Pr(>F)
## Treatment                   0.001820 **
## InitialCommunity           < 2.2e-16 ***
## Treatment:InitialCommunity  0.000189 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
    ranova(LME_Ssid1.1)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + InitialCommunity + (1 | Fragment) + Treatment:InitialCommunity
##                npar logLik     AIC   LRT Df Pr(>Chisq)
## <none>           11 2224.0 -4425.9
## (1 | Fragment)   10 2211.5 -4403.1 24.84  1  6.229e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# EMMs
    Ssid.YII.emm1.1<-emmeans(LME_Ssid1.1, ~ InitialCommunity|Treatment)
    # contrast(Ssid.YII.emm, "tukey")

    # Tukey comparison (do not trust CI to compare EMMs)
      plot(emmeans(LME_Ssid1.1, ~Treatment|InitialCommunity), comparisons = TRUE) +
      coord_flip(xlim = NULL, ylim = NULL, expand = TRUE) + facet_grid(~InitialCommunity)+
        theme_bw()
```




```
      Ssid.YII.Groups1.1<-cld(Ssid.YII.emm1.1, by=NULL) # compact-letter display
      Ssid.YII.Groups1.1<- Ssid.YII.Groups1.1[order(
        Ssid.YII.Groups1.1$InitialCommunity,
        Ssid.YII.Groups1.1$Treatment),]
      Ssid.YII.Groups1.1
```

```
##   InitialCommunity Treatment    emmean          SE       df  lower.CL
## 1               C1         A 0.5308750 0.006028392 152.4349 0.5189650
## 4               C1         N 0.5179583 0.006354483 152.4349 0.5054041
## 7               C1       N+P 0.5275750 0.006028392 152.4349 0.5156650
## 2               C3         A 0.5346583 0.004922161 152.4349 0.5249339
## 5               C3         N 0.5047266 0.004765862 152.4349 0.4953109
## 8               C3       N+P 0.5271333 0.004922161 152.4349 0.5174089
## 3                D         A 0.4737245 0.003554425 154.6118 0.4667030
## 6                D         N 0.4826500 0.003480494 152.4349 0.4757738
## 9                D       N+P 0.4922613 0.003607501 153.1957 0.4851344
##    upper.CL .group
## 1 0.5427850      5
## 4 0.5305126     45
## 7 0.5394850     45
## 2 0.5443828      5
## 5 0.5141422    34
## 8 0.5368578      5
## 3 0.4807460  1
## 6 0.4895262  12
## 9 0.4993881   23
```

```
    #write.csv( Ssid.YII.Groups1.1, "Outputs/Multicomp_SsidYII1.1.csv", row.names = F)
```

- Model for "Days" as continous variable (days 1-76)

```
LME_Ssid<-lmer(YII ~ Treatment * Days * InitialCommunity +
                     (1|Fragment) +(1|Replicate),
                   data=subset(YII.Ssid.C))
    step (LME_Ssid) #  Replicate is not significant
```

```
## Backward reduced random-effect table:
##
##                 Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                          21 2486.7 -4931.3
## (1 | Replicate)          1   20 2486.7 -4933.3  0.000  1          1
## (1 | Fragment)           0   19 2466.3 -4894.6 40.775  1  1.708e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                  Eliminated   Sum Sq   Mean Sq NumDF
## Treatment:Days:InitialCommunity          1 0.004115 0.0010287     4
## Treatment:Days                           0 0.028806 0.0144029     2
## Treatment:InitialCommunity               0 0.033666 0.0084166     4
## Days:InitialCommunity                    0 0.015350 0.0076750     2
##                                    DenDF F value    Pr(>F)
## Treatment:Days:InitialCommunity 1283.90  0.6706 0.6124001
## Treatment:Days                  1288.52  9.3992 8.861e-05 ***
## Treatment:InitialCommunity       153.14  5.4926 0.0003694 ***
## Days:InitialCommunity           1287.90  5.0087 0.0068106 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Model found:
## YII ~ Treatment + Days + InitialCommunity + (1 | Fragment) +
##     Treatment:Days + Treatment:InitialCommunity + Days:InitialCommunity
```

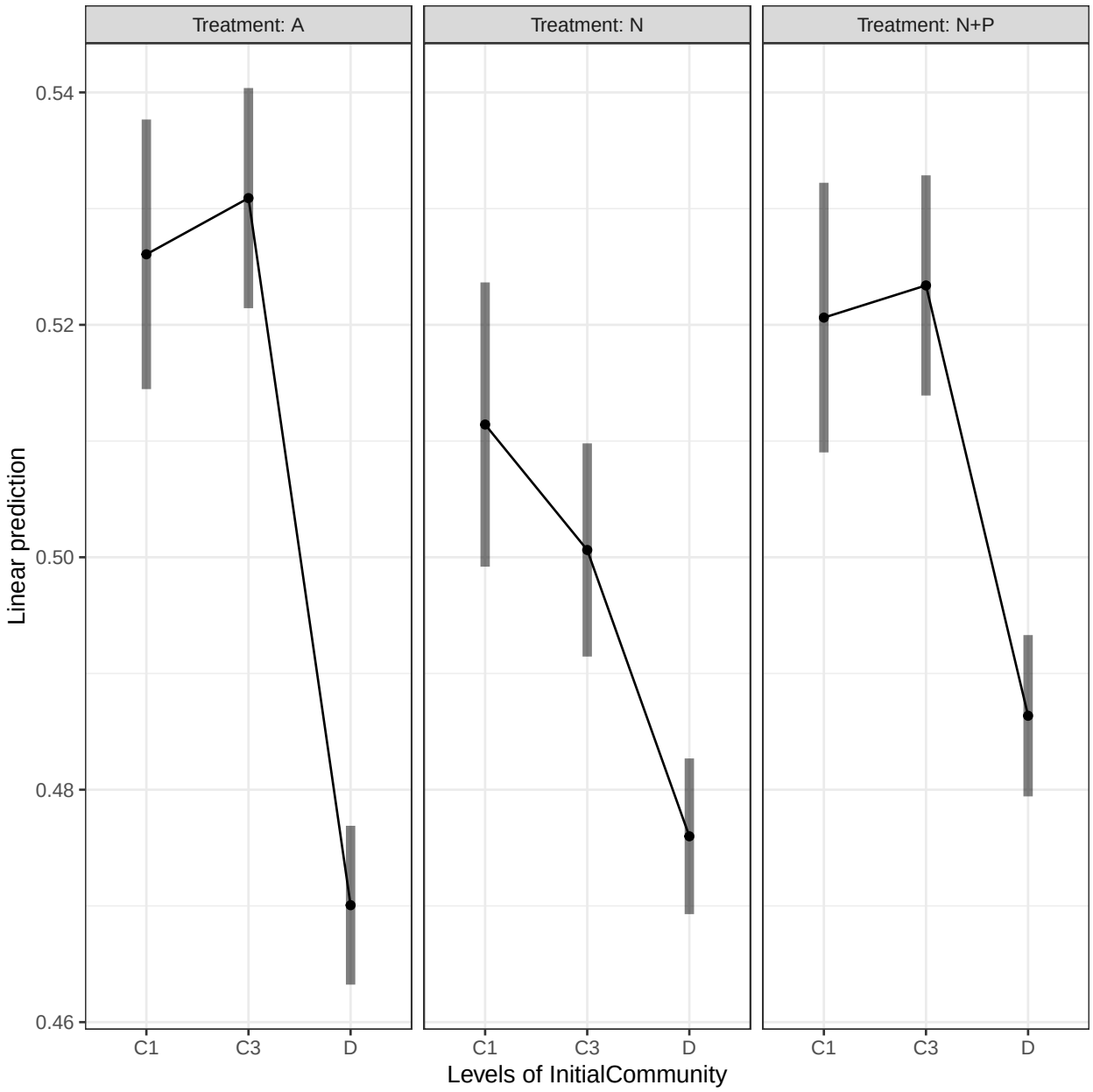
```
    anova(LME_Ssid)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                   Sum Sq  Mean Sq NumDF   DenDF  F value
## Treatment                       0.016509 0.008254     2  512.85   5.3813
## Days                            0.165811 0.165811     1 1283.77 108.0977
## InitialCommunity                0.098054 0.049027     2  512.88  31.9624
## Treatment:Days                  0.031245 0.015623     2 1283.77  10.1848
## Treatment:InitialCommunity      0.014543 0.003636     4  512.88   2.3703
## Days:InitialCommunity           0.015047 0.007524     2 1283.90   4.9049
## Treatment:Days:InitialCommunity 0.004115 0.001029     4 1283.90   0.6706
##                                    Pr(>F)
## Treatment                        0.004866 **
## Days                            < 2.2e-16 ***
## InitialCommunity                8.283e-14 ***
## Treatment:Days                  4.088e-05 ***
## Treatment:InitialCommunity       0.051566 .
## Days:InitialCommunity            0.007549 **
## Treatment:Days:InitialCommunity  0.612402
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
    ranova(LME_Ssid)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + Days + InitialCommunity + (1 | Fragment) +
##     (1 | Replicate) + Treatment:Days + Treatment:InitialCommunity +
##     Days:InitialCommunity + Treatment:Days:InitialCommunity
##                  npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>             21 2486.7 -4931.3
## (1 | Fragment)     20 2466.4 -4892.7 40.605  1  1.864e-10 ***
## (1 | Replicate)    20 2486.7 -4933.3  0.000  1           1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

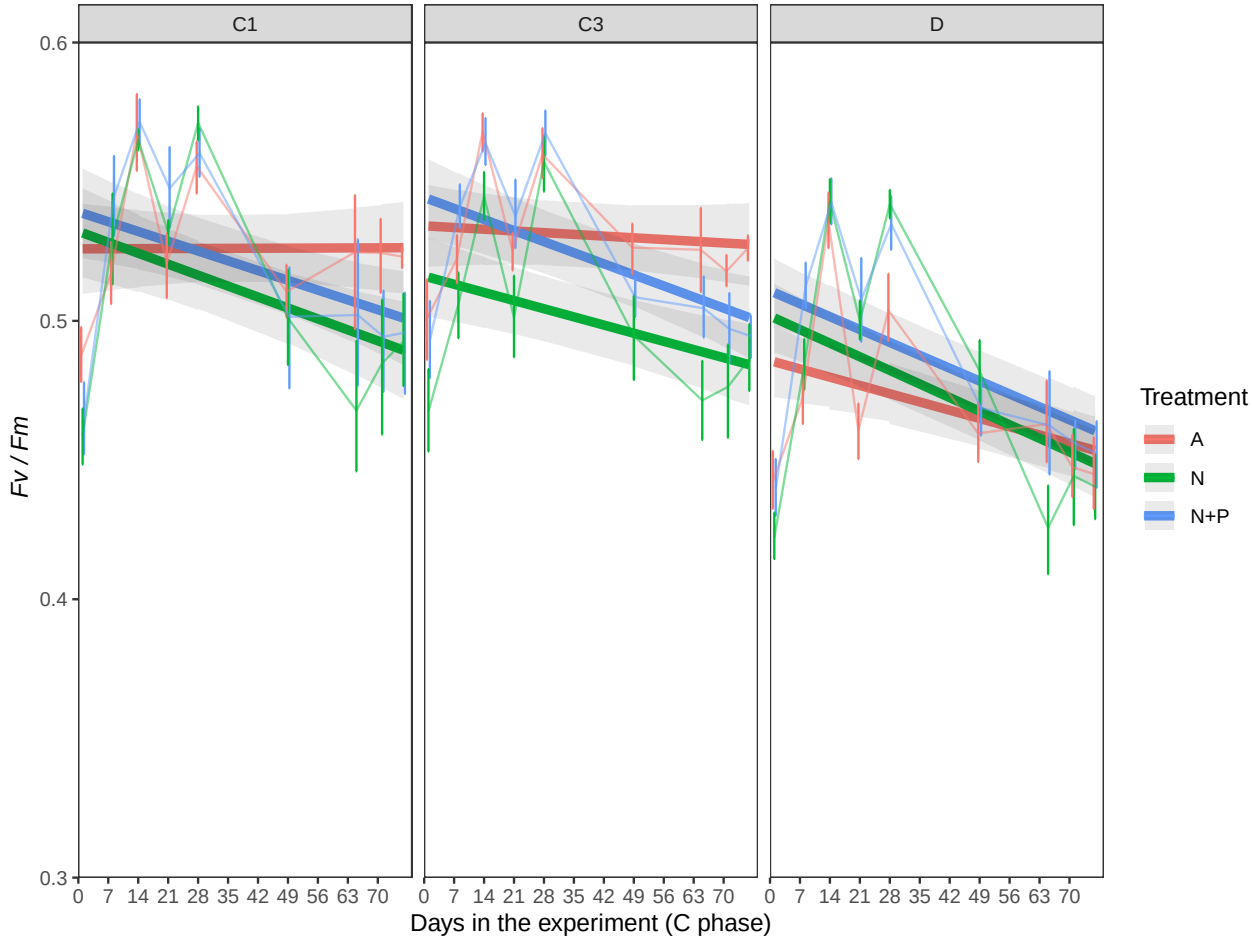
```
LME_Ssid1<-lmer(YII ~ Treatment * Days * InitialCommunity +
                      (1|Fragment),
                    data=YII.Ssid.C, na.action=na.omit)


# EMMs
      Ssid.YII.emm1<-emmeans(LME_Ssid1, ~Treatment * Days * InitialCommunity)
      # contrast(Ssid.YII.emm, "tukey")

      # Effect plot options
      emmip(LME_Ssid1, ~InitialCommunity|Treatment, CIs = TRUE) + theme_bw() # interaction plot of pred
```




```
# 2. Predict values:
    predSs1 <- predict(LME_Ssid1,re.form = NA)

# 3. Bootstrap CI:
    boot1Ss <- bootMer(LME_Ssid1, predict, nsim = 1000, re.form = NULL) # include random effects, reduc
    std.err <- apply(boot1Ss$t, 2, sd)
    CI.lo_1 <- predSs1 - std.err*1.96
    CI.hi_1 <- predSs1 + std.err*1.96
```

```
# 4. Plot
  Model1Ss_plot<- ggplot(
    YII.Ssid.C, aes(x = Days, y = YII, colour = Treatment)) +
    geom_line(aes(y = predSs1),size=2) +
    #geom_point(aes(fill=factor(Treatment)),
    #         shape = 21, colour = "black", size = 2, stroke = 0.3, alpha=0.5) +
```

```
    geom_ribbon(aes(ymin = CI.lo_1, ymax = CI.hi_1),
                size=2, alpha = 0.1, linetype = 0) +
    #scale_color_manual(values=my_colours) +
    #scale_fill_manual(values=my_colours) +
    scale_y_continuous(name=expression(~italic("Fv / Fm")),
                       limits = c(0.3, 0.6),
                       breaks = seq(0.3, 0.6, by=0.1), expand = c(0,0))+
    scale_x_continuous("Days in the experiment (C phase)", limits = c(0, 78),
                       breaks = seq(0, 76, by=7), expand = c(0,0))+

    stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                 position = position_dodge(1) )+
    stat_summary(fun.y=mean, geom="line", position = position_dodge(1),
                 linetype=1, alpha=0.5) +
    #stat_summary(fun.y=mean, geom="point", size =1,
    #               position=position_dodge(width=1), alpha=0.8)  +
    ggthe_bw # + Fill.colour

  Model1Ss_plot + facet_grid(~InitialCommunity)
```



