

# Experimental conditions

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## General project set-up

```
# Load all libraries and sources required to run the script
library(tidyverse)
library(ggthemes)
library(ggplot2)
library(plyr)
library(tidyr)

library(plotrix)
library(lme4)
library(lmerTest)
library(emmeans)
library(reshape2)

# Graphs
# Plots
MyTheme<-theme_bw() +
theme(legend.position="top",
      plot.background=element_blank(),
      #axis.text.x = element_text(angle = 90, vjust = 0.5),
      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(),
legend.title = element_blank(),
panel.background =element_rect(fill = NA,
                                color = "black"))

# Treatment colors
Treat_fill<-scale_fill_manual(values =
                              c("#2b83ba", "#003399",
                                "#d7191c", "#660000"))

Treat_colour<-scale_colour_manual(values =
                                   c("#2b83ba", "#003399",
                                     "#d7191c", "#660000"))

```

## 1. Temperature

```

# Data
Temp<-read.csv("Data/Temperature.csv", header = TRUE)
#summary(Temp)
Temp$Time<-as.POSIXct(Temp$Time, format="%m/%d/%Y %H:%M",
                      tz = "America/New_York" )
Temp<-Temp %>% filter(!between(Time, as.POSIXct('2023-05-18 08:50:00.00'),
                                as.POSIXct('2023-05-18 09:55:00.00'))

Temp <- gather(Temp, Tank, Temperature,
               Tank.1:Tank.8, factor_key=TRUE)
#Temp<-Temp[Temp$Tank!="Tank.6",]
#Temp<-Temp[Temp$Tank!="Tank.7",]
Temp<-Temp %>% mutate(Group =
                      case_when(Tank == "Tank.1" ~ "Control Temperature",
                                Tank == "Tank.2" ~ "High Temperature",
                                Tank == "Tank.3" ~ "High Temperature",
                                Tank == "Tank.4" ~ "Control Temperature",
                                Tank == "Tank.5" ~ "Control Temperature",
                                Tank == "Tank.6" ~ "Donor colonies",
                                Tank == "Tank.7" ~ "Donor colonies",
                                Tank == "Tank.8" ~ "High Temperature"))
Temp$Group<-factor(Temp$Group, levels = c("Control Temperature",
                                           "High Temperature",
                                           "Donor colonies"))

Temp<-Temp %>% mutate(Group2 =
                      case_when(Group == "Control Temperature" ~ "28 C",
                                Group == "High Temperature" ~ "31 C",
                                Group == "Donor colonies" ~ "Donor colonies"))

# Remove data from tank that had a sensor failed

```

```
Temp<-Temp %>% filter((Time<as.POSIXct('2023-06-02 00:50:00.00') |
                        Tank!="Tank.8"))
Temp$Date<-as.Date(Temp$Time)
Temp$Day<-as.numeric(difftime(Temp$Date,
                              as.Date("2023-05-01"), units="days"))
summary(Temp)
```

```
##           Time                Tank      Temperature
## Min.      :2023-05-02 07:00:00.00  Tank.1 :15290  Min.      :20.27
## 1st Qu.   :2023-05-14 21:10:00.00  Tank.2 :15290  1st Qu.   :28.01
## Median    :2023-05-27 12:05:00.00  Tank.3 :15290  Median    :28.04
## Mean      :2023-05-28 00:45:42.18  Tank.4 :15290  Mean      :28.94
## 3rd Qu.   :2023-06-10 01:56:15.00  Tank.5 :15290  3rd Qu.   :30.98
## Max.      :2023-06-24 10:45:00.00  Tank.6 :15290  Max.      :34.78
##                                     (Other):24124
##           Group      Group2      Date
## Control Temperature:45870  Length:115864  Min.      :2023-05-02
## High Temperature      :39414  Class :character  1st Qu.   :2023-05-15
## Donor colonies        :30580  Mode  :character  Median    :2023-05-27
##                                     Mean      :2023-05-27
##                                     3rd Qu.   :2023-06-10
##                                     Max.      :2023-06-24
##
##           Day
## Min.      : 1.0
## 1st Qu.   :14.0
## Median    :26.0
## Mean      :26.7
## 3rd Qu.   :40.0
## Max.      :54.0
##
```

Temperature conditions during the whole experiment

```
Temp_summary <- ddply (Temp[Temp$Day>0, ], .(Group2),
                      summarise,
                        meanT = mean (Temperature, na.rm = T),
                        sdT = sd (Temperature, na.rm = T),
                        seT = std.error (Temperature, na.rm = T))
Temp_summary
```

```
##           Group2  meanT      sdT      seT
## 1             28 C 27.98423 0.4356117 0.002033926
## 2             31 C 30.83019 0.7889764 0.003974100
## 3 Donor colonies 27.94829 0.4722004 0.002700273
```

Temperature conditions excluding ramp-up days

```
Temp_summary <- ddply (Temp[Temp$Day>5, ], .(Group2),
                      summarise,
                        meanT = mean (Temperature, na.rm = T),
                        sdT = sd (Temperature, na.rm = T),
```

```
seT = std.error (Temperature, na.rm = T))
Temp_summary
```

```
##           Group2    meanT      sdT      seT
## 1           28 C 28.00311 0.2793313 0.001363826
## 2           31 C 30.96296 0.4542417 0.002411102
## 3 Donor colonies 27.99300 0.2408386 0.001440161
```

## Plot temperature by tanks

Raw values

```
Temperature<- ggplot(Temp, aes (Time, Temperature)) +
  geom_jitter(aes(colour=Group), alpha=1, size=0.5)+
  # stat_summary(fun.data = "mean_cl_boot",
  #             geom = "errorbar", width = 0.2, color="black" )+
  # stat_summary(fun=mean, geom="point", color="black") +

  theme(legend.position = "bottom")+
  scale_y_continuous(limits = c(26, 32),
                    breaks = seq(0,32, 2),
                    # expand = c(0.01, 0.01),
                    name=("Temperature (C)")) +

  scale_x_datetime(breaks = "7 days",
                  date_labels = "%b %d",
                  limits = c(as.POSIXct("2023-05-02 12:30"),
                            as.POSIXct("2023-06-24 18:00")),
                  # expand = c(0.01, 0.01),
                  name=("Date")) +

  geom_vline(xintercept = as.POSIXct("2023-05-18"),
            linetype=2)+
  annotate("text", x = c(as.POSIXct("2023-05-13"), as.POSIXct("2023-06-12")), y = 27, label = "*")+

  MyTheme + facet_wrap(~Tank, ncol = 4)+
  #facet_wrap(~(fct_rev(Tank)), ncol = 4)+
  scale_colour_manual(
    values = c("#2b83ba", "#d7191c", "gray"))+
  theme(legend.position = "none")

#Temperature
```

Daily mean values by tank

```
Temperature<- ggplot(Temp, aes (Day, Temperature, colour=Group2)) +
  #geom_jitter(aes(colour=Group), alpha=1, size=0.5)+
  stat_summary(fun.data = "mean_cl_boot",
              geom = "errorbar", width = 0.2)+
  stat_summary(fun=mean, geom="line", alpha=0.8) +

  theme(legend.position = "bottom")+
```

```

scale_y_continuous(limits = c(27.3, 31.3),
  breaks = seq(0,32, 1),
  # expand = c(0.01, 0.01),
  name=expression(Temperature~(degree~C))) +
scale_x_continuous(breaks = seq(0, 51, 7),
  name=("Days in the experiment")) +

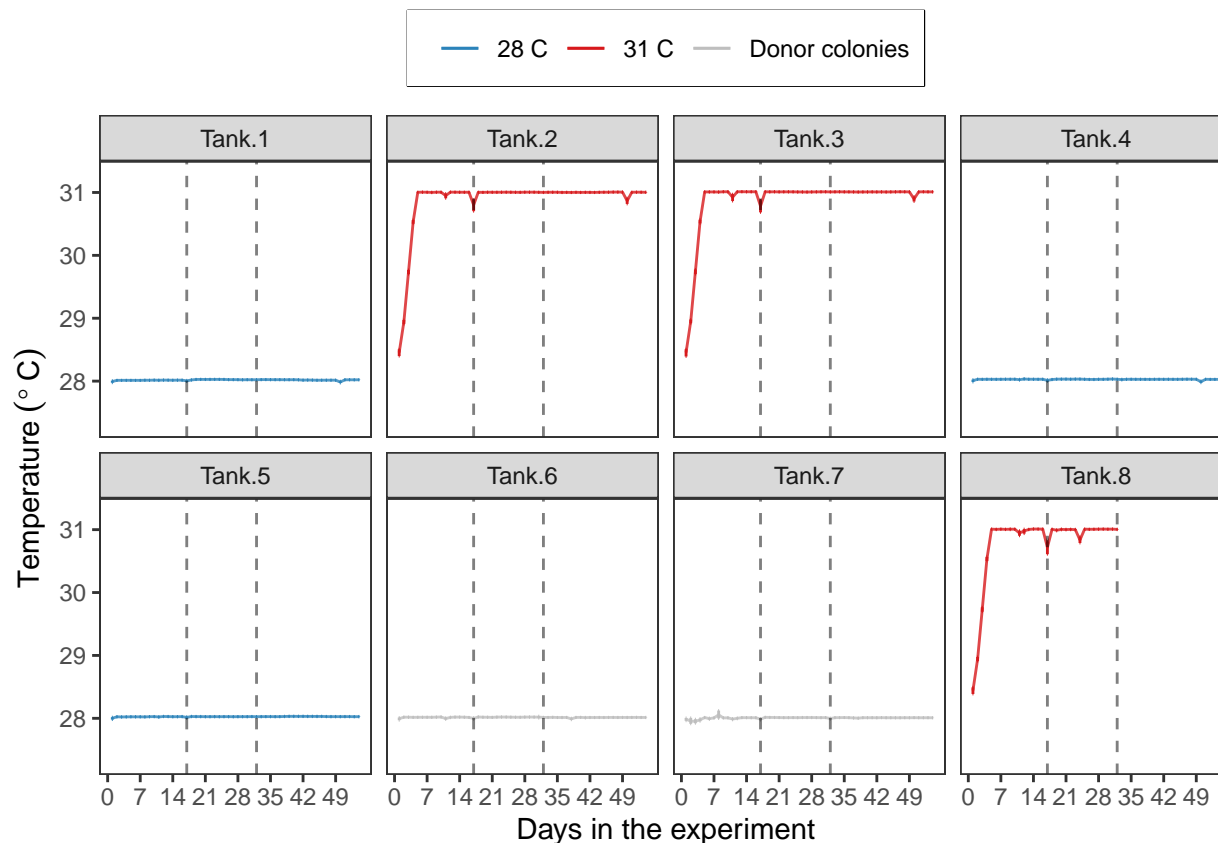
  # scale_x_date(breaks = "7 days",
  #               date_labels = "%b %d",
  #               limits = c(as.Date("2023-05-02"),
  #                           as.Date("2023-06-12")),
  #               # expand = c(0.01, 0.01),
  #               name=("Date")) +

#geom_vline(xintercept = as.Date(c("2023-05-18", "2023-06-02")),
#            linetype=2, alpha=0.5)+
# annotate("text", x = c(as.Date("2023-05-13"),
#                          as.Date("2023-06-02")), y = 27.5, label = "*")+
geom_vline(xintercept = c(17, 32),
  linetype=2, alpha=0.5)+

MyTheme + facet_wrap(~Tank, ncol = 4)+
#facet_wrap(~(fct_rev(Tank)), ncol = 4)+
scale_colour_manual(
  values = c("#2b83ba", "#d7191c", "gray"))+
theme(legend.position = "top")

```

Temperature



```
#ggsave(file="Outputs/Temperature.svg", plot=Temperature, width=8, height=4)
```

Daily mean values by treatment and experimental timeline

```
TimeLine<- ggplot(Temp, aes (Day, Temperature,
                             colour=Group2)) +
  #geom_jitter(aes(colour=Group), alpha=1, size=0.5)+
  stat_summary(fun.data = "mean_cl_boot",
               geom = "errorbar", width = 0.2)+
  stat_summary(fun=mean, geom="line", alpha=0.8) +

  theme(legend.position = "bottom")+
  scale_y_continuous(limits = c(27.3, 31.3),
                     breaks = seq(0,32, 1),
                     # expand = c(0.01, 0.01),
                     name=expression(Temperature~(degree~C))) +
  scale_x_continuous(breaks = seq(0, 51, 8),
                     name=("Days in the experiment")) +
  annotate("text", x = c(14, 31), y = 27.5, label = "*")+
  geom_vline(xintercept = c(1, 17, 32),
             linetype=2, alpha=0.5)+

  MyTheme + facet_wrap(~Group2, ncol = 1)+
  scale_colour_manual(
    values = c("#2b83ba", "#d7191c", "gray"))+
```

```

theme(legend.position = "top")

#TimeLine

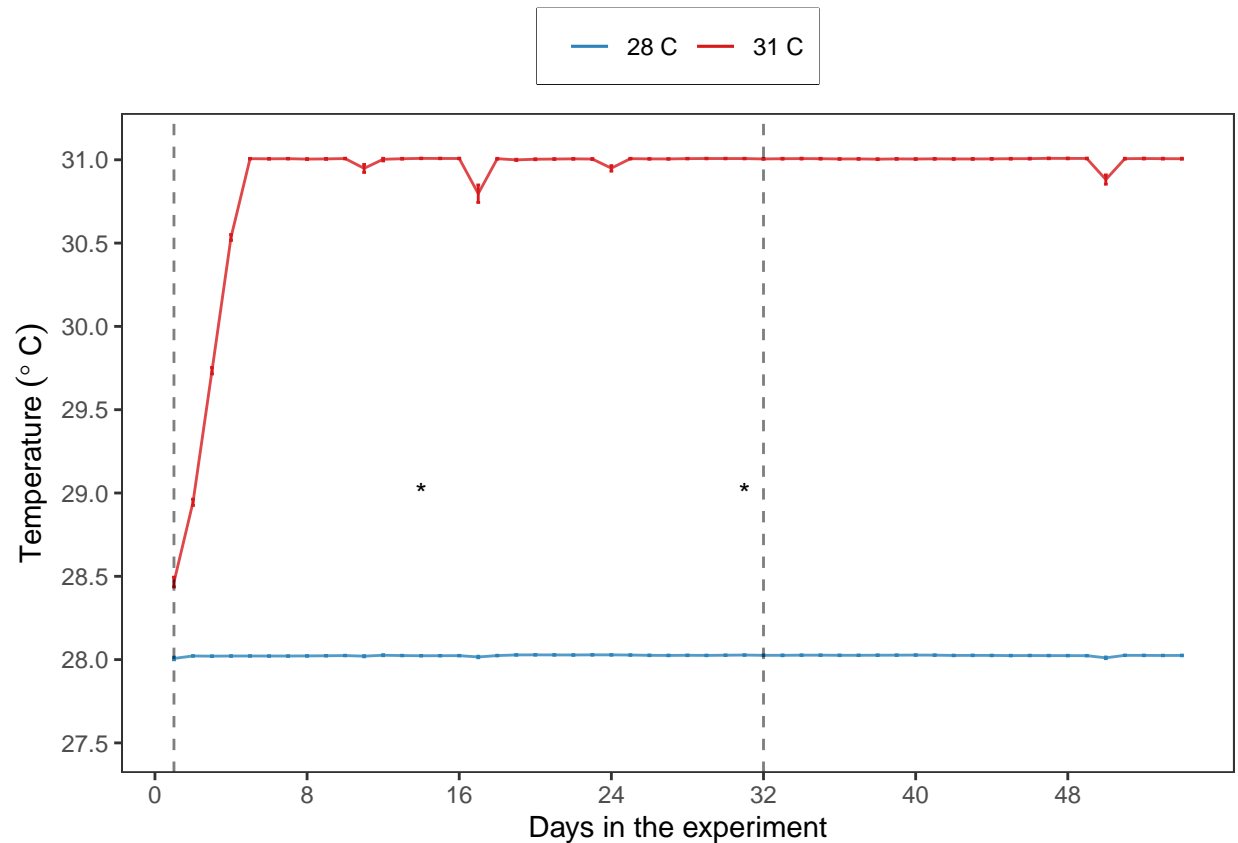
#ggsave(file="Outputs/TimeLine.svg", plot=TimeLine, width=4, height=6)

TimeLine2<- ggplot(Temp[Temp$Group!="Donor colonies", ],
  aes (Day, Temperature,
        colour=Group2)) +
  stat_summary(fun.data = "mean_cl_boot",
    geom = "errorbar", width = 0.2)+
  stat_summary(fun=mean, geom="line", alpha=0.8) +

  scale_y_continuous(limits = c(27.5, 31.1),
    breaks = seq(0,32, 0.5),
    # expand = c(0.01, 0.01),
    name=expression(Temperature~(degree~C))) +
  scale_x_continuous(breaks = seq(0, 51, 8),
    name=("Days in the experiment")) +
  annotate("text", x = c(14, 31), y = 29, label = "*")+
  geom_vline(xintercept = c(1, 32),
    linetype=2, alpha=0.5)+

  MyTheme +
  scale_colour_manual(
    values = c("#2b83ba", "#d7191c"))+
  theme(legend.position = "top")
TimeLine2

```



```
#ggsave(file="Outputs/TimeLine.svg", plot=TimeLine2, width=4, height=6)
```

## 2. Nutrients

```
# Data
data<-read.csv("Data/Nutrients.csv", header = TRUE)
#summary(data)
data$N<-as.numeric(data$N)
data$Date<-as.Date(data$Date)

library(lubridate)
data$Week<-isoweek(ymd(data$Date))
data$Week<-as.numeric(data$Week-17)

data$Target<-factor(data$Target,
                    levels=c("0", "5", "6"))
# data$Pump<-factor(data$Pump,
#                   levels=c("1", "2"))

data<-droplevels(data)
data$Treatment<-factor(data$Treatment,
                      levels = c ("LN_28", "LN_31", "HN_28", "HN_31",
                                   "Healthy", "Disease", "Stock", "VAT"))
```



```

data$Treatment3<-factor(paste(data$Nutrients,
                              data$Disease, sep = "_"))
data<-data[data$Date!="2023-05-18", ]
data$Day<-as.numeric(difftime(data$Date,
                              as.Date("2023-05-01"), units="days"))

summary(data)