- Model for "Days" as factor

```
# 1. Ssid- Days
      LME_Ssid<-lmer(YII ~ Treatment * DaysF * InitialCommunity +
```

```
                      (1|Genotype) + (1|Fragment) +(1|Replicate),
                       data=YII.Ssid.C, na.action=na.omit)
    lmerTest::step (LME_Ssid) # Replicate is not significant
```

```
## Backward reduced random-effect table:
##
##                 Eliminated npar logLik     AIC     LRT Df Pr(>Chisq)
## <none>                       85 3033.7 -5897.4
## (1 | Replicate)          1   84 3033.3 -5898.6   0.841  1      0.359
## (1 | Genotype)           0   83 2995.3 -5824.7  75.896  1     <2e-16 ***
## (1 | Fragment)           0   83 2972.7 -5779.4 121.188  1     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                  Eliminated   Sum Sq   Mean Sq NumDF
## Treatment:DaysF:InitialCommunity          1 0.019444 0.0006076    32
## Treatment:DaysF                           0 0.134201 0.0083875    16
## Treatment:InitialCommunity                0 0.020396 0.0050991     4
## DaysF:InitialCommunity                    0 0.044362 0.0027727    16
##                                    DenDF F value    Pr(>F)
## Treatment:DaysF:InitialCommunity 1220.34  1.1718    0.2354
## Treatment:DaysF                  1252.49 16.1060 < 2.2e-16 ***
## Treatment:InitialCommunity        147.69  9.7915 4.712e-07 ***
## DaysF:InitialCommunity           1252.33  5.3241 5.033e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + DaysF + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + Treatment:DaysF + Treatment:InitialCommunity +
##     DaysF:InitialCommunity
```

```
    ranova(LME_Ssid)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + DaysF + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + (1 | Replicate) + Treatment:DaysF + Treatment:InitialCommunity +
##     DaysF:InitialCommunity + Treatment:DaysF:InitialCommunity
##                 npar logLik     AIC     LRT Df Pr(>Chisq)
## <none>            85 3033.7 -5897.4
## (1 | Genotype)    84 2995.3 -5822.7  76.738  1     <2e-16 ***
## (1 | Fragment)    84 2975.1 -5782.1 117.284  1     <2e-16 ***
## (1 | Replicate)   84 3033.3 -5898.6   0.841  1      0.359
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

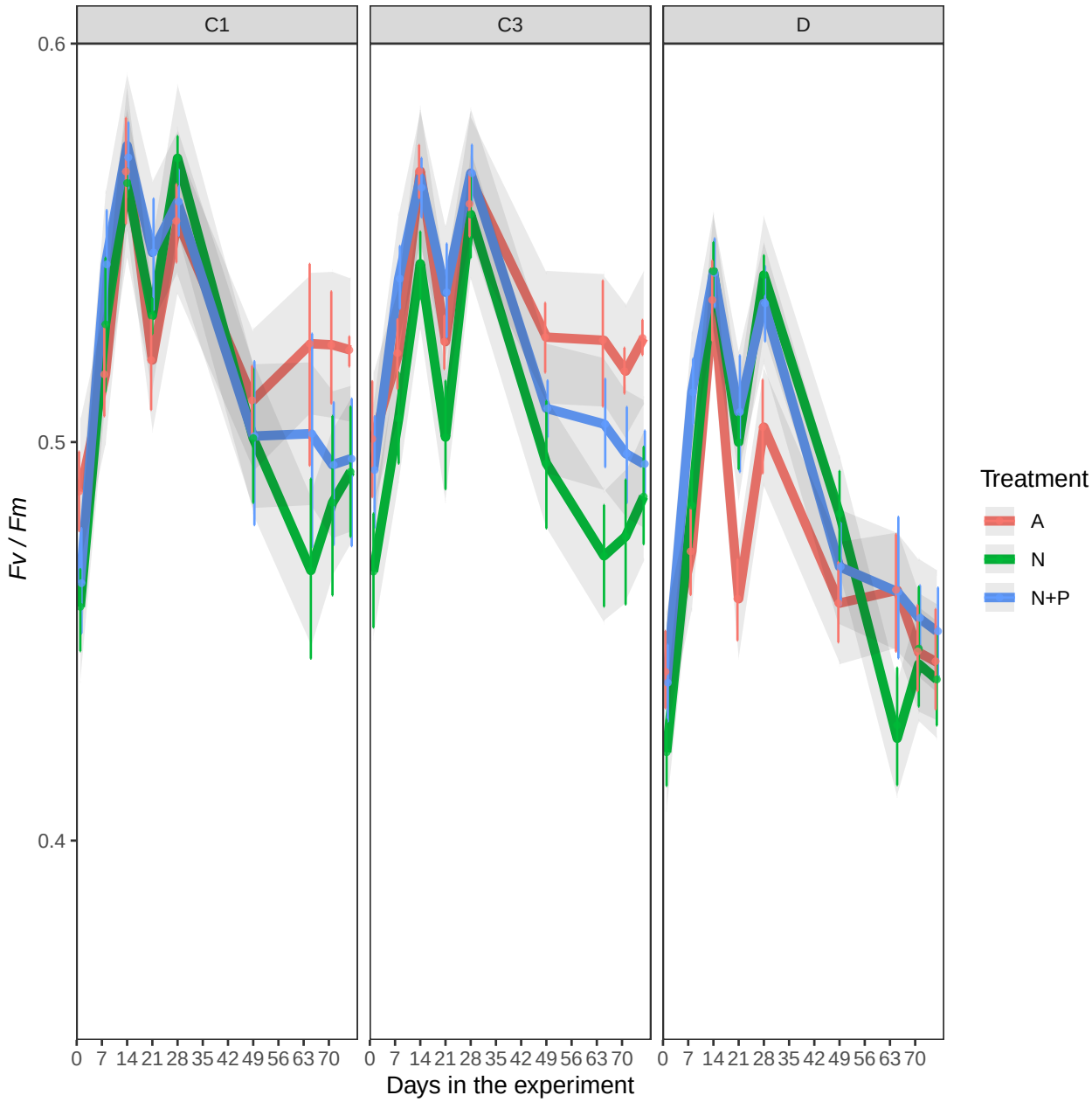
```
    LME_Ssid1.2<-lmer(YII ~ Treatment * DaysF * InitialCommunity +
                       (1|Fragment),
                     data=YII.Ssid.C, na.action=na.omit)
    lmerTest::step (LME_Ssid1.2)
```

```
## Backward reduced random-effect table:
##
##                Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                        83 2995.3 -5824.7
## (1 | Fragment)          0   82 2829.0 -5494.0 332.65  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                    Eliminated   Sum Sq   Mean Sq NumDF
## Treatment:DaysF:InitialCommunity          1 0.019389 0.0006059    32
## Treatment:DaysF                           0 0.134162 0.0083851    16
## Treatment:InitialCommunity                0 0.011521 0.0028803     4
## DaysF:InitialCommunity                    0 0.044336 0.0027710    16
##                                     DenDF F value    Pr(>F)
## Treatment:DaysF:InitialCommunity 1220.22  1.1685 0.2390861
## Treatment:DaysF                  1252.32 16.1009 < 2.2e-16 ***
## Treatment:InitialCommunity        153.05  5.5307 0.0003475 ***
## DaysF:InitialCommunity           1252.23  5.3208  5.14e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + DaysF + InitialCommunity + (1 | Fragment) +
##     Treatment:DaysF + Treatment:InitialCommunity + DaysF:InitialCommunity
```

```
# 2. Predict values:
    pred_Ssid1.2 <- predict(LME_Ssid1.2,re.form = NA)

  #3. Bootstrap CI:
    Ss.boot1.2 <- bootMer(LME_Ssid1.2, predict, nsim = 1000, re.form = NULL) # include random effects,
    std.err <- apply(Ss.boot1.2$t, 2, sd)
    CI.lo_1 <- pred_Ssid1.2 - std.err*1.96
    CI.hi_1 <- pred_Ssid1.2 + std.err*1.96
```

```
# 4. Plot
  Model_Ss_1.2_plot<- ggplot(
    YII.Ssid.C, aes(x = Days, y = YII, colour = Treatment)) +
    geom_line(aes(y = pred_Ssid1.2),size=2) +
    #geom_point(aes(fill=factor(Treatment)),
    #         shape = 21, colour = "black", size = 2, stroke = 0.3, alpha=0.3) +
    geom_ribbon(aes(ymin = CI.lo_1, ymax = CI.hi_1),
                size=2, alpha = 0.1, linetype = 0) +
    #scale_color_manual(values=my_colours) +
    #scale_fill_manual(values=my_colours) +
    scale_y_continuous(name=expression(~italic("Fv / Fm")),
                       limits = c(0.35, 0.6),
                       breaks = seq(0.4, 0.6, by=0.1), expand = c(0,0))+
    scale_x_continuous("Days in the experiment", limits = c(0, 78),
                      breaks = seq(0, 76, by=7), expand = c(0,0))+

    stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                   position = position_dodge(1) )+
```

```
    stat_summary(fun.y=mean, geom="point", size =1,
                 position=position_dodge(width=1), alpha=0.8)  +
    ggthe_bw

Model_Ss_1.2_plot + facet_grid(~InitialCommunity)
```




```
# 5. EMMs
    Ssid.YII.emmC<-emmeans(LME_Ssid1.2, ~Treatment * DaysF * InitialCommunity)
      #contrast(Ssid.YII.emm, "tukey")


       Ssid.YII_groupsC<-cld(Ssid.YII.emmC, by=NULL) # compact-letter display
       Ssid.YII_groupsC<-Ssid.YII_groupsC[order(
         Ssid.YII_groupsC$DaysF,
```

```
        Ssid.YII_groupsC$InitialCommunity,
        Ssid.YII_groupsC$Treatment),]
      Ssid.YII_groupsC
```

```
##    Treatment DaysF InitialCommunity    emmean          SE       df
## 1          A     1               C1 0.4876000 0.008975576 682.1716
## 2          N     1               C1 0.4586667 0.009461088 682.1716
## 3        N+P     1               C1 0.4646000 0.008975576 682.1716
## 28         A     1               C3 0.5008000 0.007328527 682.1716
## 29         N     1               C3 0.4675000 0.007095816 682.1716
## 30       N+P     1               C3 0.4930000 0.007328527 682.1716
## 55         A     1                D 0.4423793 0.005270640 682.1716
## 56         N     1                D 0.4221667 0.005182051 682.1716
## 57       N+P     1                D 0.4396071 0.005363933 682.1716
## 4          A     8               C1 0.5170000 0.008975576 682.1716
## 5          N     8               C1 0.5295556 0.009461088 682.1716
## 6        N+P     8               C1 0.5446000 0.008975576 682.1716
## 31         A     8               C3 0.5223333 0.007328527 682.1716
## 32         N     8               C3 0.5059375 0.007095816 682.1716
## 33       N+P     8               C3 0.5410000 0.007328527 682.1716
## 58         A     8                D 0.4725862 0.005270640 682.1716
## 59         N     8                D 0.4840667 0.005182051 682.1716
## 60       N+P     8                D 0.5125000 0.005363933 682.1716
## 7          A    14               C1 0.5712000 0.008975576 682.1716
## 8          N    14               C1 0.5650000 0.009461088 682.1716
## 9        N+P    14               C1 0.5744000 0.008975576 682.1716
## 34         A    14               C3 0.5680000 0.007328527 682.1716
## 35         N    14               C3 0.5447500 0.007095816 682.1716
## 36       N+P    14               C3 0.5663333 0.007328527 682.1716
## 61         A    14                D 0.5356552 0.005270640 682.1716
## 62         N    14                D 0.5428333 0.005182051 682.1716
## 63       N+P    14                D 0.5424643 0.005363933 682.1716
## 10         A    21               C1 0.5206000 0.008975576 682.1716
## 11         N    21               C1 0.5317778 0.009461088 682.1716
## 12       N+P    21               C1 0.5476000 0.008975576 682.1716
## 37         A    21               C3 0.5252000 0.007328527 682.1716
## 38         N    21               C3 0.5012500 0.007095816 682.1716
## 39       N+P    21               C3 0.5376000 0.007328527 682.1716
## 64         A    21                D 0.4606897 0.005270640 682.1716
## 65         N    21                D 0.4999667 0.005182051 682.1716
## 66       N+P    21                D 0.5075714 0.005363933 682.1716
## 13         A    28               C1 0.5555000 0.008975576 682.1716
## 14         N    28               C1 0.5712222 0.009461088 682.1716
## 15       N+P    28               C1 0.5603000 0.008975576 682.1716
## 40         A    28               C3 0.5659333 0.007328527 682.1716
## 41         N    28               C3 0.5571250 0.007095816 682.1716
## 42       N+P    28               C3 0.5674667 0.007328527 682.1716
## 67         A    28                D 0.5037586 0.005270640 682.1716
## 68         N    28                D 0.5419333 0.005182051 682.1716
## 69       N+P    28                D 0.5348214 0.005363933 682.1716
## 16         A    49               C1 0.5105000 0.008975576 682.1716
## 17         N    49               C1 0.5010000 0.009461088 682.1716
## 18       N+P    49               C1 0.5015000 0.008975576 682.1716
## 43         A    49               C3 0.5263333 0.007328527 682.1716
```