```

```

##      Date      Time      Sample.ID      Sample
## Min.   :2023-05-02 Length:2261 Min.    : 1 Length:2261
## 1st Qu.:2023-05-10 Class :character 1st Qu.: 566 Class :character
## Median :2023-05-19 Mode  :character Median :1134 Mode  :character
## Mean   :2023-05-22          Mean   :1133
## 3rd Qu.:2023-06-05          3rd Qu.:1699
## Max.   :2023-06-22          Max.   :2264
##
##      Arm      Tank      Beaker      Pump
## Length:2261 Length:2261 Length:2261 Length:2261
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##      TP      Coral      Genotype      Colony
## Length:2261 Length:2261 Length:2261 Length:2261
## Class :character Class :character Class :character Class :character
## Mode  :character Mode  :character Mode  :character Mode  :character
##
##
##
##      Tag      Disease      Nutrients      Temp
## Min.   : 5.0 Length:2261 Length:2261 Min.   :28.00
## 1st Qu.:250.5 Class :character Class :character 1st Qu.:28.00
## Median :526.0 Mode  :character Mode  :character Median :28.00
## Mean   :467.5          Mean   :29.42
## 3rd Qu.:544.0          3rd Qu.:31.00
## Max.   :873.0          Max.   :31.00
## NA's   :562          NA's   :184
##      Treatment Treatment2 Target Beaker.conditions
## LN_28 :575 Length:2261 0:1153 Length:2261
## HN_28 :521 Class :character 5:1016 Class :character
## HN_31 :495 Mode  :character 6: 92 Mode  :character
## LN_31 :486
## Stock : 92
## VAT   : 46
## (Other): 46
##      Notes      NH4      NO2      N.N
## Length:2261 Min.   : 0.000 Min.   :0.0000 Min.   : 0.000
## Class :character 1st Qu.: 0.120 1st Qu.:0.0200 1st Qu.: 0.060
## Mode  :character Median : 0.370 Median :0.0700 Median : 0.300
##          Mean   : 1.430 Mean   :0.3217 Mean   : 1.381

```

```
##           3rd Qu.: 1.462    3rd Qu.:0.5700    3rd Qu.: 2.250
##           Max.      :60.030    Max.      :2.7900    Max.      :14.020
##           NA's      :17        NA's      :560      NA's      :560
##           NO3          PO4          N          Week
## Min.      :-0.01    Min.      :0.0000    Min.      : 0.000    Min.      :1.000
## 1st Qu.: 0.03    1st Qu.:0.0600    1st Qu.: 0.240    1st Qu.:2.000
## Median : 0.20    Median :0.1000    Median : 1.025    Median :3.000
## Mean      : 1.06    Mean      :0.3993    Mean      : 3.184    Mean      :3.825
## 3rd Qu.: 1.53    3rd Qu.:0.2550    3rd Qu.: 4.400    3rd Qu.:6.000
## Max.      :12.97    Max.      :4.9500    Max.      :212.630    Max.      :8.000
## NA's      :560      NA's      :560      NA's      :563
##           Treatment3      Day
## HN_Placebo      :230    Min.      : 1.00
## HN_SCTLD        :786    1st Qu.: 9.00
## LN_Placebo      :269    Median :18.00
## LN_SCTLD        :792    Mean      :21.77
## Other_Placebo   :161    3rd Qu.:35.00
## Other_SCTLD     : 23    Max.      :52.00
##
```

## Exploratory plots

```
NH4_plot<- ggplot(data, aes (Target, NH4)) +
  #geom_boxplot ()+
  geom_jitter(aes(colour=Arm, shape=Pump), alpha=1)+
  # stat_summary(fun.data = "mean_cl_boot",
  #              geom = "errorbar", width = 0.2, color="black" )+
  # stat_summary(fun=mean, geom="point", color="black") +
  #geom_point(shape=21)+

  theme(legend.position = "bottom")+
  scale_y_continuous(limits = c(0, 11),
                    breaks = seq(0,12, 2.5),
                    # expand = c(0.01, 0.01),
                    name=("NH4 [umol/L]")) +
  # geom_hline(yintercept = 4.1, linetype=2)+
  # geom_hline(yintercept = 0.3, linetype=2)+
  MyTheme +
  facet_grid(Beaker.conditions~Date, scales = "free_y")

#NH4_plot
```

```
NH4_genotype<- ggplot(data, aes (Date, NH4)) +
  geom_boxplot ()+
  geom_jitter(aes(colour=Genotype, shape=Arm), alpha=1)+
  # stat_summary(fun.data = "mean_cl_boot",
  #              geom = "errorbar", width = 0.2, color="black" )+
  # stat_summary(fun=mean, geom="point", color="black") +
  #geom_point(shape=21)+

  theme(legend.position = "bottom")+

```

```

scale_y_continuous(limits = c(0, 12),
                   breaks = seq(0,10, 1),
                   # expand = c(0.01, 0.01),
                   name=("NH4 [umol/L]")) +
# geom_hline(yintercept = 4.1, linetype=2)+
# geom_hline(yintercept = 0.3, linetype=2)+
MyTheme +
facet_wrap(Disease~Nutrients, scales = "free_y")
#NH4_genotype

```

```

NH4_Arms<- ggplot(data, aes (Day, NH4)) +
  #geom_boxplot ()+
  geom_jitter(aes(colour=Arm, shape=Beaker.conditions), alpha=1)+
  stat_summary(fun.data = "mean_cl_boot",
              geom = "errorbar", width = 0.2, color="black" )+
  stat_summary(fun=mean, geom="point", color="black") +
  #geom_point(shape=21)+

  theme(legend.position = "bottom")+
  geom_vline(xintercept = c(17, 32),
            linetype=2, alpha=0.5)+
  scale_x_continuous(limits = c(0, 55),
                    breaks = seq(0,55, 7),
                    # expand = c(0.01, 0.01),
                    name=("Days in the experiment")) +
  scale_y_continuous(limits = c(0, 15),
                    breaks = seq(0,20, 1),
                    # expand = c(0.01, 0.01),
                    name=("NH4 [umol/L]")) +
  # geom_hline(yintercept = 4.1, linetype=2)+
  # geom_hline(yintercept = 0.3, linetype=2)+
  MyTheme +
  facet_wrap(Disease~Nutrients)

#NH4_Arms

```

Remove VAT and stock solution values

```

NH4_Temp<- ggplot(data, aes (Day, NH4, fill=Treatment,
                             colour=Treatment,
                             shape=Beaker.conditions)) +

  #geom_jitter(aes(colour=Treatment, shape=Beaker.conditions),
  #alpha=1, size =1)+
  #geom_boxplot ()+
  scale_shape_manual(values=c(21, 22))+
  scale_color_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000",
                              '#CC9900', '#FF33FF', '#FF6600', '#999999'))+
  scale_fill_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000",
                              '#CC9900', '#FF33FF', '#FF6600', '#999999'))+

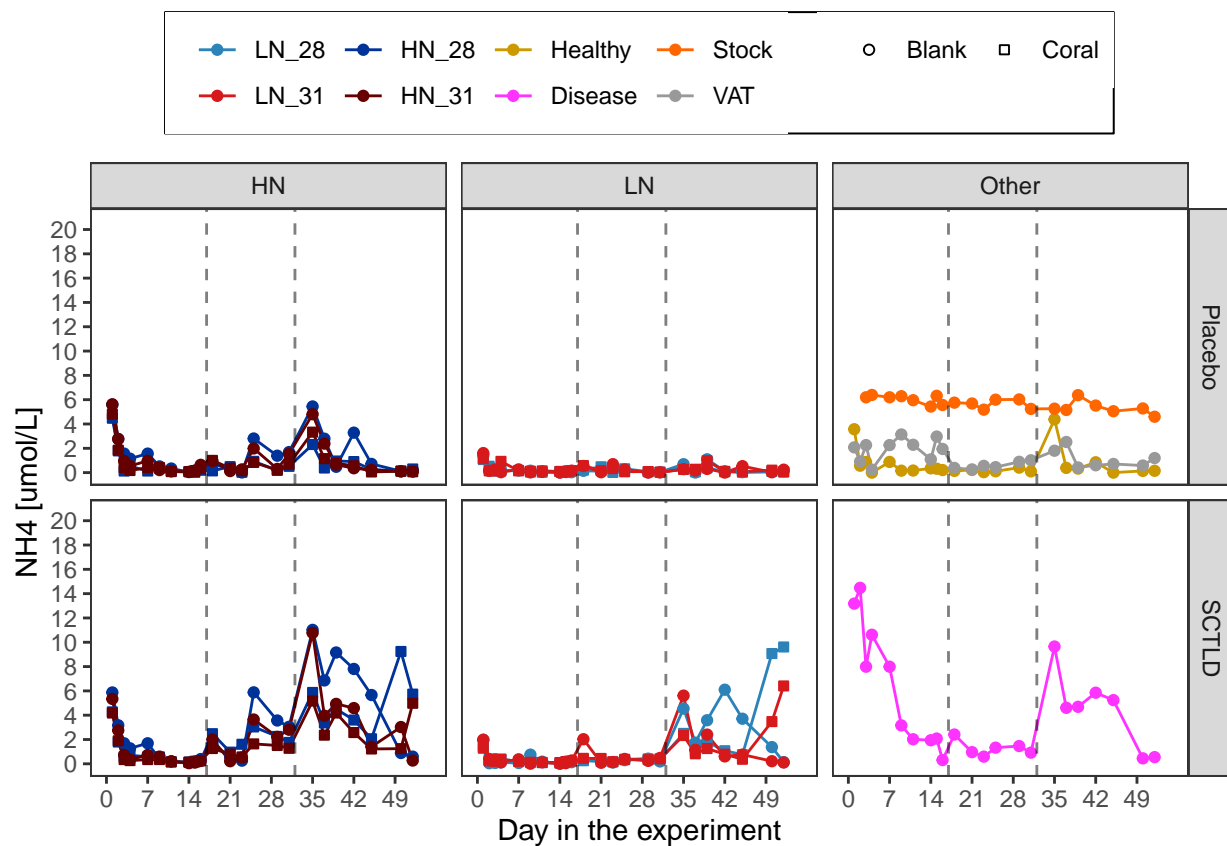
  # stat_summary(fun.data = "mean_cl_boot",
  #              geom = "errorbar", width = 0.2)+
  stat_summary(fun.data = "mean_cl_boot",

```

```

    geom = "line")+
stat_summary(fun=mean, geom="point") +
#geom_point(shape=21)+
    geom_vline(xintercept = c(17, 32),
               linetype=2, alpha=0.5)+
scale_x_continuous(limits = c(0, 55),
                   breaks = seq(0,55, 7),
                   # expand = c(0.01, 0.01),
                   name="Day in the experiment")) +
scale_y_continuous(#limits = c(0, 60),
                  breaks = seq(0, 20, 2),
                  # expand = c(0.01, 0.01),
                  name="NH4 [umol/L]")) +
# geom_hline(yintercept = 4.1, linetype=2)+
# geom_hline(yintercept = 0.3, linetype=2)+
#ylim()+
MyTheme
#NH4_Temp+facet_wrap(~Nutrients)
NH4_Temp+facet_grid(Disease~Nutrients)

```



```

NH4_W<- ggplot(data, aes (Week, NH4, fill=Treatment, colour=Treatment)) +

    geom_jitter(aes(colour=Treatment, shape=Beaker.conditions),
               alpha=1, size =1)+
    geom_boxplot(aes (Week, NH4, fill=Treatment, group=Week))+

```

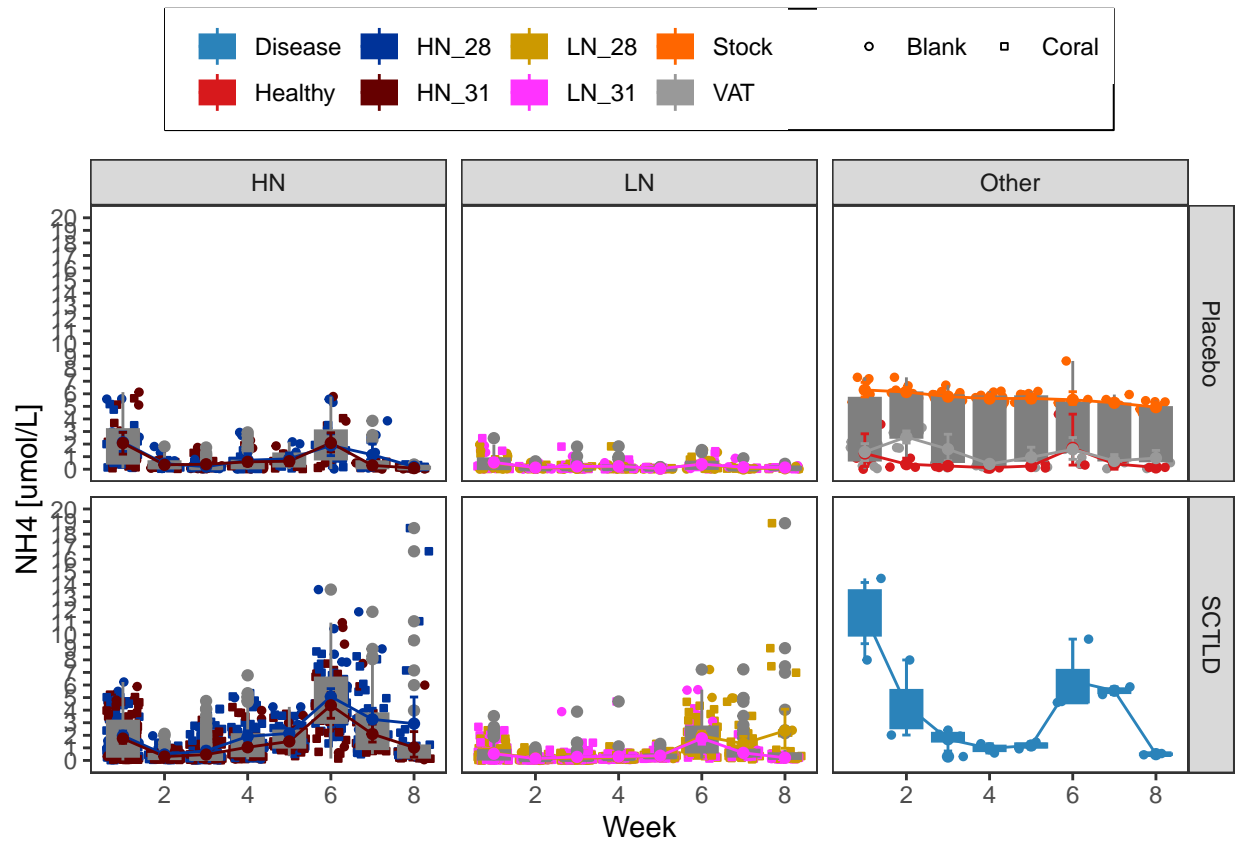
```

scale_shape_manual(values=c(21, 22))+
scale_color_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000",
                             '#CC9900', '#FF33FF', '#FF6600', '#999999'))+
scale_fill_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000",
                             '#CC9900', '#FF33FF', '#FF6600', '#999999'))+

stat_summary(fun.data = "mean_cl_boot",
             geom = "errorbar", width = 0.2)+
stat_summary(fun.data = "mean_cl_boot",
             geom = "line")+
stat_summary(fun=mean, geom="point") +
#geom_point(shape=21)+

theme(legend.position = "bottom")+
scale_y_continuous(limits = c(0, 20),
                   breaks = seq(0,20, 1),
                   # expand = c(0.01, 0.01),
                   name=("NH4 [umol/L]")) +
# geom_hline(yintercept = 4.1, linetype=2)+
# geom_hline(yintercept = 0.3, linetype=2)+
MyTheme
#NH4_Temp+facet_wrap(~Nutrients)
NH4_W+facet_grid(Disease~Nutrients)

```



Remove Stock solution, VAT and donor tank samples

```

Corals<-data[data$Nutrients!="Other", ]

Concentrations <- ddply (Corals, .(Treatment, Disease, Beaker.conditions, Nutrients, Day), summarise,
  meanNH4 = mean (NH4, na.rm = T),
  sdNH4 = sd (NH4, na.rm = T),
  seNH4 = std.error (NH4, na.rm = T))
#Concentrations

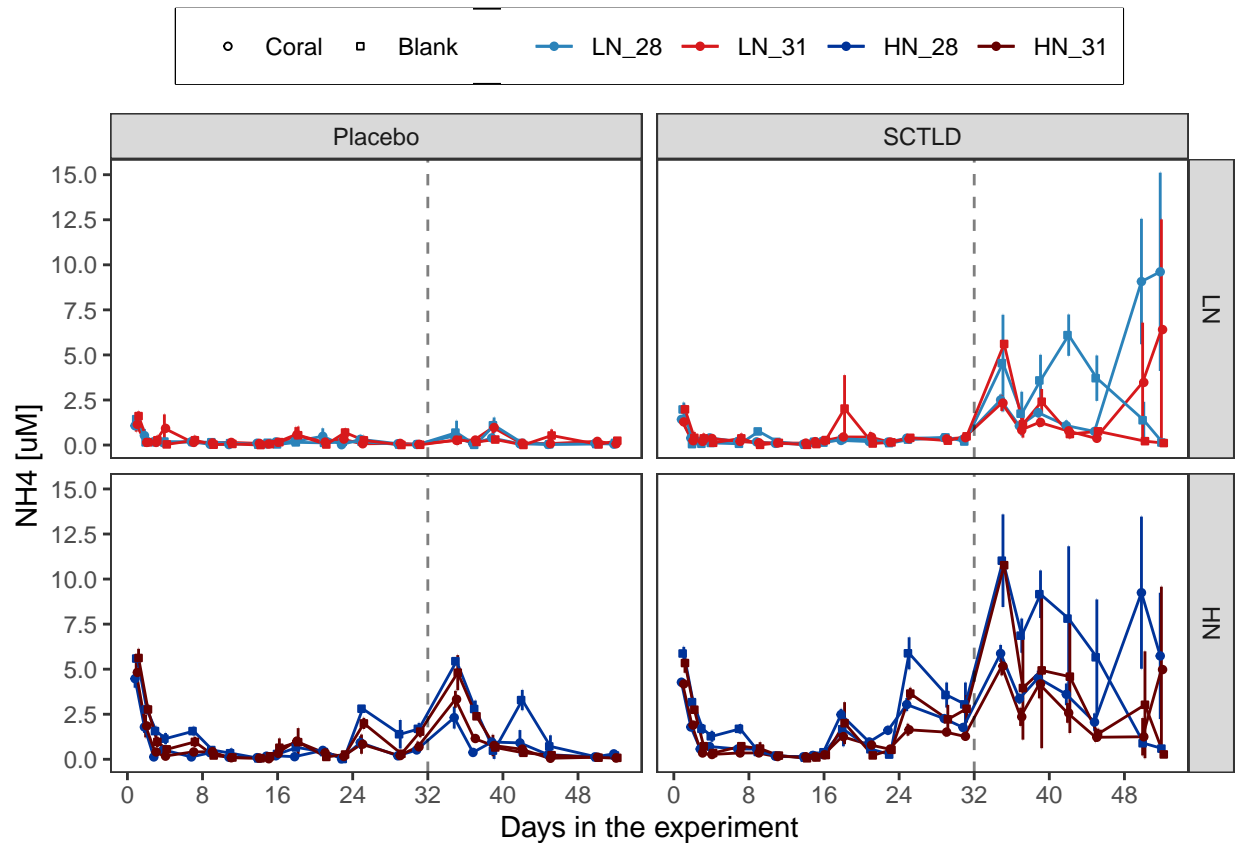
Concentrations$Beaker.conditions<-factor(Concentrations$Beaker.conditions,
  levels=c("Coral", "Blank"))
Concentrations$Nutrients<-factor(Concentrations$Nutrients,
  levels=c("LN", "HN"))

write.csv(Concentrations, "Outputs/Concentrations.csv")

# Standard error of the mean

NH4_day<-ggplot(Concentrations,
  aes(x=Day, y=(meanNH4), shape=Beaker.conditions,
    colour=Treatment)) +
  geom_errorbar(aes(ymin=(meanNH4-seNH4), ymax=(meanNH4+seNH4)),
    width=.1, position=position_dodge(0.5)) +
  geom_line(position=position_dodge(0.5)) +
  geom_point(position=position_dodge(0.5), aes(fill=Treatment), size=1)+
  scale_shape_manual(values=c(21, 22))+
  scale_color_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000"))+
  scale_fill_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000"))+
  geom_vline(xintercept = c(32),
    linetype=2, alpha=0.5)+
  scale_x_continuous(#limits = c(0, 55),
    breaks = seq(0,55, 8),
    # expand = c(0.01, 0.01),
    name=("Days in the experiment")) +
  scale_y_continuous(#limits = c(0, 60),
    breaks = seq(0, 35, 2.5),
    # expand = c(0.01, 0.01),
    name=("NH4 [uM]")) + MyTheme +
  facet_grid(Nutrients~Disease)
NH4_day