```
## 44         N    49              C3 0.4946875 0.007095816 682.1716
## 45       N+P    49              C3 0.5084667 0.007328527 682.1716
## 70         A    49               D 0.4595862 0.005270640 682.1716
## 71         N    49               D 0.4820000 0.005182051 682.1716
## 72       N+P    49               D 0.4687143 0.005363933 682.1716
## 19         A    65              C1 0.5247000 0.008975576 682.1716
## 20         N    65              C1 0.4677778 0.009461088 682.1716
## 21       N+P    65              C1 0.5021000 0.008975576 682.1716
## 46         A    65              C3 0.5255333 0.007328527 682.1716
## 47         N    65              C3 0.4714375 0.007095816 682.1716
## 48       N+P    65              C3 0.5045333 0.007328527 682.1716
## 73         A    65               D 0.4628424 0.005337022 704.3547
## 74         N    65               D 0.4256667 0.005182051 682.1716
## 75       N+P    65               D 0.4624674 0.005433973 705.1685
## 22         A    71              C1 0.5244000 0.008975576 682.1716
## 23         N    71              C1 0.4847778 0.009461088 682.1716
## 24       N+P    71              C1 0.4943000 0.008975576 682.1716
## 49         A    71              C3 0.5178000 0.007328527 682.1716
## 50         N    71              C3 0.4763125 0.007095816 682.1716
## 51       N+P    71              C3 0.4971333 0.007328527 682.1716
## 76         A    71               D 0.4472311 0.005337722 704.3258
## 77         N    71               D 0.4443000 0.005182051 682.1716
## 78       N+P    71               D 0.4558929 0.005363933 682.1716
## 25         A    76              C1 0.5231000 0.008975576 682.1716
## 26         N    76              C1 0.4925556 0.009461088 682.1716
## 27       N+P    76              C1 0.4958000 0.008975576 682.1716
## 52         A    76              C3 0.5261333 0.007328527 682.1716
## 53         N    76              C3 0.4863125 0.007095816 682.1716
## 54       N+P    76              C3 0.4945333 0.007328527 682.1716
## 79         A    76               D 0.4447668 0.005337722 704.3258
## 80         N    76               D 0.4404333 0.005182051 682.1716
## 81       N+P    76               D 0.4525357 0.005363933 682.1716
##     lower.CL  upper.CL
## 1  0.4699769 0.5052231
## 2  0.4400903 0.4772430
## 3  0.4469769 0.4822231
## 28 0.4864108 0.5151892
## 29 0.4535677 0.4814323
## 30 0.4786108 0.5073892
## 55 0.4320307 0.4527279
## 56 0.4119920 0.4323414
## 57 0.4290753 0.4501389
## 4  0.4993769 0.5346231
## 5  0.5109792 0.5481319
## 6  0.5269769 0.5622231
## 31 0.5079442 0.5367225
## 32 0.4920052 0.5198698
## 33 0.5266108 0.5553892
## 58 0.4622376 0.4829348
## 59 0.4738920 0.4942414
## 60 0.5019682 0.5230318
## 7  0.5535769 0.5888231
## 8  0.5464236 0.5835764
## 9  0.5567769 0.5920231
```

```
## 34 0.5536108 0.5823892
## 35 0.5308177 0.5586823
## 36 0.5519442 0.5807225
## 61 0.5253065 0.5460038
## 62 0.5326586 0.5530080
## 63 0.5319325 0.5529961
## 10 0.5029769 0.5382231
## 11 0.5132014 0.5503541
## 12 0.5299769 0.5652231
## 37 0.5108108 0.5395892
## 38 0.4873177 0.5151823
## 39 0.5232108 0.5519892
## 64 0.4503410 0.4710383
## 65 0.4897920 0.5101414
## 66 0.4970396 0.5181032
## 13 0.5378769 0.5731231
## 14 0.5526459 0.5897986
## 15 0.5426769 0.5779231
## 40 0.5515442 0.5803225
## 41 0.5431927 0.5710573
## 42 0.5530775 0.5818558
## 67 0.4934100 0.5141072
## 68 0.5317586 0.5521080
## 69 0.5242896 0.5453532
## 16 0.4928769 0.5281231
## 17 0.4824236 0.5195764
## 18 0.4838769 0.5191231
## 43 0.5119442 0.5407225
## 44 0.4807552 0.5086198
## 45 0.4940775 0.5228558
## 70 0.4492376 0.4699348
## 71 0.4718253 0.4921747
## 72 0.4581825 0.4792461
## 19 0.5070769 0.5423231
## 20 0.4492014 0.4863541
## 21 0.4844769 0.5197231
## 46 0.5111442 0.5399225
## 47 0.4575052 0.4853698
## 48 0.4901442 0.5189225
## 73 0.4523641 0.4733208
## 74 0.4154920 0.4358414
## 75 0.4517987 0.4731361
## 22 0.5067769 0.5420231
## 23 0.4662014 0.5033541
## 24 0.4766769 0.5119231
## 49 0.5034108 0.5321892
## 50 0.4623802 0.4902448
## 51 0.4827442 0.5115225
## 76 0.4367514 0.4577109
## 77 0.4341253 0.4544747
## 78 0.4453611 0.4664247
## 25 0.5054769 0.5407231
## 26 0.4739792 0.5111319
## 27 0.4781769 0.5134231
```

```
## 52 0.5117442 0.5405225
## 53 0.4723802 0.5002448
## 54 0.4801442 0.5089225
## 79 0.4342871 0.4552466
## 80 0.4302586 0.4506080
## 81 0.4420039 0.4630675
##
## 1       567890ABCDEFGHIJKLMN
## 2   1234567890ABCDEFG
## 3   1234567890ABCDEFGHI
## 28            ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmno
## 29    34567890ABC E
## 30          90ABCDEFGHIJKLMN
## 55  1234
## 56  1
## 57  123
## 4                   HIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 5                      LMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 6                                XYZabcdefghijklmno    tuv     z2z3z4z5z6z7    z0zAzBzCzDzEzFzGzH
## 31                     MNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 32              D FG IJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuv       z3              zAzBzC  zE
## 33                           TUVW    bcd  g   klm o  rs  v x z1  z3  z5  z7  z9z0    zC  zE  zG
## 58       67890AB DEF
## 59         890ABCDEFGHIJKL
## 60                    JKLMNOPQRSTUVWXYZabcdefghijklmnop r t vwx   z2    z5z6z7z8z9  zA  zCzD    zGzH
## 7
## 8
## 9
## 34
## 35                                                    wxyz1z2  z4z5z6z7z8z9z0      zD  zFzGzH
## 36
## 61                        P  ST  W Y ab    gh jk   opqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 62                                              rs  v x z1  z3  z5        z0    zC  zE  zG
## 63                                             q s u   yz1  z3z4          z0  zB    zEzF
## 10                    JKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 11                       NOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 12                                        hijklmno                                zAzBzCzDzEzFzGzH
## 37                      MNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 38             BCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmno
## 39                          PQRSTUVW YZabcde ghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 64    34567890
## 65             BCDEFGHIJKLMN   R
## 66                   HIJKLMN P R T V  Y  b def h  k mn                    z6z7z8z9                zH
## 13
## 14
## 15
## 40
## 41
## 42
## 67              C   GHIJKLMNO QR  UV X Z  cdef  i  lmn
## 68                                                 pqrstuvwxyz1z2z3z4z5        z0zAzBzCzDzEzFzG
## 69                         O Q S U WX Za c   g ij l  opqrstuvwxyz1z2z3z4z5        z0zAzBzCzDzEzFzG
## 16             BCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 17           90ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
```

```
## 18           0ABCDEFGHIJKLMNOPQRSTUVW                  pqrs   wxyz1           z8z9
## 43                      MNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 44           0ABCDEFGHIJKLMN   R
## 45              C EFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 70    34567890
## 71         890ABCDEFGHIJK
## 72     4567890AB D
## 19                     KLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 20  1234567890ABCDEFGHIJ
## 21           0ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefg        pqrstuvwxyz1z2z3z4z5z6z7z8z9z0
## 46                      MNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 47    34567890ABC E  H
## 48             BCDEFGHIJKLMNOPQRS    XYZa   ef hij   n pq  tu w y  z2  z4  z6  z8    zAzB  zD  zF  zH
## 73    34567890A
## 74  12
## 75    34567890A
## 22                     KLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 23    34567890ABCDEFGHIJKLM
## 24         890ABCDEFGHIJKLMNOPQRSTUVW
## 49                    JKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 50    34567890ABCDEFGHIJK
## 51           0ABCDEFGHIJKLMNO        X       f
## 76  1234567
## 77  123456
## 78   23456789
## 25                     KLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 26        7890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmno
## 27         890ABCDEFGHIJKLMNOPQRSTUVW
## 52                      MNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzH
## 53         890ABCDEFGHIJKLMN
## 54           0ABCDEFGHIJKLMN
## 79  12345
## 80  1234
## 81  12345678
```

```
      #write.csv(Ssid.YII_groupsC, "Outputs/Multicomp_SsidYIIC.csv", row.names = F)
```

H: Effect of pre-exposure to nutrient treatments during heat challenge

Ofav

- Model for "Days" as continous variable (days 84-110)

```
# 1. Ofav- Days
     LME_Ofav.H<-lmer(YII ~ Treatment * Days * InitialCommunity +
                        (1|Genotype) + (1|Fragment) +(1|Replicate),
                         data=YII.Ofav.H, na.action=na.omit)
     lmerTest::step (LME_Ofav.H) # Replicate is not significant
```

```
## Backward reduced random-effect table:
##
##                 Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                          16 666.73 -1301.5
## (1 | Replicate)          1   15 666.73 -1303.5 0.0000  1   1.000000
```

```
## (1 | Genotype)           0   14 662.44 -1296.9 8.5781  1   0.003402 **
## (1 | Fragment)           0   14 663.16 -1298.3 7.1280  1   0.007589 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                Eliminated    Sum Sq   Mean Sq NumDF
## Treatment:Days:InitialCommunity          1 0.0022744 0.0011372     2
## Treatment:InitialCommunity               2 0.0016208 0.0008104     2
## Treatment:Days                           0 0.0189804 0.0094902     2
## Days:InitialCommunity                    0 0.0088774 0.0088774     1
##                                 DenDF F value   Pr(>F)
## Treatment:Days:InitialCommunity 390.99  0.7378 0.478849
## Treatment:InitialCommunity       89.11  0.5261 0.592744
## Treatment:Days                  390.47  6.1692 0.002302 **
## Days:InitialCommunity           393.25  5.7709 0.016757 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + Days + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + Treatment:Days + Days:InitialCommunity
```

```
ranova(LME_Ofav.H)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + Days + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + (1 | Replicate) + Treatment:Days + Treatment:InitialCommunity +
##     Days:InitialCommunity + Treatment:Days:InitialCommunity
##                 npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>            16 666.73 -1301.5
## (1 | Genotype)    15 662.44 -1294.9 8.5781  1   0.003402 **
## (1 | Fragment)    15 663.16 -1296.3 7.1282  1   0.007588 **
## (1 | Replicate)   15 666.73 -1303.5 0.0000  1   1.000000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