```



```
#ggsave(file="Outputs/Nutrients.svg", plot=NH4_day, width=7.5, height=5)
```

Remove empty beakers

```
Concentrations2 <- ddply (Corals[Corals$Beaker.conditions=="Coral", ],
  .(Treatment, Nutrients, Day),
  summarise,
    meanNH4 = mean (NH4, na.rm = T),
    sdNH4 = sd (NH4, na.rm = T),
    seNH4 = std.error (NH4, na.rm = T))
#Concentrations2

Concentrations2$Nutrients<-factor(Concentrations2$Nutrients,
  levels=c("LN", "HN"))

# Standard error of the mean

NH4_day<-ggplot(Concentrations2,
  aes(x=Day, y=(meanNH4),
    colour=Treatment)) +
  geom_errorbar(aes(ymin=(meanNH4-seNH4), ymax=(meanNH4+seNH4)),
    width=.1, position=position_dodge(0.5)) +
  geom_line(position=position_dodge(0.5)) +
  geom_point(position=position_dodge(0.5), aes(fill=Treatment), size=1)+
  scale_shape_manual(values=c(21, 22))+
```

```

scale_color_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000"))+
scale_fill_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000"))+
geom_vline(xintercept = c(1, 32),
           linetype=2, alpha=0.5)+
scale_x_continuous(#limits = c(0, 55),
                  breaks = seq(0,55, 8),
                  # expand = c(0.01, 0.01),
                  name="Days in the experiment")) +
scale_y_continuous(#limits = c(0, 60),
                  breaks = seq(0, 20, 2),
                  # expand = c(0.01, 0.01),
                  name="NH4 [uM]")) + MyTheme #+
#facet_grid(~Disease)
NH4_day

```

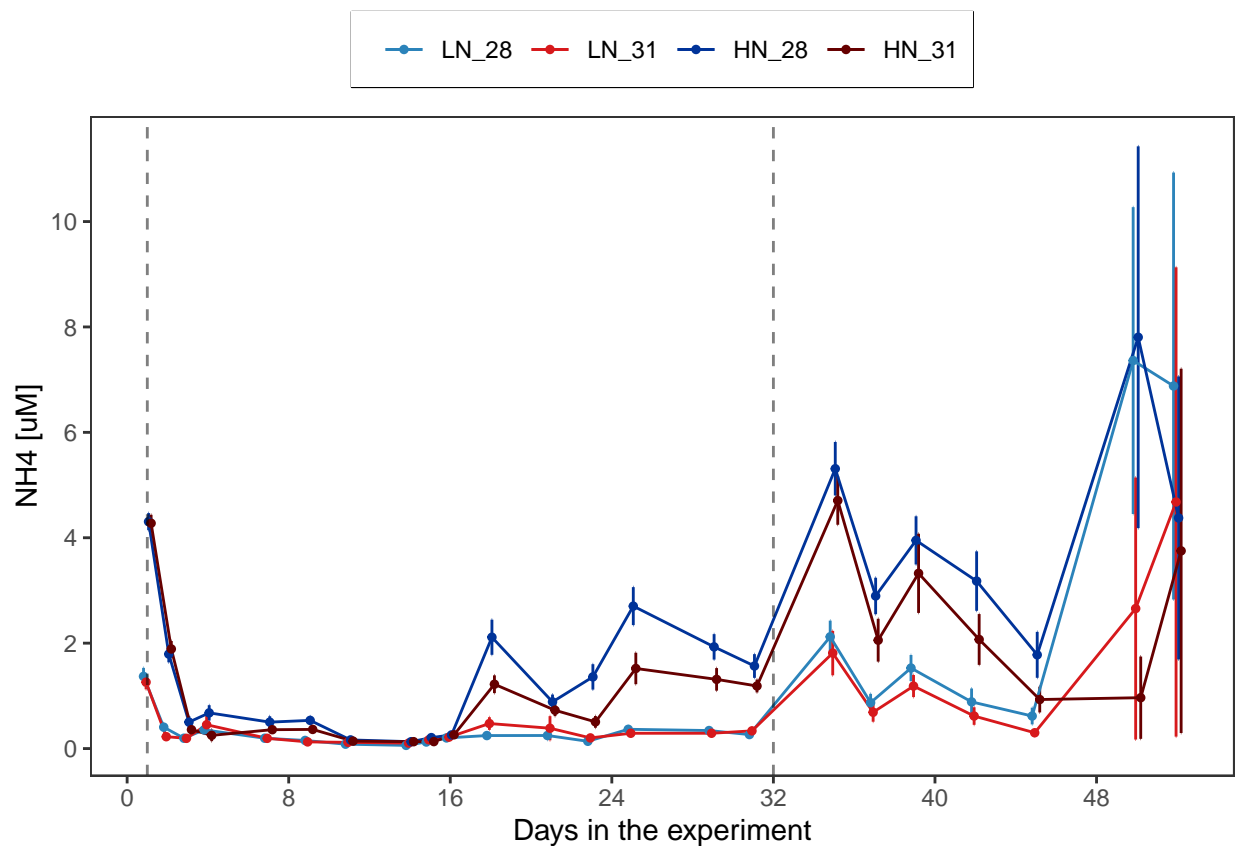


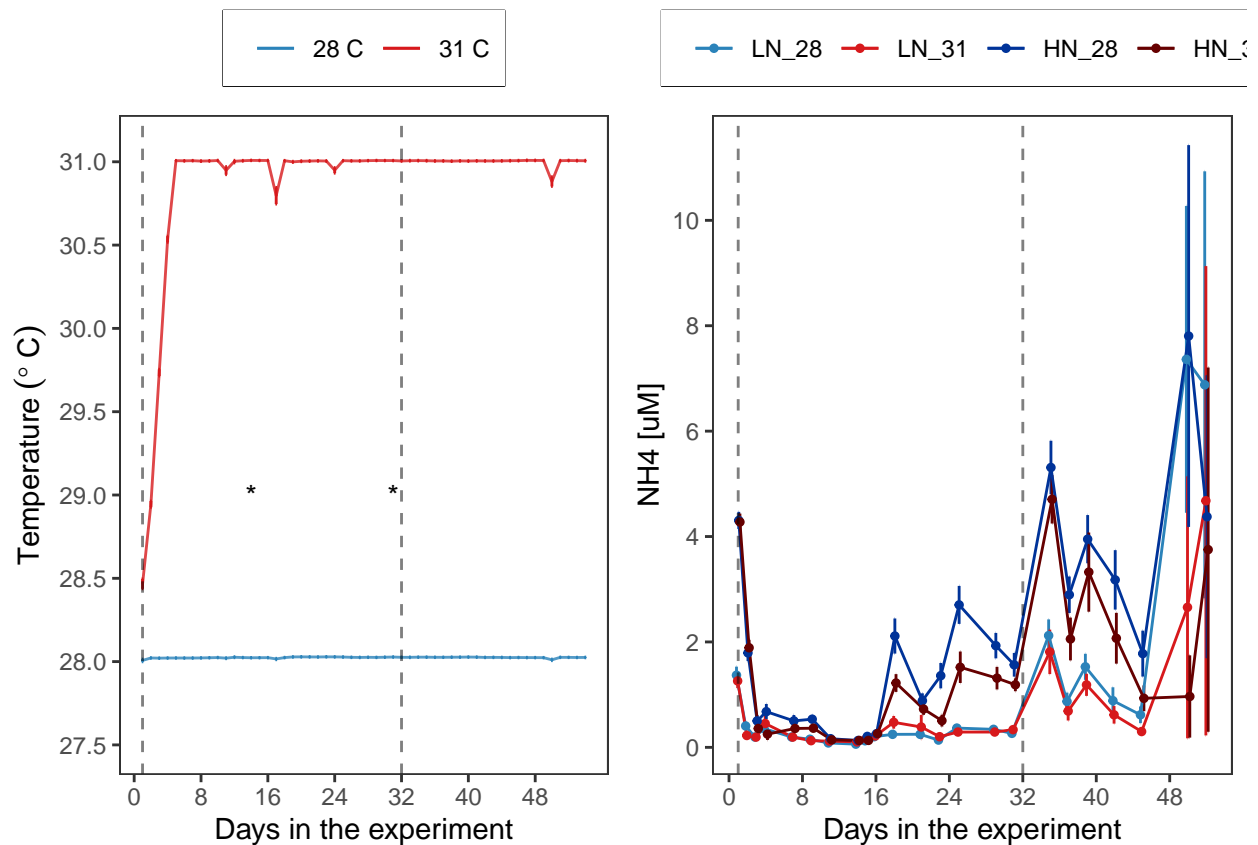
Figure: Experimental conditions

```

library(gridExtra)
experiment<-grid.arrange(TimeLine2, NH4_day, ncol = 2)

```





```
experiment
```

```
## TableGrob (1 x 2) "arrange": 2 grobs
##   z      cells   name      grob
## 1 1 (1-1,1-1) arrange gtable[layout]
## 2 2 (1-1,2-2) arrange gtable[layout]
```

```
#ggsave(file="Outputs/Experiment_conditions.svg", plot=experiment, width=8.5, height=4)
```

## Other figures

```
NH4_by_coral<- ggplot(Corals[Corals$Beaker.conditions=="Coral", ],
  aes (Day, NH4, fill=Treatment,
    colour=Treatment)) +

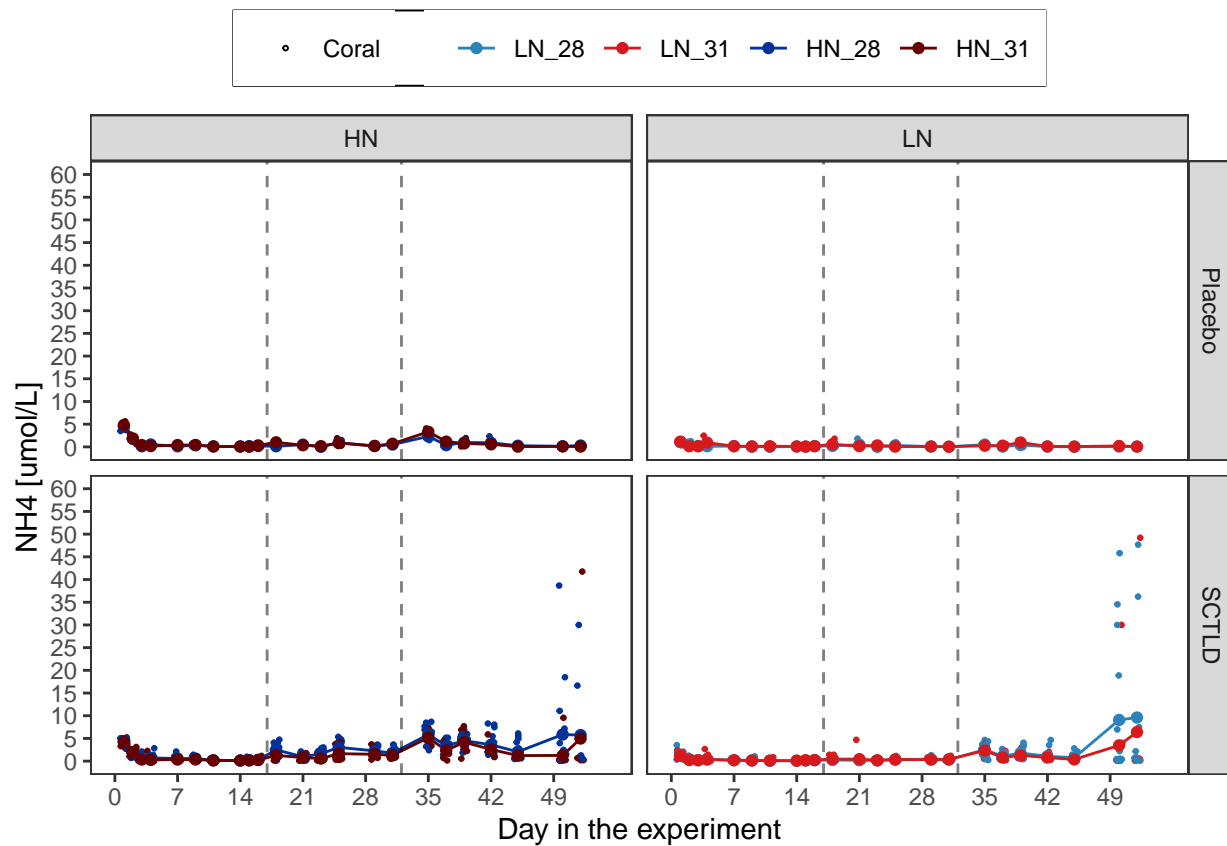
  geom_jitter(aes(colour=Treatment, shape=Beaker.conditions),
    alpha=1, size =0.5)+
  scale_shape_manual(values=c(21, 22))+
  scale_color_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000"))+
  scale_fill_manual(values=c("#2b83ba", "#d7191c", "#003399", "#660000"))+
  # stat_summary(fun.data = "mean_cl_boot",
  #             geom = "errorbar", width = 0.2)+
  stat_summary(fun.data = "mean_cl_boot",
```

```

    geom = "line")+
  stat_summary(fun=mean, geom="point") +
  #geom_point(shape=21)+
  geom_vline(xintercept = c(17, 32),
    linetype=2, alpha=0.5)+
  scale_x_continuous(limits = c(0, 55),
    breaks = seq(0,55, 7),
    # expand = c(0.01, 0.01),
    name="Day in the experiment")) +
  scale_y_continuous(limits = c(0, 60),
    breaks = seq(0, 60, 5),
    # expand = c(0.01, 0.01),
    name="NH4 [umol/L]") +

  MyTheme
#NH4_Temp+facet_wrap(~Nutrients)
NH4_by_coral+facet_grid(Disease~Nutrients)

```



```

Concentrations <- ddply (data, .(Nutrients, Disease, Date),
  summarise,
    meanNH4 = mean (NH4, na.rm = T),
    sdNH4 = sd (NH4, na.rm = T))
#Concentrations

Concentrations<-Concentrations %>%
  mutate_if(is.numeric, round, digits=2)

```

```

Concentrations_Day_Beaker <- ddply (data, .(Nutrients, Day, Beaker.conditions),
  summarise,
    meanNH4 = mean (NH4, na.rm = T),
    sdNH4 = sd (NH4, na.rm = T))
Concentrations_Day_Beaker

```

##	Nutrients	Day	Beaker.conditions	meanNH4	sdNH4
## 1	HN	1	Blank	5.6050000	0.48685580
## 2	HN	1	Coral	4.2902564	0.70357541
## 3	HN	2	Blank	2.8625000	0.29528437
## 4	HN	2	Coral	1.8423077	0.67117909
## 5	HN	3	Blank	1.2362500	0.50036951
## 6	HN	3	Coral	0.4279487	0.37932891
## 7	HN	4	Blank	0.8287500	0.48792381
## 8	HN	4	Coral	0.4587179	0.60078536
## 9	HN	7	Blank	1.2362500	0.50036951
## 10	HN	7	Coral	0.4279487	0.37932891
## 11	HN	9	Blank	0.4300000	0.26316752
## 12	HN	9	Coral	0.4466667	0.29381639
## 13	HN	11	Blank	0.2112500	0.18357073
## 14	HN	11	Coral	0.1521795	0.13800169
## 15	HN	14	Blank	0.0625000	0.02314550
## 16	HN	14	Coral	0.1303846	0.09637772
## 17	HN	15	Blank	0.1487500	0.10020515
## 18	HN	15	Coral	0.1678947	0.19496580
## 19	HN	16	Blank	0.3900000	0.33170555
## 20	HN	16	Coral	0.2602564	0.21599814
## 21	HN	18	Blank	1.3200000	1.07631647
## 22	HN	18	Coral	1.6548718	1.21934597
## 23	HN	21	Blank	0.3250000	0.29587642
## 24	HN	21	Coral	0.8043590	0.54990212
## 25	HN	23	Blank	0.2662500	0.26180350
## 26	HN	23	Coral	0.9221795	0.91281505
## 27	HN	25	Blank	3.5800000	1.64163681
## 28	HN	25	Coral	2.0961538	1.55516350
## 29	HN	29	Blank	1.8687500	1.45688942
## 30	HN	29	Coral	1.6133333	1.03921803
## 31	HN	31	Blank	2.2681250	1.07258678
## 32	HN	31	Coral	1.3721795	0.80108544
## 33	HN	35	Blank	8.0093750	3.42885491
## 34	HN	35	Coral	5.0762903	1.98945050
## 35	HN	37	Blank	3.9975000	2.48364795
## 36	HN	37	Coral	2.5706452	1.50530326
## 37	HN	39	Blank	3.8068750	4.52110048
## 38	HN	39	Coral	3.7082258	2.22852513
## 39	HN	42	Blank	4.0087500	3.95710730
## 40	HN	42	Coral	2.7490323	2.22416892
## 41	HN	45	Blank	2.0012500	2.89665047
## 42	HN	45	Coral	1.4501613	1.61399942
## 43	HN	50	Blank	1.0312500	2.03934470
## 44	HN	50	Coral	5.1574194	12.79517597
## 45	HN	52	Blank	0.2400000	0.19555050
## 46	HN	52	Coral	4.0637500	10.48866596