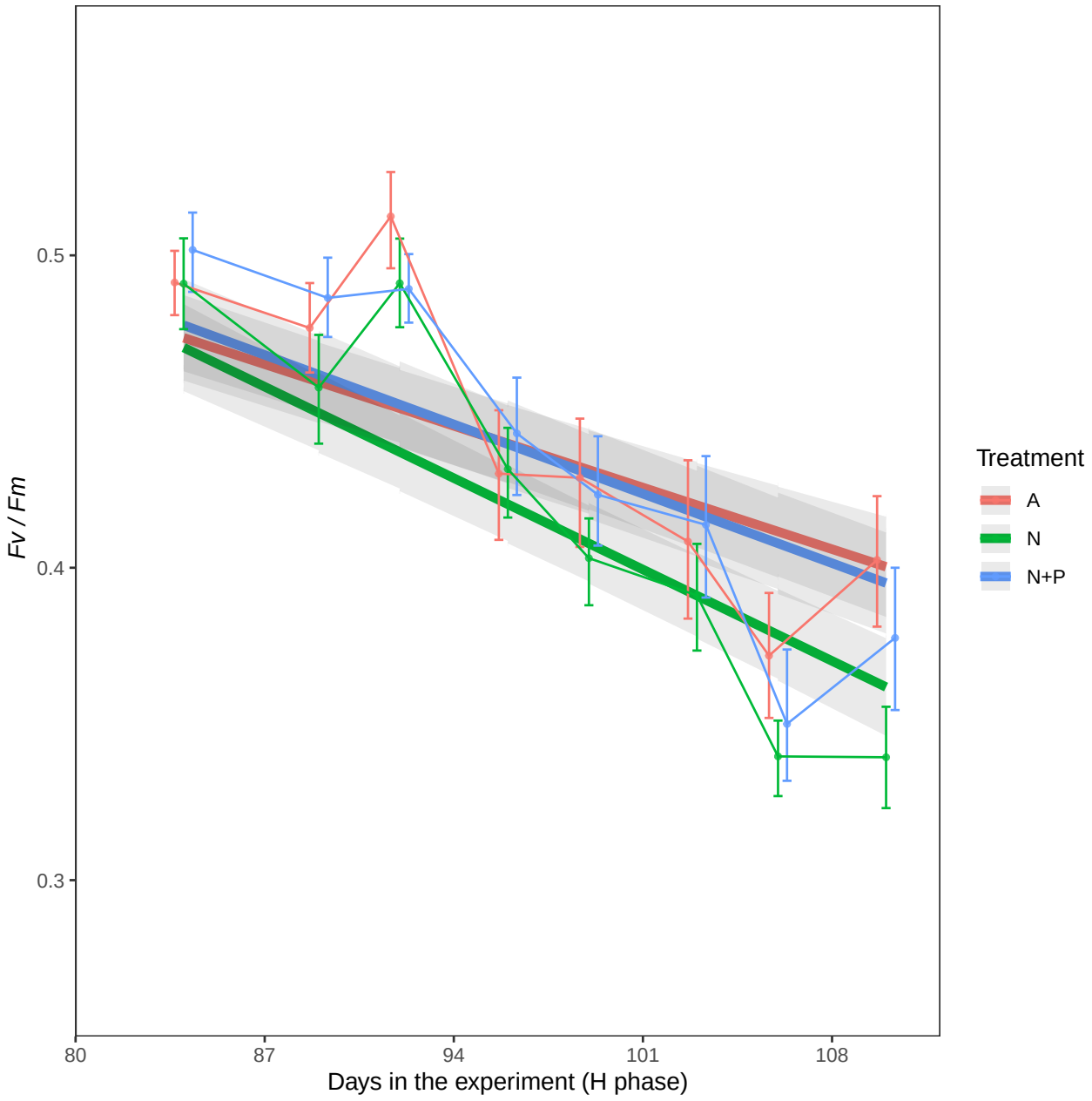
```
LME_Ofav.H1<-lmer(YII ~ Treatment * Days +
                    (1 | Genotype/Fragment),
                  data=YII.Ofav.H, na.action=na.omit)
lmerTest::step (LME_Ofav.H1)
```

```
## Backward reduced random-effect table:
##
##                         Eliminated npar logLik     AIC     LRT Df
## <none>                                9 687.23 -1356.5
## (1 | Fragment:Genotype)          0    8 683.59 -1351.2  7.2867  1
## (1 | Genotype)                   0    8 674.23 -1332.5 26.0040  1
##                         Pr(>Chisq)
## <none>
## (1 | Fragment:Genotype)   0.006947 **
```

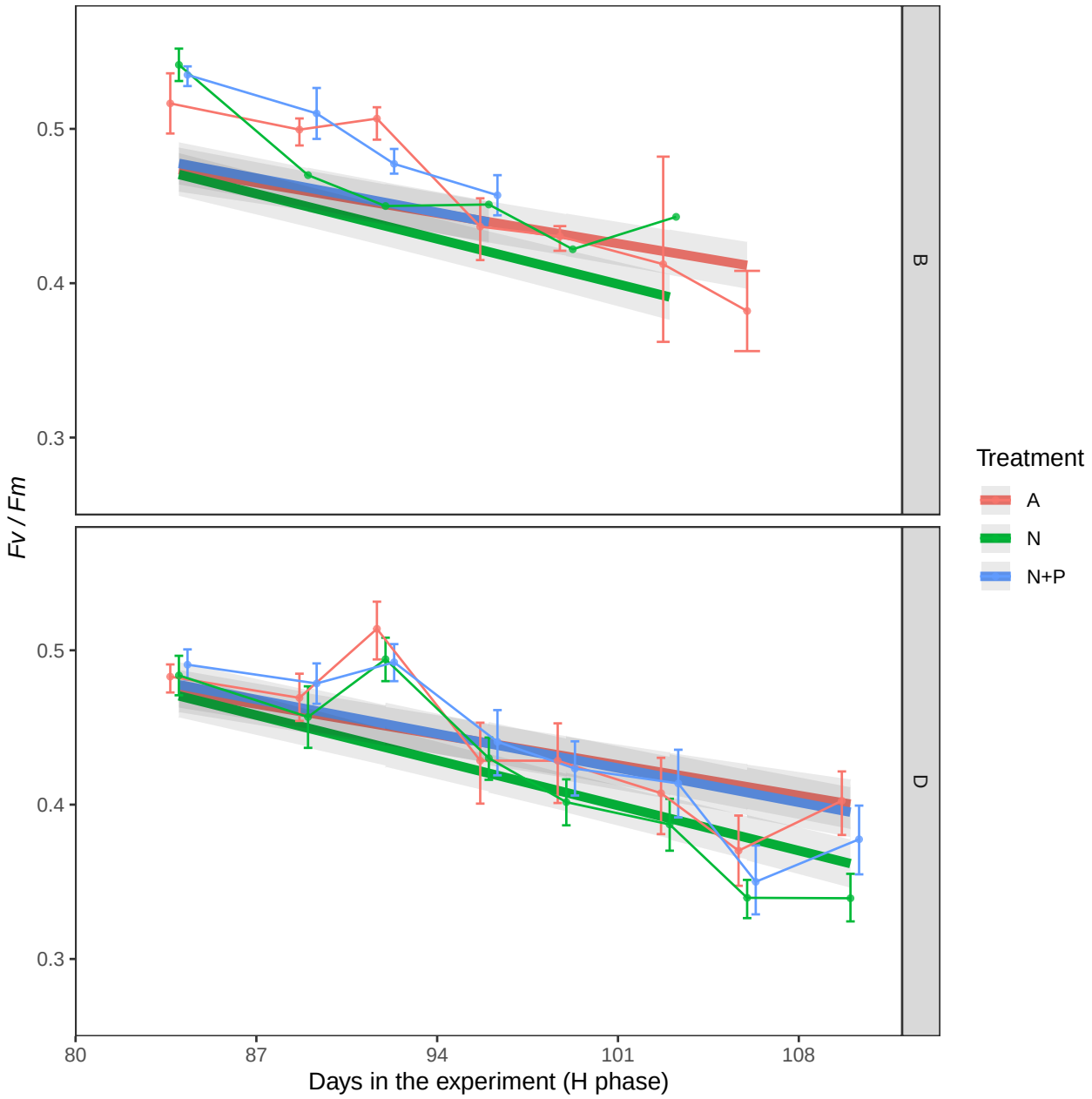
```
## (1 | Genotype)           3.407e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                Eliminated   Sum Sq   Mean Sq NumDF DenDF F value  Pr(>F)
## Treatment:Days          0 0.015625 0.0078127     2   390  5.0081 0.00712
##
## Treatment:Days **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment * Days + (1 | Genotype/Fragment)
```

```
# 2. Predict values:
    pred_Ofav.H <- predict(LME_Ofav.H1,re.form = NA)

#3. Bootstrap CI:
    OF.bootH <- bootMer(LME_Ofav.H1, predict, nsim = 1000, re.form = NULL) # include random effects, re
    std.err <- apply(OF.bootH$t, 2, sd)
    CI.lo_H <- pred_Ofav.H - std.err*1.96
    CI.hi_H <- pred_Ofav.H + std.err*1.96
```

```
 # 4 .Plot
  Model_of_H_plot<- ggplot(
    YII.Ofav.H, aes(x = Days, y = YII, colour = Treatment)) +
    geom_line(aes(y = pred_Ofav.H),size=2) +
    #geom_point(aes(fill=factor(Treatment)),
    #          shape = 21, colour = "black", size = 2, stroke = 0.3, alpha=0.3) +
    geom_ribbon(aes(ymin = CI.lo_H, ymax = CI.hi_H),
                size=2, alpha = 0.1, linetype = 0) +
    #scale_color_manual(values=my_colours) +
    #scale_fill_manual(values=my_colours) +
    scale_y_continuous(name=expression(~italic("Fv / Fm")),
                       limits = c(0.25, 0.58),
                       breaks = seq(0.3, 0.5, by=0.1), expand = c(0,0))+
    scale_x_continuous("Days in the experiment (H phase)", limits = c(80, 112),
                       breaks = seq(80, 110, by=7), expand = c(0,0))+

    stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                 position = position_dodge(1) )+
    stat_summary(fun.y=mean, geom="line", position = position_dodge(1),
                 linetype=1, alpha=1) +
    stat_summary(fun.y=mean, geom="point", size =1,
                 position=position_dodge(width=1), alpha=0.8)  +
    ggthe_bw

  Model_of_H_plot
```




```
Model_of_H_plot+ facet_grid(InitialCommunity~.)
```



- Model for "Days" as factor (daysF 84-110)

```
# 1. Ofav- Days
    LME_Ofav.HF<-lmer(YII ~ Treatment * DaysF * Community +
                        (1|Genotype) + (1|Fragment) +(1|Replicate),
                         data=YII.Ofav.H, na.action=na.omit)
      lmerTest::step (LME_Ofav.HF) # Replicate is not significant
```

```
## Backward reduced random-effect table:
##
##                  Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                        49 740.58 -1383.2
## (1 | Replicate)           1   48 740.58 -1385.2  0.000  1   1.000000
## (1 | Genotype)            0   47 735.75 -1377.5  9.650  1   0.001894 **
## (1 | Fragment)            0   47 715.64 -1337.3 49.865  1  1.647e-12 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                           Eliminated   Sum Sq   Mean Sq NumDF  DenDF
## Treatment:DaysF:Community          1 0.001743 0.0002179     8 330.04
## Treatment:Community                2 0.000134 0.0000672     2 110.06
## Treatment:DaysF                    0 0.033700 0.0021062    16 330.20
## DaysF:Community                    0 0.047109 0.0067299     7 336.98
##                           F value    Pr(>F)
## Treatment:DaysF:Community  0.3417    0.9492
## Treatment:Community        0.1071    0.8986
## Treatment:DaysF            3.3619 1.663e-05 ***
## DaysF:Community           10.7421 3.153e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + DaysF + Community + (1 | Genotype) + (1 | Fragment) +
##     Treatment:DaysF + DaysF:Community
```

```
ranova(LME_Ofav.HF)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + DaysF + Community + (1 | Genotype) + (1 | Fragment) +
##     (1 | Replicate) + Treatment:DaysF + Treatment:Community +
##     DaysF:Community + Treatment:DaysF:Community
##                  npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>             49 740.58 -1383.2
## (1 | Genotype)     48 735.75 -1375.5  9.649  1   0.001894 **
## (1 | Fragment)     48 715.64 -1335.3 49.865  1  1.647e-12 ***
## (1 | Replicate)    48 740.58 -1385.2  0.000  1   1.000000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

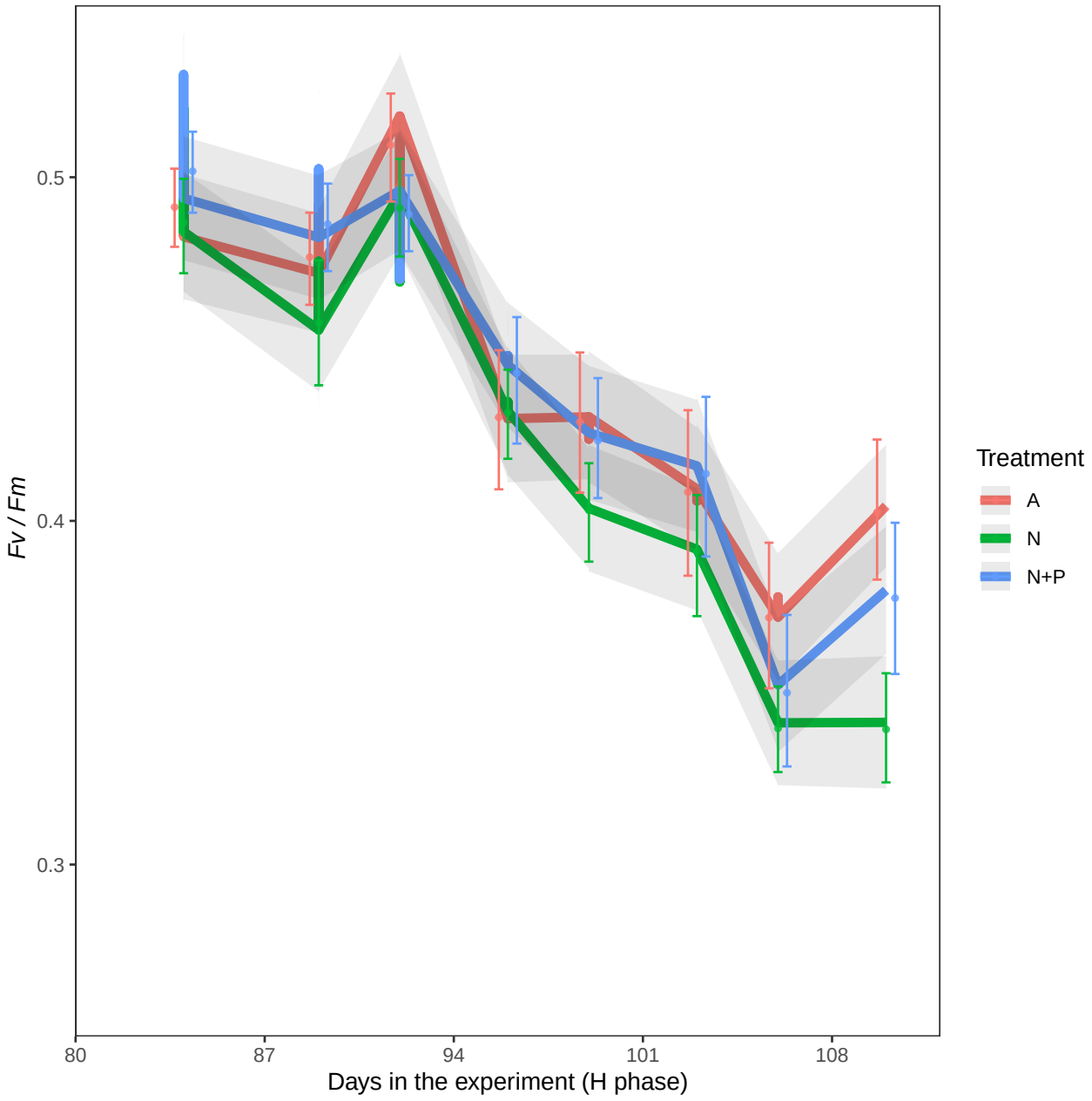
```
LME_Ofav.HF.1<-lmer(YII ~ Treatment + DaysF + Community +
                      (1 | Genotype) + (1 | Fragment) +
                      Treatment:DaysF + DaysF:Community,
                    data=YII.Ofav.H, na.action=na.omit)
lmerTest::step (LME_Ofav.HF.1)
```

```
## Backward reduced random-effect table:
##
##                Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                        38 767.61 -1459.2
## (1 | Genotype)          0   37 762.53 -1451.1 10.158  1   0.001437 **
## (1 | Fragment)          0   37 742.39 -1410.8 50.450  1  1.222e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
```

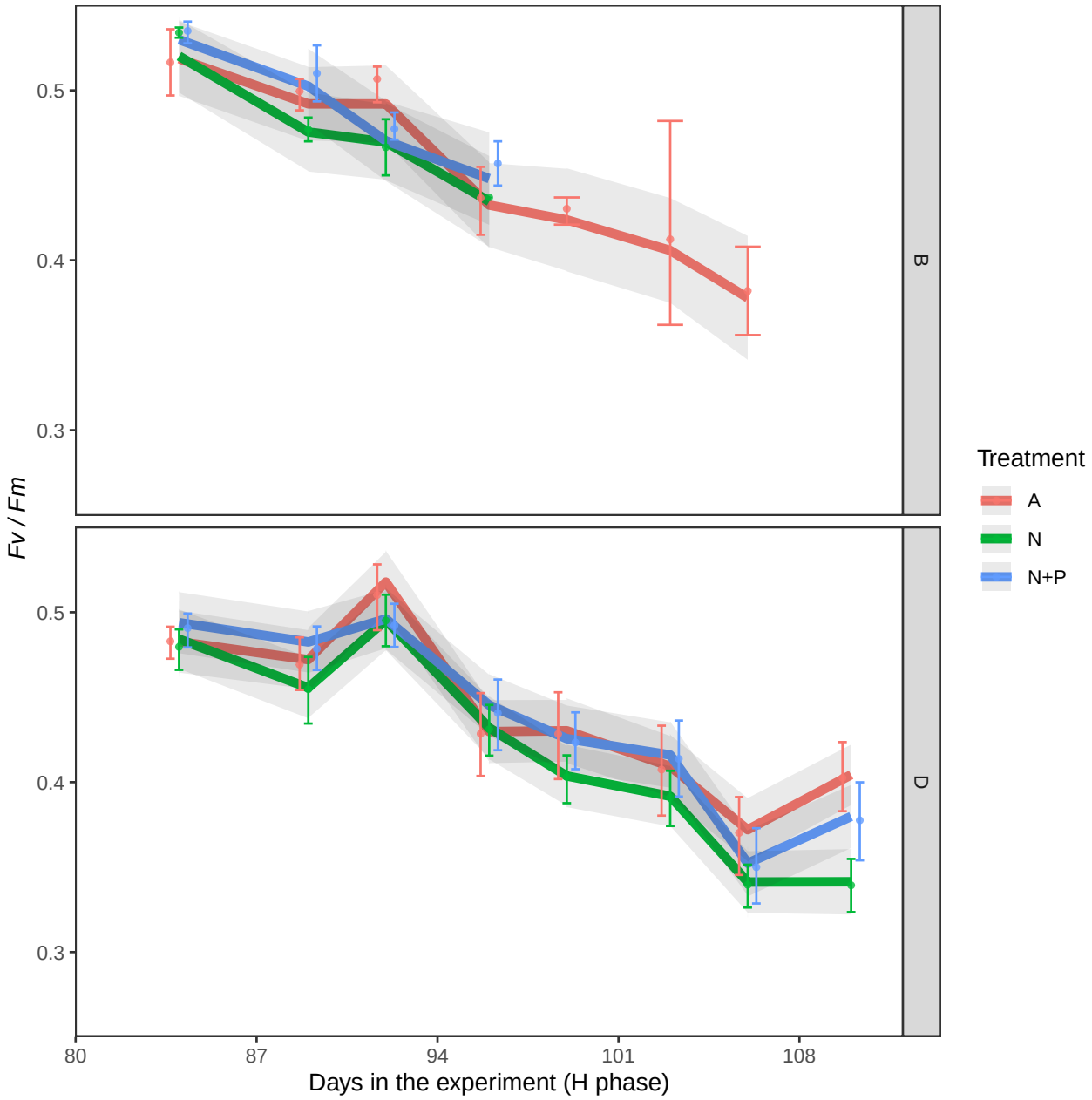
```
## Degrees of freedom method: Satterthwaite
##
##                  Eliminated   Sum Sq   Mean Sq NumDF  DenDF F value
## Treatment:DaysF           0 0.033700 0.0021062    16 330.20  3.3619
## DaysF:Community           0 0.047109 0.0067299     7 336.98 10.7421
##                     Pr(>F)
## Treatment:DaysF 1.663e-05 ***
## DaysF:Community 3.153e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + DaysF + Community + (1 | Genotype) + (1 | Fragment) +
##     Treatment:DaysF + DaysF:Community
```

```
# 2. Predict values:
    pred_OfavHF <- predict(LME_Ofav.HF.1,re.form = NA)

# 3. Bootstrap CI:
    OF.bootHF <- bootMer(LME_Ofav.HF.1, predict, nsim = 1000, re.form = NULL) # include random effects,
    std.err <- apply(OF.bootHF$t, 2, sd)
    CI.lo_HF <- pred_OfavHF - std.err*1.96
    CI.hi_HF <- pred_OfavHF + std.err*1.96
```

```
# 4. Plot
  Model_of_HF_plot<- ggplot(
    YII.Ofav.H, aes(x = Days, y = YII, colour = Treatment)) +
    geom_line(aes(y = pred_OfavHF),size=2) +
    #geom_point(aes(fill=factor(Treatment)),
    #         shape = 21, colour = "black", size = 2, stroke = 0.3, alpha=0.3) +
    geom_ribbon(aes(ymin = CI.lo_HF, ymax = CI.hi_HF),
                size=2, alpha = 0.1, linetype = 0) +
    #scale_color_manual(values=my_colours) +
    #scale_fill_manual(values=my_colours) +
    scale_y_continuous(name=expression(~italic("Fv / Fm")),
                       limits = c(0.25, 0.55),
                       breaks = seq(0.3, 0.5, by=0.1), expand = c(0,0))+
    scale_x_continuous("Days in the experiment (H phase)", limits = c(80, 112),
                      breaks = seq(80, 110, by=7), expand = c(0,0))+

    stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                 position = position_dodge(1) )+
    stat_summary(fun.y=mean, geom="point", size =1,
                 position=position_dodge(width=1), alpha=0.8)  +
    ggthe_bw

  Model_of_HF_plot
```




```
Model_of_HF_plot + facet_grid(Community~.)
```




```
# 5. EMMs
      Ofav.YII.emmH<-emmeans(LME_Ofav.HF.1, ~ Treatment:DaysF + DaysF:Community)
      #contrast(Ofav.YII.emmH, "tukey")

      Ofav.YII_groupsH<-cld(Ofav.YII.emmH, by=NULL) # compact-letter display
      Ofav.YII_groupsH<-Ofav.YII_groupsH[order(
        Ofav.YII_groupsH$Days,
        Ofav.YII_groupsH$Treatment,
        Ofav.YII_groupsH$Community),]
      Ofav.YII_groupsH
```

```
##    Treatment DaysF Community    emmean          SE         df  lower.CL
## 1          A    76         B 0.5210288 0.012613323  14.922875 0.4941321
## 28         A    76         D 0.4494904 0.008969100   8.301352 0.4289376
```

```
## 2          N    76         B 0.5295096 0.013007706  15.631647 0.5018816
## 29         N    76         D 0.4579712 0.008800041   8.009569 0.4376824
## 3        N+P    76         B 0.5232788 0.012613323  14.922875 0.4963821
## 30       N+P    76         D 0.4517404 0.008969100   8.301352 0.4311876
## 4          A    84         B 0.5186628 0.013724669  22.951364 0.4902678
## 31         A    84         D 0.4826724 0.009914445  12.542421 0.4611739
## 5          N    84         B 0.5201820 0.014320556  24.694535 0.4906698
## 32         N    84         D 0.4841917 0.009673596  11.904891 0.4630961
## 6        N+P    84         B 0.5298619 0.013724669  22.951364 0.5014670
## 33       N+P    84         D 0.4938716 0.009914445  12.542421 0.4723730
## 7          A    89         B 0.4920634 0.013865015  24.126731 0.4634553
## 34         A    89         D 0.4721222 0.009936118  12.667539 0.4505991
## 8          N    89         B 0.4755140 0.014866327  29.266376 0.4451210
## 35         N    89         D 0.4555729 0.009768913  12.352852 0.4343555
## 9        N+P    89         B 0.5024500 0.013865015  24.126731 0.4738420
## 36       N+P    89         D 0.4825089 0.009936118  12.667539 0.4609858
## 10         A    92         B 0.4920256 0.014565528  30.097540 0.4622828
## 37         A    92         D 0.5177948 0.010026426  13.090243 0.4961491
## 11         N    92         B 0.4695689 0.015159517  34.160557 0.4387664
## 38         N    92         D 0.4953381 0.010042442  13.407324 0.4737096
## 12       N+P    92         B 0.4703263 0.014565528  30.097540 0.4405836
## 39       N+P    92         D 0.4960955 0.010026426  13.090243 0.4744499
## 13         A    96         B 0.4324907 0.015319807  36.099926 0.4014237
## 40         A    96         D 0.4297618 0.010098455  13.430016 0.4080162
## 14         N    96         B 0.4346908 0.016877692  45.294298 0.4007035
## 41         N    96         D 0.4319619 0.009838768  12.983667 0.4107038
## 15       N+P    96         B 0.4480812 0.015841033  41.485786 0.4161010
## 42       N+P    96         D 0.4453524 0.010141063  13.603811 0.4235424
## 16         A    99         B 0.4237945 0.018497075  68.141416 0.3868855
## 43         A    99         D 0.4302692 0.010433672  15.112609 0.4080448
## 17         N    99         B 0.3971821 0.022004291  96.180900 0.3535050
## 44         N    99         D 0.4036568 0.009717208  12.779601 0.3826272
## 18       N+P    99         B 0.4191579 0.021582125 113.878203 0.3764034
## 45       N+P    99         D 0.4256326 0.010690292  16.631937 0.4030400
## 19         A   103         B 0.4057945 0.018497075  68.141416 0.3688855
## 46         A   103         D 0.4092692 0.010433672  15.112609 0.3870448
## 20         N   103         B 0.3882535 0.022004291  96.180900 0.3445764
## 47         N   103         D 0.3917282 0.009717208  12.779601 0.3706986
## 21       N+P   103         B 0.4125216 0.021582125 113.878203 0.3697671
## 48       N+P   103         D 0.4159963 0.010690292  16.631937 0.3934037
## 22         A   106         B 0.3778894 0.021387686 110.660476 0.3355069
## 49         A   106         D 0.3720192 0.010433672  15.112609 0.3497948
## 23         N   106         B 0.3471057 0.024378618 139.625535 0.2989068
## 50         N   106         D 0.3412355 0.009961939  13.810328 0.3198417
## 24       N+P   106         B 0.3581393 0.024105590 154.871806 0.3105211
## 51       N+P   106         D 0.3522690 0.010690292  16.631937 0.3296764
## 25         A   110         B        NA          NA         NA        NA
## 52         A   110         D 0.4043525 0.010433672  15.112609 0.3821281
## 26         N   110         B        NA          NA         NA        NA
## 53         N   110         D 0.3413755 0.010270961  15.034314 0.3194879
## 27       N+P   110         B        NA          NA         NA        NA
## 54       N+P   110         D 0.3798145 0.010690292  16.631937 0.3572218
##     upper.CL
## 1  0.5479256
```