## 47	LN	1	Blank	1.6860000	0.42573335
## 48	LN	1	Coral	1.3176316	0.65252290
## 49	LN	2	Blank	0.1800000	0.22715633
## 50	LN	2	Coral	0.3179487	0.28889244
## 51	LN	3	Blank	0.2080000	0.27655821
## 52	LN	3	Coral	0.1951282	0.17187621
## 53	LN	4	Blank	0.1320000	0.18029605
## 54	LN	4	Coral	0.4025641	0.61046021
## 55	LN	7	Blank	0.2080000	0.27655821
## 56	LN	7	Coral	0.1951282	0.17187621
## 57	LN	9	Blank	0.2190000	0.32962774
## 58	LN	9	Coral	0.1405128	0.18085977
## 59	LN	11	Blank	0.1130000	0.07528465
## 60	LN	11	Coral	0.1003846	0.15404367
## 61	LN	14	Blank	0.0125000	0.01388730
## 62	LN	14	Coral	0.0804878	0.09655830
## 63	LN	15	Blank	0.1025000	0.07959720
## 64	LN	15	Coral	0.1439024	0.13947900
## 65	LN	16	Blank	0.1512500	0.12777631
## 66	LN	16	Coral	0.2092683	0.15289523
## 67	LN	18	Blank	0.7637500	1.29792073
## 68	LN	18	Coral	0.3580488	0.40511862
## 69	LN	21	Blank	0.1300000	0.12071217
## 70	LN	21	Coral	0.3150000	0.75952946
## 71	LN	23	Blank	0.2800000	0.30430248
## 72	LN	23	Coral	0.1691463	0.14956563
## 73	LN	25	Blank	0.2868750	0.16972536
## 74	LN	25	Coral	0.3290244	0.23026675
## 75	LN	29	Blank	0.1737500	0.18552532
## 76	LN	29	Coral	0.3167073	0.22899675
## 77	LN	31	Blank	0.1837500	0.21025070
## 78	LN	31	Coral	0.2997561	0.24228328
## 79	LN	35	Blank	2.7825000	2.90042731
## 80	LN	35	Coral	2.0084848	1.41056808
## 81	LN	37	Blank	0.7687500	1.07999256
## 82	LN	37	Coral	0.8048485	0.71313731
## 83	LN	39	Blank	1.8475000	1.60351177
## 84	LN	39	Coral	1.4034848	1.00651742
## 85	LN	42	Blank	1.7062500	2.79341413
## 86	LN	42	Coral	0.7880303	0.98959741
## 87	LN	45	Blank	1.2600000	1.68860889
## 88	LN	45	Coral	0.5019697	0.60870757
## 89	LN	50	Blank	0.4193750	0.81024880
## 90	LN	50	Coral	5.6512121	11.91667923
## 91	LN	52	Blank	0.1616667	0.09174239
## 92	LN	52	Coral	5.9112000	14.71519632
## 93	Other	1	Blank	5.2275000	5.34849745
## 94	Other	2	Blank	4.2200000	6.87828952
## 95	Other	3	Blank	4.5700000	2.78492370
## 96	Other	4	Blank	4.5837500	3.97196223
## 97	Other	7	Blank	4.5700000	2.78492370
## 98	Other	9	Blank	4.3425000	2.30303992
## 99	Other	11	Blank	3.8250000	2.40220732
## 100	Other	14	Blank	2.5566667	2.30242191

## 101	Other	15	Blank	3.8985714	2.82568829
## 102	Other	16	Blank	3.3325000	2.51078673
## 103	Other	18	Blank	2.9414286	2.74629101
## 104	Other	21	Blank	3.0556250	2.82506566
## 105	Other	23	Blank	2.8081250	2.54535422
## 106	Other	25	Blank	3.2937500	2.92201465
## 107	Other	29	Blank	3.4675000	2.77377386
## 108	Other	31	Blank	3.0012500	2.45654483
## 109	Other	35	Blank	4.8337500	2.51139084
## 110	Other	37	Blank	3.8325000	1.87864503
## 111	Other	39	Blank	3.5692857	3.23125418
## 112	Other	42	Blank	3.7468750	2.54635725
## 113	Other	45	Blank	3.3587500	2.42737623
## 114	Other	50	Blank	2.8593750	2.61078592
## 115	Other	52	Blank	2.6856250	2.10544437

```
Concentrations_Nutrients_Day <- ddpby (data, .(Nutrients, Day),
  summarise,
    meanNH4 = mean (NH4, na.rm = T),
    sdNH4 = sd (NH4, na.rm = T))
Concentrations_Nutrients_Day
```

##	Nutrients	Day	meanNH4	sdNH4
## 1	HN	1	4.51404255	0.83333447
## 2	HN	2	2.01595745	0.73184894
## 3	HN	3	0.56553191	0.50124978
## 4	HN	4	0.52170213	0.59511168
## 5	HN	7	0.56553191	0.50124978
## 6	HN	9	0.44382979	0.28617077
## 7	HN	11	0.16223404	0.14616403
## 8	HN	14	0.11882979	0.09175945
## 9	HN	15	0.16456522	0.18130032
## 10	HN	16	0.28234043	0.24023732
## 11	HN	18	1.59787234	1.19193109
## 12	HN	21	0.72276596	0.54432029
## 13	HN	23	0.81053191	0.87226170
## 14	HN	25	2.34872340	1.65098965
## 15	HN	29	1.65680851	1.10659850
## 16	HN	31	1.52468085	0.90611234
## 17	HN	35	5.67794872	2.59423899
## 18	HN	37	2.86333333	1.80717879
## 19	HN	39	3.72846154	2.77267711
## 20	HN	42	3.00743590	2.65622255
## 21	HN	45	1.56320513	1.91129003
## 22	HN	50	4.31102564	11.52670995
## 23	HN	52	3.29900000	9.46982671
## 24	LN	1	1.39437500	0.62670332
## 25	LN	2	0.28979592	0.28089507
## 26	LN	3	0.19775510	0.19430716
## 27	LN	4	0.34734694	0.55969402
## 28	LN	7	0.19775510	0.19430716
## 29	LN	9	0.15653061	0.21746217
## 30	LN	11	0.10295918	0.14097842
## 31	LN	14	0.06938776	0.09188213

```
## 32      LN  15 0.13714286 0.13181426
## 33      LN  16 0.19979592 0.14943630
## 34      LN  18 0.42428571 0.63670375
## 35      LN  21 0.28479592 0.69830894
## 36      LN  23 0.18724490 0.18400934
## 37      LN  25 0.32214286 0.22053203
## 38      LN  29 0.29336735 0.22708843
## 39      LN  31 0.28081633 0.23925089
## 40      LN  35 2.15951220 1.77774745
## 41      LN  37 0.79780488 0.78177926
## 42      LN  39 1.49012195 1.13673518
## 43      LN  42 0.96719512 1.51152863
## 44      LN  45 0.64987805 0.94229141
## 45      LN  50 4.63036585 10.86862120
## 46      LN  52 4.79838710 13.36273926
## 47  Other   1 5.22750000 5.34849745
## 48  Other   2 4.22000000 6.87828952
## 49  Other   3 4.57000000 2.78492370
## 50  Other   4 4.58375000 3.97196223
## 51  Other   7 4.57000000 2.78492370
## 52  Other   9 4.34250000 2.30303992
## 53  Other  11 3.82500000 2.40220732
## 54  Other  14 2.55666667 2.30242191
## 55  Other  15 3.89857143 2.82568829
## 56  Other  16 3.33250000 2.51078673
## 57  Other  18 2.94142857 2.74629101
## 58  Other  21 3.05562500 2.82506566
## 59  Other  23 2.80812500 2.54535422
## 60  Other  25 3.29375000 2.92201465
## 61  Other  29 3.46750000 2.77377386
## 62  Other  31 3.00125000 2.45654483
## 63  Other  35 4.83375000 2.51139084
## 64  Other  37 3.83250000 1.87864503
## 65  Other  39 3.56928571 3.23125418
## 66  Other  42 3.74687500 2.54635725
## 67  Other  45 3.35875000 2.42737623
## 68  Other  50 2.85937500 2.61078592
## 69  Other  52 2.68562500 2.10544437
```

```
Concentrations_Nutrients_Week <- ddply (data, .(Nutrients, Week),
  summarise,
    meanNH4 = mean (NH4, na.rm = T),
    sdNH4 = sd (NH4, na.rm = T))
Concentrations_Nutrients_Week
```

```
##      Nutrients Week  meanNH4      sdNH4
## 1      HN      1 1.9043085 1.7599295
## 2      HN      2 0.3905319 0.3810693
## 3      HN      3 0.5429144 0.8688467
## 4      HN      4 1.2940071 1.3432905
## 5      HN      5 1.5907447 1.0080741
## 6      HN      6 4.0899145 2.6815205
## 7      HN      7 2.2853205 2.4110082
## 8      HN      8 3.8710145 10.6183037
```

```
## 9      LN      1 0.5530256 0.6608567
## 10     LN      2 0.1524150 0.1897650
## 11     LN      3 0.2076531 0.3598637
## 12     LN      4 0.2647279 0.4366877
## 13     LN      5 0.2870918 0.2321292
## 14     LN      6 1.4824797 1.4042235
## 15     LN      7 0.8085366 1.2618301
## 16     LN      8 4.7027083 11.9166468
## 17    Other     1 4.6282609 4.1934187
## 18    Other     2 4.2317391 2.3958253
## 19    Other     3 3.2100000 2.5114464
## 20    Other     4 3.0525000 2.6533768
## 21    Other     5 3.2343750 2.5425524
## 22    Other     6 4.1006522 2.5077327
## 23    Other     7 3.5528125 2.4115721
## 24    Other     8 2.7725000 2.2929522
```

```
Concentrations<-Concentrations %>%
  mutate_if(is.numeric, round, digits=2)

# write.csv(Concentrations, "Outputs/weekly_NH4.csv", row.names = F)
```