```
## 28 0.4700432
## 2  0.5571376
## 29 0.4782599
## 3  0.5501756
## 30 0.4722932
## 4  0.5470577
## 31 0.5041710
## 5  0.5496943
## 32 0.5052874
## 6  0.5582569
## 33 0.5153702
## 7  0.5206714
## 34 0.4936453
## 8  0.5059070
## 35 0.4767903
## 9  0.5310581
## 36 0.5040320
## 10 0.5217683
## 37 0.5394404
## 11 0.5003715
## 38 0.5169667
## 12 0.5000691
## 39 0.5177411
## 13 0.4635577
## 40 0.4515074
## 14 0.4686781
## 41 0.4532200
## 15 0.4800615
## 42 0.4671623
## 16 0.4607034
## 43 0.4524936
## 17 0.4408592
## 44 0.4246864
## 18 0.4619125
## 45 0.4482253
## 19 0.4427034
## 46 0.4314936
## 20 0.4319307
## 47 0.4127579
## 21 0.4552761
## 48 0.4385889
## 22 0.4202720
## 49 0.3942436
## 23 0.3953047
## 50 0.3626293
## 24 0.4057574
## 51 0.3748616
## 25        NA
## 52 0.4265769
## 26        NA
## 53 0.3632632
## 27        NA
## 54 0.4024071
##
```

```
## 1                                                                                                z0zAzBzCzDzEzFzGzI
## 28            AB      IJ LMN PQR TUVW YZ  cdefg i  lmnopq     w y
## 2                                                                                                                  zI
## 29                    IJ LMN PQR TUVW YZabcdefghi klmnopqrs   wxyz1        z6z7z8z9
## 3                                                                                          zB    zEzFzGzI
## 30                    IJ LMN PQR TUVW YZ  cdefg i  lmnopq     w y
## 4                                                                                  z6z7z8z9z0zAzBzCzDzEzFzGzI
## 31                           QR   V   Zab   f hijk m  p rstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzI
## 5                                                                                    z8z9z0zAzBzCzDzEzFzGzI
## 32                                V   Zab   f hijk m  p rstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzI
## 6                                                                                          zB    zEzFzGzI
## 33                                    ab     h jk      rstuv x z1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzI
## 7                                        e g i k   opq s uvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzI
## 34                       M  PQR  UV  YZabc ef hijklm op rstuvwxyz1z2z3    z6z7z8z9z0  zB  zD  zF  zI
## 8                          STUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzG
## 35                    IJ LMN PQR TUVW YZabcdefghi klmnopqrs   wxyz1        z6z7
## 9                                                          wxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzI
## 36                           QR   V   Zab   f hijk m  p rstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzI
## 10                              cdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzI
## 37                                                        z4z5          zA  zC  zE  zG
## 11                     KLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzG
## 38                                      j         tuv     z2z3z4z5        z0zAzBzCzDzEzFzGzI
## 12                     KLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5z6z7z8z9z0zA  zCzD
## 39                                       h jk      rstuv x z1z2z3z4z5z6z7z8z9z0zAzBzCzDzEzFzGzI
## 13     456 890ABCDEFGHIJKLMNOPQRSTUVWXYZabcd f h j lmn   r t
## 40      56  90ABC EFG IJKL NO   ST  WX     d  g      n  q
## 14     456 890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuv
## 41       6   0AB  E G IJKLMNOP  STU WXY   cde g    l no q
## 15             CDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3z4z5
## 42       6   0AB  E G IJKLMNOPQRSTUVWXYZ  cdefg i  lmnopq     w y
## 16    34567890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuv
## 43      56  90ABC EFG IJKL NO   ST  WX     d  g      n  q
## 17  1234567890ABCDEFGHIJKLMNOPQRSTUVWXYZab
## 44     456 890  CDEFGH
## 18  1234567890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz1z2z3
## 45      56  90ABC EFG IJKL NO   ST  WX     d  g      n  q
## 19  1234567890ABCDEFGHIJKLMNOPQRSTUVWXYZ
## 46     456 890  CDEFGH  K   O   S    X
## 20  1234567890ABCDEFGHIJKLMNOPQR
## 47    345 789   CD F H
## 21  1234567890ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuv
## 48     456 890ABCDEFGHIJKL NO   ST  WX
## 22  1234567890ABCDEFGHIJ
## 49  1234  78
## 23  1234567890AB
## 50  12
## 24  1234567890ABCDEFGHIJ
## 51  123   7
## 25
## 52     456 890  CDEFGH  K   O   S    X
## 26
## 53  12
## 27
## 54  1234  78     D   H
```

```
      #write.csv(Ofav.YII_groupsH, "Outputs/Multicomp_OfavYII_H.csv", row.names = F)
```

Ssid

- Model for "Days" as continous variable (days 84-110)

```
# 1. Ssid- Days
      LME_Ssid.H<-lmer(YII ~ Treatment * Days * InitialCommunity +
                         (1|Genotype) + (1|Fragment) +(1|Replicate),
                          data=YII.Ssid.H, na.action=na.omit)
      lmerTest::step (LME_Ssid.H) # Replicate is not significant
```

```
## Backward reduced random-effect table:
##
##                 Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                       22 1692.9 -3341.9
## (1 | Replicate)          1   21 1692.9 -3343.9 0.0000  1   1.000000
## (1 | Genotype)           0   20 1690.8 -3341.5 4.3147  1   0.037785 *
## (1 | Fragment)           0   20 1688.9 -3337.9 7.9765  1   0.004739 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                Eliminated   Sum Sq  Mean Sq NumDF DenDF
## Treatment:Days:InitialCommunity          0 0.043395 0.010849     4  1029
##                                F value    Pr(>F)
## Treatment:Days:InitialCommunity  4.6856 0.0009452 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + Days + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + Treatment:Days + Treatment:InitialCommunity +
##     Days:InitialCommunity + Treatment:Days:InitialCommunity
```

```
      ranova(LME_Ssid.H)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + Days + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + (1 | Replicate) + Treatment:Days + Treatment:InitialCommunity +
##     Days:InitialCommunity + Treatment:Days:InitialCommunity
##                 npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>            22 1692.9 -3341.9
## (1 | Genotype)    21 1690.8 -3339.5 4.3147  1   0.037785 *
## (1 | Fragment)    21 1688.9 -3335.9 7.9765  1   0.004739 **
## (1 | Replicate)   21 1692.9 -3343.9 0.0000  1   1.000000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
    LME_Ssid.H1<-lmer(YII ~ Treatment * Days * InitialCommunity +
                        (1 | Genotype/Fragment),
                      data=YII.Ssid.H, na.action=na.omit)
    lmerTest::step (LME_Ssid.H1)
```

```
## Backward reduced random-effect table:
##
##                          Eliminated npar logLik     AIC    LRT Df
## <none>                                21 1692.9 -3343.9
## (1 | Fragment:Genotype)          0   20 1688.9 -3337.9 7.9765  1
## (1 | Genotype)                   0   20 1690.8 -3341.5 4.3147  1
##                          Pr(>Chisq)
## <none>
## (1 | Fragment:Genotype)   0.004739 **
## (1 | Genotype)            0.037785 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                Eliminated   Sum Sq  Mean Sq NumDF DenDF
## Treatment:Days:InitialCommunity          0 0.043395 0.010849     4  1029
##                                F value    Pr(>F)
## Treatment:Days:InitialCommunity  4.6856 0.0009452 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment * Days * InitialCommunity + (1 | Genotype/Fragment)
```

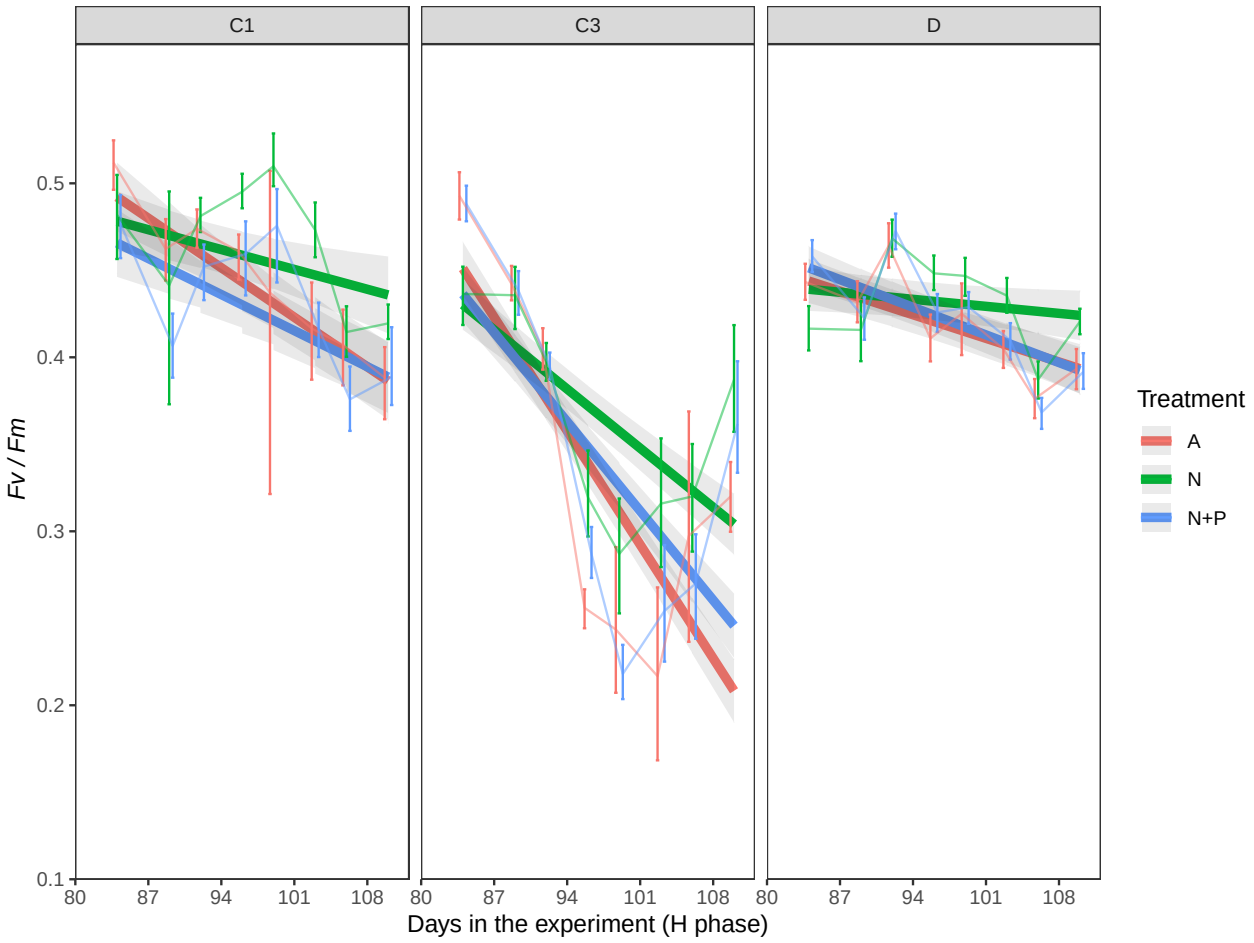
```
    anova(LME_Ssid.H1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                 Sum Sq Mean Sq NumDF   DenDF  F value
## Treatment                      0.11600 0.05800     2 1028.54  25.0508
## Days                           1.54813 1.54813     1 1031.59 668.6284
## InitialCommunity               0.53863 0.26932     2  592.49 116.3168
## Treatment:Days                 0.13358 0.06679     2 1030.56  28.8453
## Treatment:InitialCommunity     0.04043 0.01011     4 1028.02   4.3649
## Days:InitialCommunity          0.74822 0.37411     2 1029.91 161.5765
## Treatment:Days:InitialCommunity 0.04340 0.01085     4 1028.98   4.6856
##                                    Pr(>F)
## Treatment                      2.384e-11 ***
## Days                           < 2.2e-16 ***
## InitialCommunity               < 2.2e-16 ***
## Treatment:Days                 6.467e-13 ***
## Treatment:InitialCommunity     0.0016675 **
## Days:InitialCommunity          < 2.2e-16 ***
## Treatment:Days:InitialCommunity 0.0009452 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# 2. Predict values:
    pred_Ssid.H <- predict(LME_Ssid.H1,re.form = NA)
```

```r
#3. Bootstrap CI:
    Ss.bootH <- bootMer(LME_Ssid.H1, predict, nsim = 1000, re.form = NULL) # include random effects, re
    std.errSH <- apply(Ss.bootH$t, 2, sd)
    CI.lo_SH <- pred_Ssid.H - std.errSH*1.96
    CI.hi_SH <- pred_Ssid.H + std.errSH*1.96
```