#3. Treatment effects on NH4 concentrations

```
## model 1: LMER for both species
fit1<-lmerTest::lmer(NH4 ~Nutrients * Temp * Disease * Week +
  (1|Beaker.conditions), data=data[data$Nutrients!="Other", ])
isSingular(fit1)
```

```
## [1] FALSE
```

```
anova(fit1)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##               Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
## Nutrients           1.354    1.354      1 2058.4  0.1328 0.715615
## Temp               14.267   14.267      1 2058.7  1.3989 0.237050
## Disease            12.826   12.826      1 2058.6  1.2576 0.262243
## Week              78.526   78.526      1 2058.9  7.6996 0.005573 **
## Nutrients:Temp       0.527    0.527      1 2058.4  0.0517 0.820141
## Nutrients:Disease    0.475    0.475      1 2058.6  0.0466 0.829173
## Temp:Disease         9.238    9.238      1 2058.3  0.9058 0.341337
## Nutrients:Week       0.637    0.637      1 2058.5  0.0625 0.802686
## Temp:Week           62.996   62.996      1 2058.9  6.1768 0.013022 *
## Disease:Week        65.411   65.411      1 2058.1  6.4136 0.011399 *
## Nutrients:Temp:Disease 0.508    0.508      1 2058.5  0.0498 0.823436
## Nutrients:Temp:Week   0.658    0.658      1 2058.4  0.0646 0.799445
## Nutrients:Disease:Week 0.080    0.080      1 2058.5  0.0078 0.929571
## Temp:Disease:Week    47.866   47.866      1 2058.1  4.6933 0.030395 *
## Nutrients:Temp:Disease:Week 0.028    0.028      1 2058.5  0.0028 0.958040
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
step(fit1)
```

```
## Backward reduced random-effect table:
##
##               Eliminated npar  logLik   AIC   LRT Df Pr(>Chisq)
## <none>                        18 -5371.2 10778
## (1 | Beaker.conditions)       1  17 -5371.8 10778 1.142  1      0.2852
##
## Backward reduced fixed-effect table:
##               Eliminated Df Sum of Sq   RSS    AIC F value
## Nutrients:Temp:Disease:Week      1  1      0.01 21023 4835.0  0.0006
## Nutrients:Temp:Week              2  1      1.14 21024 4833.1  0.1121
## Nutrients:Temp:Disease           3  1      3.01 21027 4831.4  0.2955
## Nutrients:Disease:Week           4  1      4.84 21032 4829.9  0.4751
## Nutrients:Week                   5  1      1.34 21034 4828.0  0.1311
## Nutrients:Disease                6  1      9.33 21043 4826.9  0.9156
## Nutrients:Temp                   7  1     21.20 21064 4827.0  2.0809
## Nutrients                        0  1     479.21 21543 4871.7 47.0018
## Temp:Disease:Week                0  1      47.84 21112 4829.7  4.6923
##
##               Pr(>F)
## Nutrients:Temp:Disease:Week 0.97967
## Nutrients:Temp:Week         0.73785
## Nutrients:Temp:Disease      0.58675
## Nutrients:Disease:Week      0.49075
## Nutrients:Week              0.71733
## Nutrients:Disease           0.33874
## Nutrients:Temp              0.14931
## Nutrients                   9.332e-12 ***
## Temp:Disease:Week           0.03041 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Model found:
## NH4 ~ Nutrients + Temp + Disease + Week + Temp:Disease + Temp:Week + Disease:Week + Temp:Disease:Week
```

```
ranova(fit1)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## NH4 ~ Nutrients + Temp + Disease + Week + (1 | Beaker.conditions) + Nutrients:Temp + Nutrients:Disease
##               npar  logLik   AIC   LRT Df Pr(>Chisq)
## <none>                18 -5371.2 10778
## (1 | Beaker.conditions) 17 -5371.8 10778 1.142  1      0.2852
```

```
summary(fit1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: NH4 ~ Nutrients * Temp * Disease * Week + (1 | Beaker.conditions)
## Data: data[data$Nutrients != "Other", ]
##
```



```

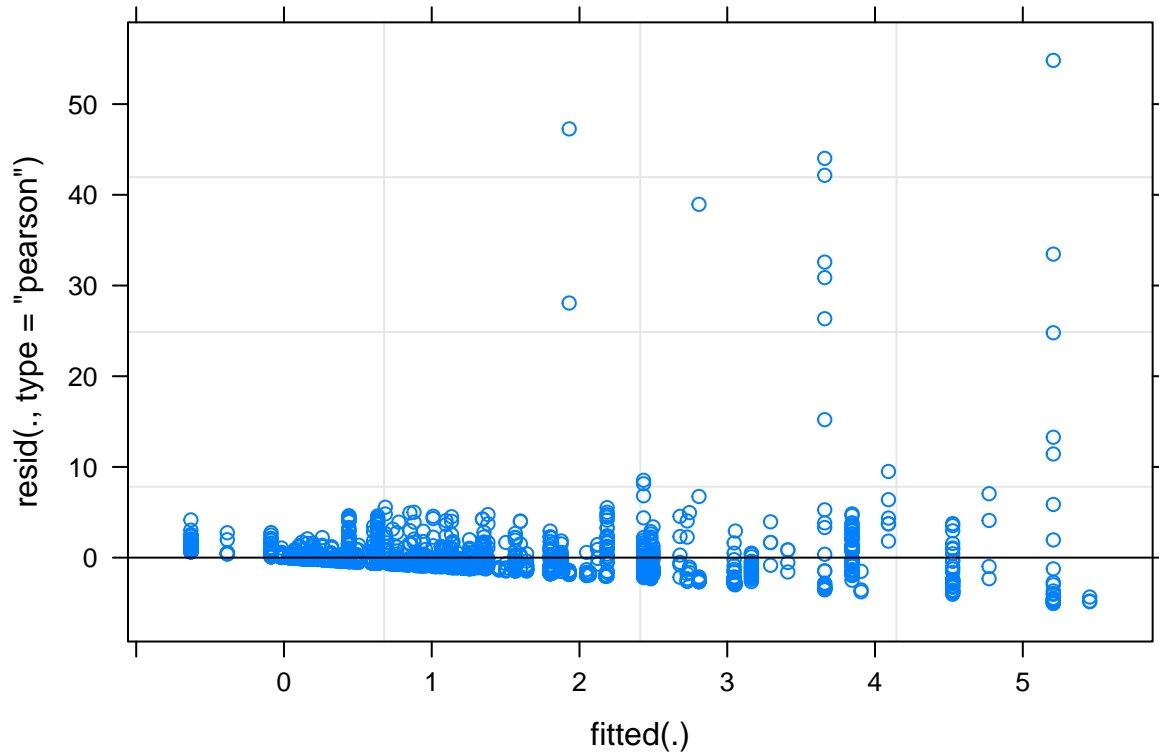
## REML criterion at convergence: 10742.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.5834 -0.2982 -0.1176  0.0647 17.1669
##
## Random effects:
##      Groups             Name             Variance Std.Dev.
## Beaker.conditions (Intercept)  0.04324  0.2079
## Residual                      10.19870  3.1935
## Number of obs: 2075, groups: Beaker.conditions, 2
##
## Fixed effects:
##
##              Estimate Std. Error      df t value
## (Intercept)    5.766e-01  8.471e+00  2.059e+03   0.068
## NutrientsLN    -9.787e-01  1.151e+01  2.059e+03  -0.085
## Temp           2.537e-02  2.868e-01  2.058e+03   0.088
## DiseaseSCTLD   -5.966e+00  9.608e+00  2.058e+03  -0.621
## Week           2.967e-01  1.846e+00  2.058e+03   0.161
## NutrientsLN:Temp  9.441e-04  3.908e-01  2.059e+03   0.002
## NutrientsLN:DiseaseSCTLD -2.843e+00  1.318e+01  2.059e+03  -0.216
## Temp:DiseaseSCTLD  1.629e-01  3.253e-01  2.058e+03   0.501
## NutrientsLN:Week -2.367e-01  2.528e+00  2.059e+03  -0.094
## Temp:Week       -1.298e-02  6.251e-02  2.058e+03  -0.208
## DiseaseSCTLD:Week  3.841e+00  2.125e+00  2.058e+03   1.808
## NutrientsLN:Temp:DiseaseSCTLD  9.979e-02  4.472e-01  2.059e+03   0.223
## NutrientsLN:Temp:Week  1.003e-02  8.581e-02  2.059e+03   0.117
## NutrientsLN:DiseaseSCTLD:Week -2.591e-01  2.931e+00  2.059e+03  -0.088
## Temp:DiseaseSCTLD:Week -1.105e-01  7.201e-02  2.058e+03  -1.534
## NutrientsLN:Temp:DiseaseSCTLD:Week  5.240e-03  9.958e-02  2.058e+03   0.053
##
##              Pr(>|t|)
## (Intercept)    0.9457
## NutrientsLN    0.9323
## Temp           0.9295
## DiseaseSCTLD   0.5347
## Week           0.8724
## NutrientsLN:Temp  0.9981
## NutrientsLN:DiseaseSCTLD  0.8292
## Temp:DiseaseSCTLD  0.6166
## NutrientsLN:Week  0.9254
## Temp:Week       0.8356
## DiseaseSCTLD:Week  0.0708
## NutrientsLN:Temp:DiseaseSCTLD  0.8234
## NutrientsLN:Temp:Week  0.9069
## NutrientsLN:DiseaseSCTLD:Week  0.9296
## Temp:DiseaseSCTLD:Week  0.1252
## NutrientsLN:Temp:DiseaseSCTLD:Week  0.9580
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

par(mfrow=c(2,2))
plot(fit1)

```



```
par(mfrow=c(1,1))
```

```
#Pairwise comparisons
```

```
Sw.emmc<-multcomp::cld(emmeans(fit1, specs=c("Nutrients", "Disease")))
```

```
Sw.emmc
```

```
##  Nutrients Disease emmean    SE   df lower.CL upper.CL .group
##  LN          Placebo  0.272 0.246 3.79   -0.428   0.971    1
##  HN          Placebo  0.997 0.259 4.63    0.315   1.678   12
##  LN          SCTLD   1.031 0.212 1.41   -0.365   2.427    2
##  HN          SCTLD   2.054 0.212 1.41    0.661   3.447    3
##
## Results are averaged over the levels of: Temp
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 4 estimates
## significance level used: alpha = 0.05
## NOTE: If two or more means share the same grouping symbol,
##       then we cannot show them to be different.
##       But we also did not show them to be the same.
```

## Packages used

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

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