```r
 # 4 .Plot
  Model_Ss_H_plot<- ggplot(
    YII.Ssid.H, aes(x = Days, y = YII, colour = Treatment)) +
    geom_line(aes(y = pred_Ssid.H),size=2) +
    #geom_point(aes(fill=factor(Treatment)),
    #          shape = 21, colour = "black", size = 2, stroke = 0.3, alpha=0.3) +
    geom_ribbon(aes(ymin = CI.lo_SH, ymax = CI.hi_SH),
                size=2, alpha = 0.1, linetype = 0) +
    #scale_color_manual(values=my_colours) +
    #scale_fill_manual(values=my_colours) +
    scale_y_continuous(name=expression(~italic("Fv / Fm")),
                       limits = c(0.1, 0.58),
                       breaks = seq(0.1, 0.5, by=0.1), expand = c(0,0))+
    scale_x_continuous("Days in the experiment (H phase)", limits = c(80, 112),
                     breaks = seq(80, 110, by=7), expand = c(0,0))+

    stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                   position = position_dodge(1) )+
    stat_summary(fun.y=mean, geom="line", position = position_dodge(1),
                   linetype=1, alpha=0.5) +
    #stat_summary(fun.y=mean, geom="point", size =1,
    #               position=position_dodge(width=1), alpha=0.8)  +
    ggthe_bw

  Model_Ss_H_plot+ facet_grid(~InitialCommunity)
```



- Model for "Days" as factor (daysF 84-110)

```
# 1. Ssid- Days
      LME_Ssid.HF<-lmer(YII ~ Treatment * DaysF * InitialCommunity +
                        (1|Genotype) + (1|Fragment) +(1|Replicate),
                         data=YII.Ssid.H, na.action=na.omit)
      lmerTest::step (LME_Ssid.HF) # Replicate is not significant
```

```
## Backward reduced random-effect table:
##
##                  Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                        85 1885.7 -3601.5
## (1 | Replicate)           1   84 1885.7 -3603.5 -0.010  1     1.0000
## (1 | Genotype)            0   83 1883.2 -3600.3  5.153  1     0.0232 *
## (1 | Fragment)            0   83 1846.5 -3526.9 78.534  1     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                    Eliminated   Sum Sq   Mean Sq NumDF
## Treatment:DaysF:InitialCommunity            0 0.081998 0.0025624    32
##                                     DenDF F value   Pr(>F)
## Treatment:DaysF:InitialCommunity 929.23   2.275 8.27e-05 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment + DaysF + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + Treatment:DaysF + Treatment:InitialCommunity +
##     DaysF:InitialCommunity + Treatment:DaysF:InitialCommunity
```

```
ranova(LME_Ssid.HF)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## YII ~ Treatment + DaysF + InitialCommunity + (1 | Genotype) +
##     (1 | Fragment) + (1 | Replicate) + Treatment:DaysF + Treatment:InitialCommunity +
##     DaysF:InitialCommunity + Treatment:DaysF:InitialCommunity
##                  npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>             85 1885.7 -3601.5
## (1 | Genotype)     84 1883.2 -3598.3  5.144  1    0.02333 *
## (1 | Fragment)     84 1846.5 -3524.9 78.525  1    < 2e-16 ***
## (1 | Replicate)    84 1885.7 -3603.5 -0.010  1    1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
LME_Ssid.HF.1<-lmer(YII ~ Treatment * DaysF * InitialCommunity + (1 | Fragment),
                    data=YII.Ssid.H, na.action=na.omit)
lmerTest::step (LME_Ssid.HF.1)
```

```
## Backward reduced random-effect table:
##
##                Eliminated npar logLik     AIC    LRT Df Pr(>Chisq)
## <none>                     83 1883.2 -3600.3
## (1 | Fragment)          0   82 1835.2 -3506.5 95.807  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Backward reduced fixed-effect table:
## Degrees of freedom method: Satterthwaite
##
##                                  Eliminated   Sum Sq   Mean Sq NumDF
## Treatment:DaysF:InitialCommunity          0 0.081916 0.0025599    32
##                                   DenDF F value    Pr(>F)
## Treatment:DaysF:InitialCommunity 928.77  2.2693 8.706e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## YII ~ Treatment * DaysF * InitialCommunity + (1 | Fragment)
```

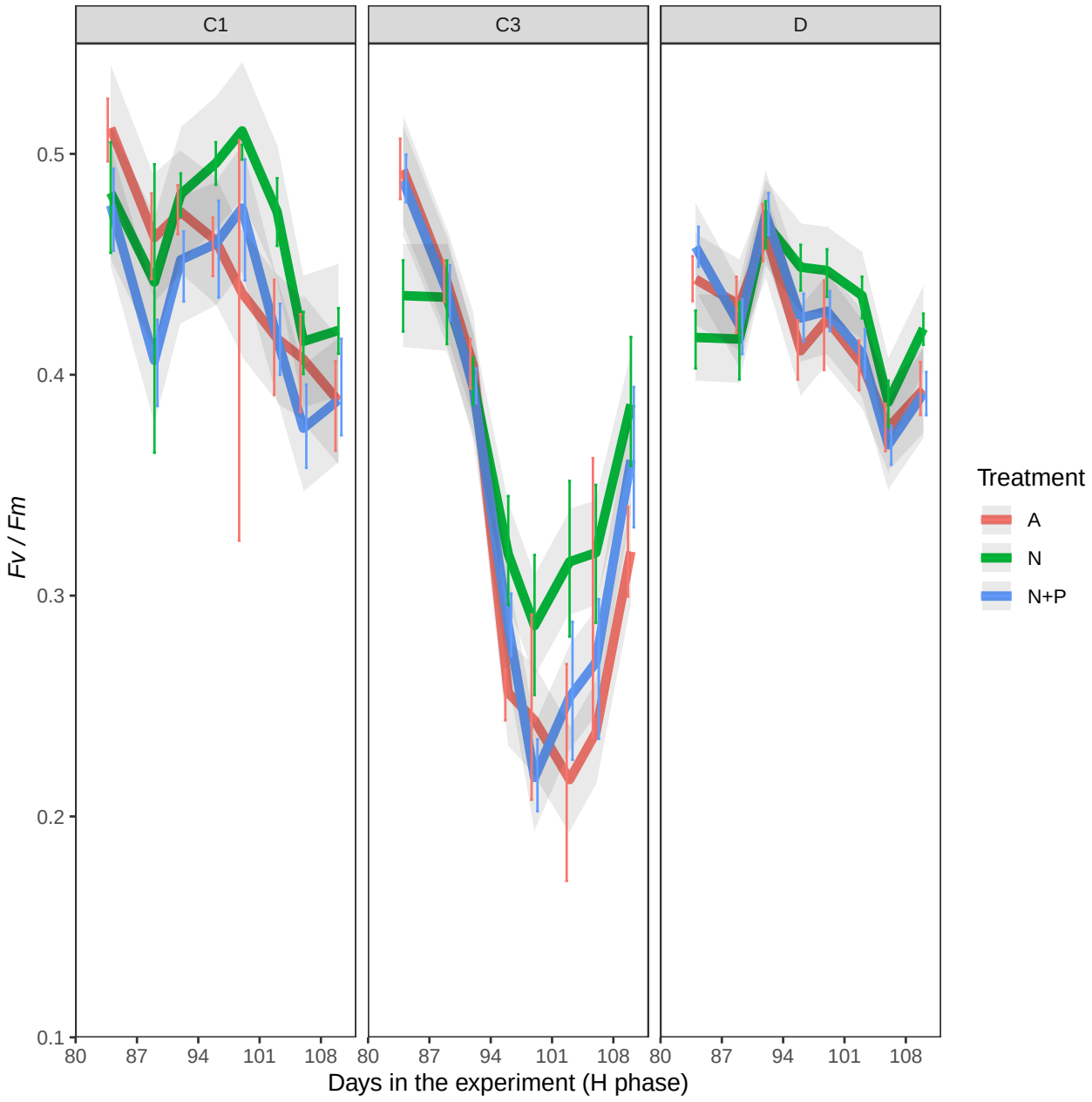
```
anova(LME_Ssid.HF.1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                                  Sum Sq  Mean Sq NumDF  DenDF  F value
## Treatment                       0.02021 0.010107     2 139.81   8.9593
## DaysF                           1.73159 0.216449     8 929.05 191.8792
## InitialCommunity                0.42229 0.211146     2 139.28 187.1781
```

```
## Treatment:DaysF                  0.18733 0.011708    16 929.05  10.3792
## Treatment:InitialCommunity       0.00816 0.002041     4 139.26   1.8093
## DaysF:InitialCommunity           1.59131 0.099457    16 928.78  88.1676
## Treatment:DaysF:InitialCommunity 0.08192 0.002560    32 928.77   2.2693
##                                     Pr(>F)
## Treatment                        0.0002182 ***
## DaysF                            < 2.2e-16 ***
## InitialCommunity                 < 2.2e-16 ***
## Treatment:DaysF                  < 2.2e-16 ***
## Treatment:InitialCommunity       0.1304012
## DaysF:InitialCommunity           < 2.2e-16 ***
## Treatment:DaysF:InitialCommunity 8.706e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# 2. Predict values:
    pred_SsidHF <- predict(LME_Ssid.HF.1,re.form = NA)

# 3. Bootstrap CI:
    Ss.bootHF <- bootMer(LME_Ssid.HF.1, predict, nsim = 1000, re.form = NULL) # include random effects,
    std.err <- apply(Ss.bootHF$t, 2, sd)
    CI.lo_HF.S <- pred_SsidHF - std.err*1.96
    CI.hi_HF.S <- pred_SsidHF + std.err*1.96
```

```
# 4. Plot
  Model_Ss_HF_plot<- ggplot(
    YII.Ssid.H, aes(x = Days, y = YII, colour = Treatment)) +
    geom_line(aes(y = pred_SsidHF),size=2) +
    #geom_point(aes(fill=factor(Treatment)),
    #         shape = 21, colour = "black", size = 2, stroke = 0.3, alpha=0.3) +
    geom_ribbon(aes(ymin = CI.lo_HF.S, ymax = CI.hi_HF.S),
                size=2, alpha = 0.1, linetype = 0) +
    #scale_color_manual(values=my_colours) +
    #scale_fill_manual(values=my_colours) +
    scale_y_continuous(name=expression(~italic("Fv / Fm")),
                       limits = c(0.1, 0.55),
                       breaks = seq(0.1, 0.5, by=0.1), expand = c(0,0))+
    scale_x_continuous("Days in the experiment (H phase)", limits = c(80, 112),
                     breaks = seq(80, 110, by=7), expand = c(0,0))+

    stat_summary(fun.data = "mean_cl_boot",geom = "errorbar", width = 1,
                   position = position_dodge(1) )+
    #stat_summary(fun.y=mean, geom="point", size =1,
    #               position=position_dodge(width=1), alpha=0.8)  +
    ggthe_bw

  Model_Ss_HF_plot + facet_grid(~InitialCommunity)
```




```
# 5. EMMs
    Ssid.YII.emmH<-emmeans(LME_Ssid.HF.1, ~ Treatment*DaysF*InitialCommunity)
      #contrast(Ssid.YII.emmH, "tukey")

      Ssid.YII_groupsH<-cld(Ssid.YII.emmH, by=NULL) # compact-letter display
      Ssid.YII_groupsH<-Ssid.YII_groupsH[order(
        Ssid.YII_groupsH$Days,
        Ssid.YII_groupsH$Treatment,
        Ssid.YII_groupsH$InitialCommunity),]
      Ssid.YII_groupsH
```

```
##    Treatment DaysF InitialCommunity    emmean          SE       df
## 1          A    76               C1 0.5231000 0.011848713 804.2337
## 28         A    76               C3 0.5261333 0.009674433 804.2337
```

```
## 55         A    76              D 0.4450000 0.007080960 804.2337
## 2          N    76             C1 0.4925556 0.012489640 804.2337
## 29         N    76             C3 0.4863125 0.009367230 804.2337
## 56         N    76              D 0.4404333 0.006840857 804.2337
## 3        N+P    76             C1 0.4958000 0.011848713 804.2337
## 30       N+P    76             C3 0.4945333 0.009674433 804.2337
## 57       N+P    76              D 0.4525357 0.007080960 804.2337
## 4          A    84             C1 0.5117084 0.014084168 862.8882
## 31         A    84             C3 0.4927729 0.011242188 856.4291
## 58         A    84              D 0.4432483 0.008138997 853.1904
## 5          N    84             C1 0.4824338 0.015203280 869.3190
## 32         N    84             C3 0.4358231 0.010766881 853.1904
## 59         N    84              D 0.4168966 0.007779468 849.9462
## 6        N+P    84             C1 0.4767617 0.014084168 862.8882
## 33       N+P    84             C3 0.4878222 0.011242188 856.4291
## 60       N+P    84              D 0.4578990 0.007957098 846.2325
## 7          A    89             C1 0.4621369 0.014084168 862.8882
## 34         A    89             C3 0.4421366 0.011242188 856.4291
## 61         A    89              D 0.4315816 0.008138997 853.1904
## 8          N    89             C1 0.4419338 0.015203280 869.3190
## 35         N    89             C3 0.4350731 0.010766881 853.1904
## 62         N    89              D 0.4161575 0.007779468 849.9462
## 9        N+P    89             C1 0.4064760 0.014084168 862.8882
## 36       N+P    89             C3 0.4379131 0.011242188 856.4291
## 63       N+P    89              D 0.4225354 0.007957098 846.2325
## 10         A    92             C1 0.4737084 0.014084168 862.8882
## 37         A    92             C3 0.4042275 0.011242188 856.4291
## 64         A    92              D 0.4640578 0.008138997 853.1904
## 11         N    92             C1 0.4817671 0.015203280 869.3190
## 38         N    92             C3 0.3967397 0.010766881 853.1904
## 65         N    92              D 0.4687662 0.007779468 849.9462
## 12       N+P    92             C1 0.4520474 0.014084168 862.8882
## 39       N+P    92             C3 0.3942767 0.011242188 856.4291
## 66       N+P    92              D 0.4725809 0.007957098 846.2325
## 13         A    96             C1 0.4607084 0.014084168 862.8882
## 40         A    96             C3 0.2559547 0.011242188 856.4291
## 67         A    96              D 0.4108673 0.008138997 853.1904
## 14         N    96             C1 0.4957671 0.015203280 869.3190
## 41         N    96             C3 0.3188231 0.010766881 853.1904
## 68         N    96              D 0.4486792 0.007779468 849.9462
## 15       N+P    96             C1 0.4593331 0.014084168 862.8882
## 42       N+P    96             C3 0.2864585 0.011242188 856.4291
## 69       N+P    96              D 0.4257172 0.007957098 846.2325
## 16         A    99             C1 0.4369941 0.014084168 862.8882
## 43         A    99             C3 0.2435002 0.011242188 856.4291
## 70         A    99              D 0.4250102 0.008138997 853.1904
## 17         N    99             C1 0.5104338 0.015203280 869.3190
## 44         N    99             C3 0.2864064 0.010766881 853.1904
## 71         N    99              D 0.4472010 0.007779468 849.9462
## 18       N+P    99             C1 0.4754760 0.014084168 862.8882
## 45       N+P    99             C3 0.2176403 0.011242188 856.4291
## 72       N+P    99              D 0.4287627 0.007957098 846.2325
## 19         A   103             C1 0.4164226 0.014084168 862.8882
## 46         A   103             C3 0.2166820 0.011242188 856.4291
```

```
## 73         A   103              D 0.4047721 0.008138997 853.1904
## 20         N   103             C1 0.4737671 0.015203280 869.3190
## 47         N   103             C3 0.3153231 0.010766881 853.1904
## 74         N   103              D 0.4358531 0.007779468 849.9462
## 21       N+P   103             C1 0.4164760 0.014084168 862.8882
## 48       N+P   103             C3 0.2539131 0.011242188 856.4291
## 75       N+P   103              D 0.4096718 0.007957098 846.2325
## 22         A   106             C1 0.4069941 0.014084168 862.8882
## 49         A   106             C3 0.2379547 0.011242188 856.4291
## 76         A   106              D 0.3761054 0.008138997 853.1904
## 23         N   106             C1 0.4151004 0.015203280 869.3190
## 50         N   106             C3 0.3194064 0.010766881 853.1904
## 77         N   106              D 0.3876357 0.007779468 849.9462
## 24       N+P   106             C1 0.3757617 0.014084168 862.8882
## 51       N+P   106             C3 0.2697313 0.011242188 856.4291
## 78       N+P   106              D 0.3682627 0.007957098 846.2325
## 25         A   110             C1 0.3881369 0.014084168 862.8882
## 52         A   110             C3 0.3199547 0.011242188 856.4291
## 79         A   110              D 0.3932959 0.008138997 853.1904
## 26         N   110             C1 0.4201004 0.015203280 869.3190
## 53         N   110             C3 0.3865731 0.010766881 853.1904
## 80         N   110              D 0.4209401 0.007779468 849.9462
## 27       N+P   110             C1 0.3886188 0.014084168 862.8882
## 54       N+P   110             C3 0.3613676 0.011242188 856.4291
## 81       N+P   110              D 0.3915809 0.007957098 846.2325
##     lower.CL  upper.CL                                .group
## 1  0.4998419 0.5463581                                   bc
## 28 0.5071432 0.5451235                                    c
## 55 0.4311007 0.4588993          GHIJKLMNOPQRSTUVWXYZ
## 2  0.4680394 0.5170717                      TUVWXYZabc
## 29 0.4679254 0.5046996                   O  RS UVWXYZabc
## 56 0.4270053 0.4538614        B   FGHIJKLMNOPQRSTUVW Y
## 3  0.4725419 0.5190581                     S   WXYZabc
## 30 0.4755432 0.5135235                       X Zabc
## 57 0.4386364 0.4664351            H JKLMNOPQRSTUVWXYZa
## 4  0.4840651 0.5393516                           abc
## 31 0.4707075 0.5148384                     RS  VWXYZabc
## 58 0.4272735 0.4592231        B   FGHIJKLMNOPQRSTUVWXYZa
## 5  0.4525943 0.5122732             JKLMNOPQRSTUVWXYZabc
## 32 0.4146904 0.4569557       0ABCDEFGHIJKLMNOPQRSTUVWXYZ
## 59 0.4016274 0.4321658      890ABCDEFGHIJK
## 6  0.4491185 0.5044049           IJKLMNOPQRSTUVWXYZabc
## 33 0.4657567 0.5098876               NO  RSTUVWXYZabc
## 60 0.4422811 0.4735170            JKLMNOPQRSTUVWXYZa
## 7  0.4344937 0.4897802          GHIJKLMNOPQRSTUVWXYZabc
## 34 0.4200711 0.4642020       0ABCDEFGHIJKLMNOPQRSTUVWXYZa
## 61 0.4156068 0.4475564       0ABCDEFGHIJKLMN PQ  T
## 8  0.4120943 0.4717732      90ABCDEFGHIJKLMNOPQRSTUVWXYZab
## 35 0.4139404 0.4562057       0ABCDEFGHIJKLMNOPQRSTUVWXYZ
## 62 0.4008883 0.4314267      890ABCDEFGHIJ
## 9  0.3788327 0.4341192     7890ABCDEFGHIJKLM
## 36 0.4158476 0.4599785       0ABCDEFGHIJKLMNOPQRSTUVWXYZa
## 63 0.4069174 0.4381534      90ABCDEFGHIJKL
## 10 0.4460651 0.5013516           IJKLMNOPQRSTUVWXYZabc
```

```
## 37 0.3821620 0.4262929        7890ABCDEFGHIJ
## 64 0.4480830 0.4800326                    KLMNOPQRSTUVWXYZab
## 11 0.4519277 0.5116065                   IJKLMNOPQRSTUVWXYZabc
## 38 0.3756071 0.4178724        7890ABCDEFG
## 65 0.4534970 0.4840354                     LMNOPQRSTUVWXYZab
## 12 0.4244042 0.4796906             CDEFGHIJKLMNOPQRSTUVWXYZab
## 39 0.3722112 0.4163422        7890ABCDEFG
## 66 0.4569629 0.4881988                      MNOP RSTUVWXYZab
## 13 0.4330651 0.4883516               EFGHIJKLMNOPQRSTUVWXYZabc
## 40 0.2338893 0.2780202  123
## 67 0.3948925 0.4268421        7890ABCDEFGHIJ
## 14 0.4659277 0.5256065                       NOPQRSTUVWXYZabc
## 41 0.2976904 0.3399557    345
## 68 0.4334100 0.4639484                GHIJKLMNOPQRSTUVWXYZa
## 15 0.4316899 0.4869764              DEFGHIJKLMNOPQRSTUVWXYZabc
## 42 0.2643931 0.3085240   234
## 69 0.4100993 0.4413352          0ABCDEFGHIJKL    Q
## 16 0.4093508 0.4646373         890ABCDEFGHIJKLMNOPQRSTUVWXYZa
## 43 0.2214347 0.2655657  12
## 70 0.4090354 0.4409850          0ABCDEFGHIJKLM  PQ
## 17 0.4805943 0.5402732                                  YZabc
## 44 0.2652737 0.3075391   234
## 71 0.4319317 0.4624702                GHIJKLMNOPQRSTUVWXYZa
## 18 0.4478327 0.5031192                  IJKLMNOPQRSTUVWXYZabc
## 45 0.1955749 0.2397058  1
## 72 0.4131447 0.4443806          0ABCDEFGHIJKL    Q
## 19 0.3887794 0.4440659        7890ABCDEFGHIJKLMNOPQ  TU
## 46 0.1946166 0.2387475  1
## 73 0.3887973 0.4207469        7890ABCDEFG
## 20 0.4439277 0.5036065                  GHIJKLMNOPQRSTUVWXYZabc
## 47 0.2941904 0.3364557    345
## 74 0.4205839 0.4511224           AB DEFGHIJKLMNOPQR TUV
## 21 0.3888327 0.4441192        7890ABCDEFGHIJKLMNOPQ  TU
## 48 0.2318476 0.2759785  1234
## 75 0.3940538 0.4252897        7890ABCDEFG I
## 22 0.3793508 0.4346373        7890ABCDEFGHIJKLM
## 49 0.2158893 0.2600202  12
## 76 0.3601306 0.3920802      6789
## 23 0.3852610 0.4449398        7890ABCDEFGHIJKLMNOPQRS
## 50 0.2982737 0.3405391    3456
## 77 0.3723665 0.4029050        7890  C
## 24 0.3481185 0.4034049     567890AB
## 51 0.2476658 0.2917967  1234
## 78 0.3526447 0.3838806     567
## 25 0.3604937 0.4157802     567890ABCDEFGH
## 52 0.2978893 0.3420202    456
## 79 0.3773211 0.4092707        7890A CDE
## 26 0.3902610 0.4499398        7890ABCDEFGHIJKLMNOPQRSTUVWX
## 53 0.3654404 0.4077057        7890ABCDEF
## 80 0.4056709 0.4362093          90ABCDEFGHIJK
## 27 0.3609756 0.4162621      567890ABCDEFGH
## 54 0.3393021 0.3834331      5678
## 81 0.3759629 0.4071988        7890A CD
```

```
#write.csv(Ssid.YII_groupsH, "Outputs/Multicomp_SsidYIIH.csv", row.names = F)
```

Packages used

```
# Creates bibliography
#knitr::write_bib(c(.packages()), "packages.bib")
```


Arnold, Jeffrey B. 2019. *Ggthemes: Extra Themes, Scales and Geoms for 'Ggplot2'*. https://CRAN.R-project.org/package=ggthemes.

Bates, Douglas, and Martin Maechler. 2019. *Matrix: Sparse and Dense Matrix Classes and Methods*. https://CRAN.R-project.org/package=Matrix.

Bates, Douglas, Martin Maechler, Ben Bolker, and Steven Walker. 2019. *Lme4: Linear Mixed-Effects Models Using 'Eigen' and S4*. https://CRAN.R-project.org/package=lme4.

Fox, John, Sanford Weisberg, and Brad Price. 2018. *CarData: Companion to Applied Regression Data Sets*. https://CRAN.R-project.org/package=carData.

Fox, John, Sanford Weisberg, Brad Price, Michael Friendly, and Jangman Hong. 2019. *Effects: Effect Displays for Linear, Generalized Linear, and Other Models*. https://CRAN.R-project.org/package=effects.

Genz, Alan, Frank Bretz, Tetsuhisa Miwa, Xuefei Mi, and Torsten Hothorn. 2019. *Mvtnorm: Multivariate Normal and T Distributions*. https://CRAN.R-project.org/package=mvtnorm.

Gohel, David, Hadley Wickham, Lionel Henry, and Jeroen Ooms. 2019. *Gdtools: Utilities for Graphical Rendering*. https://CRAN.R-project.org/package=gdtools.

Henry, Lionel, and Hadley Wickham. 2019. *Purrr: Functional Programming Tools*. https://CRAN.R-project.org/package=purrr.

Hothorn, Torsten. 2019. *TH.data: TH's Data Archive*. https://CRAN.R-project.org/package=TH.data.

Hothorn, Torsten, Frank Bretz, and Peter Westfall. 2019. *Multcomp: Simultaneous Inference in General Parametric Models*. https://CRAN.R-project.org/package=multcomp.

Kuznetsova, Alexandra, Per Bruun Brockhoff, and Rune Haubo Bojesen Christensen. 2019. *LmerTest: Tests in Linear Mixed Effects Models*. https://CRAN.R-project.org/package=lmerTest.

Lenth, Russell. 2019. *Emmeans: Estimated Marginal Means, Aka Least-Squares Means*. https://CRAN.R-project.org/package=emmeans.

Müller, Kirill, and Hadley Wickham. 2019. *Tibble: Simple Data Frames*. https://CRAN.R-project.org/package=tibble.

R Core Team. 2020. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. https://www.R-project.org/.

Ripley, Brian. 2019. *MASS: Support Functions and Datasets for Venables and Ripley's Mass*. https://CRAN.R-project.org/package=MASS.

Therneau, Terry M. 2019. *Survival: Survival Analysis*. https://CRAN.R-project.org/package=survival.

Wickham, Hadley. 2017. *Tidyverse: Easily Install and Load the 'Tidyverse'*. https://CRAN.R-project.org/package=tidyverse.

———. 2019a. *Forcats: Tools for Working with Categorical Variables (Factors)*. https://CRAN.R-project.org/package=forcats.

———. 2019b. *Stringr: Simple, Consistent Wrappers for Common String Operations*. https://CRAN.

R-project.org/package=stringr.

Wickham, Hadley, and Lionel Henry. 2020. *Tidyr: Tidy Messy Data*. https://CRAN.R-project.org/package=tidyr.

Wickham, Hadley, Winston Chang, Lionel Henry, Thomas Lin Pedersen, Kohske Takahashi, Claus Wilke, Kara Woo, and Hiroaki Yutani. 2019. *Ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics*. https://CRAN.R-project.org/package=ggplot2.

Wickham, Hadley, Romain François, Lionel Henry, and Kirill Müller. 2019. *Dplyr: A Grammar of Data Manipulation*. https://CRAN.R-project.org/package=dplyr.

Wickham, Hadley, Jim Hester, and Romain Francois. 2018. *Readr: Read Rectangular Text Data*. https://CRAN.R-project.org/package=readr.