## Figure 1e

```
library(readxl)
library(lubridate)
##
## Attaching package: 'lubridate'
## The following objects are masked from 'package:base':
##
##
       date, intersect, setdiff, union
library(mgcv)
## Loading required package: nlme
## This is mgcv 1.8-34. For overview type 'help("mgcv-package")'.
library(ggplot2)
library(ggsignif)
library(readr)
library(emmeans)
library(tidyr)
library(plyr)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:plyr':
##
##
       arrange, count, desc, failwith, id, mutate, rename, summarise,
##
       summarize
## The following object is masked from 'package:nlme':
##
##
       collapse
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
#load in raw data
dat <- data.frame(read_csv("1d+e_data.csv"))</pre>
##
## -- Column specification -----
## cols(
##
     `Repeat(Date)` = col_character(),
##
     Algae = col_character(),
```

```
##
     Well_ID = col_character(),
##
     Larvae = col_double(),
     `Number of Symbionts` = col_double(),
##
     Time_post_infection = col_double()
##
## )
head(dat)
     Repeat.Date. Algae Well_ID Larvae Number.of.Symbionts Time_post_infection
## 1
                I SSB01
                             SI1
                                      1
## 2
                I SSB01
                             SI1
                                      2
                                                           1
                                                                               1
## 3
                I SSB01
                             SI1
                                      3
                                                           3
                                                                               1
## 4
                I SSB01
                            SI1
                                      4
                                                           2
                                                                               1
## 5
                I SSB01
                            SI1
                                                           4
                                                                               1
## 6
                I SSB01
                            SI1
                                      6
                                                           4
                                                                               1
#clean up raw data
dat$Algae <- factor(dat$Algae, levels= c("SSB01", "M. gaditana", "N. oculata", "C. velia"))
dat$Well_ID <- factor(dat$Well_ID)</pre>
dat$Time_post_infection <- factor(as.double(dat$Time_post_infection))</pre>
dat$Repeat.Date. <- factor(as.character(dat$Repeat.Date.))</pre>
dat$infected <- ifelse(dat$Number.of.Symbionts>=1,1,0)
head(dat)
##
     Repeat.Date. Algae Well_ID Larvae Number.of.Symbionts Time_post_infection
## 1
                I SSB01
                             SI1
                                      1
                                                                               1
## 2
                I SSB01
                             SI1
                                      2
                                                           1
                                                                               1
## 3
                I SSB01
                             SI1
                                      3
                                                           3
                                                                               1
## 4
                I SSB01
                            SI1
                                      4
                                                           2
                                                                               1
                I SSB01
                            SI1
                                      5
                                                           4
                                                                               1
                I SSB01
                            SI1
                                                           4
## 6
                                      6
                                                                               1
##
     infected
## 1
            0
## 2
            1
## 3
            1
## 4
            1
## 5
            1
## 6
            1
#model data with generalized linear mixed modes
mod <- gam(Number.of.Symbionts ~ Algae + Time_post_infection + s(Well_ID, bs="re"),data=dat,family=nb()</pre>
S <- summary(mod)$p.table
S
##
                           Estimate Std. Error
                                                   z value
                                                                Pr(>|z|)
## (Intercept)
                          2.2709388 0.2839641
                                                  7.997276 1.272021e-15
## AlgaeM. gaditana
                         -1.7196165 0.2858519 -6.015761 1.790433e-09
## AlgaeN. oculata
                         -3.7828161 0.3091895 -12.234621 2.030508e-34
## AlgaeC. velia
                         -1.3633748 0.2818657 -4.836966 1.318360e-06
## Time_post_infection2 -0.6728683 0.3202546 -2.101042 3.563729e-02
## Time_post_infection3 -1.1276807 0.3234755 -3.486139 4.900465e-04
## Time_post_infection6 -1.2798536 0.3239162 -3.951187 7.776463e-05
## Time_post_infection10 -1.9957867 0.3335057 -5.984266 2.173675e-09
#model pairwise comparison (Tukey)
mod.emm.s <- emmeans(mod, c("Algae", "Time_post_infection"))</pre>
```

```
## NOTE: A nesting structure was detected in the fitted model:
       Well_ID %in% (Algae*Time_post_infection)
pairwise <- data.frame(pairs(mod.emm.s))</pre>
pairwise$label <- ifelse(pairwise$p.value < 0.001, "***",ifelse(pairwise$p.value < 0.01, "**",ifelse(pairwise
pairwise <- pairwise %>% separate(contrast, c("start", "end"), " - ")
pairwise <- pairwise %>% separate(start, c("Algae_1", "t.p.i_1"), sep="\\s+(?=\\S*$)")
pairwise <- pairwise %>% separate(end, c("Algae_2", "t.p.i_2"), sep="\\s+(?=\\S*$)")
head(pairwise)
##
    Algae 1 t.p.i 1
                         Algae 2 t.p.i 2 estimate
                                                           SE
                                                                          t.ratio
## 1
      SSB01
                  1 M. gaditana
                                     1 -0.2230427 0.1478362 4517.078 -1.508715
## 2
      SSB01
                   1 N. oculata
                                       1 1.2768239 0.1617624 4517.078 7.893204
## 3
      SSB01
                        C. velia
                                      1 0.3598090 0.1491615 4517.078 2.412211
                   1
## 4
      SSB01
                   1
                           SSB01
                                       2 -0.2527391 0.1484267 4517.078 -1.702787
## 5
                                      2 0.5020817 0.1592841 4517.078 3.152115
       SSB01
                   1 M. gaditana
## 6
       SSB01
                   1 N. oculata
                                       2 3.2462206 0.2748150 4517.078 11.812385
##
         p.value label
## 1 9.947136e-01
## 2 4.336698e-08
## 3 6.521989e-01
## 4 9.789622e-01
## 5 1.591631e-01
## 6 4.336605e-08
                    ***
write_csv(pairwise, "1e_pairwise.csv")
#clean up results for graph
result <- data.frame(mod.emm.s)</pre>
summary <- data.frame(Algae=result$Algae)</pre>
#Transform data (linkfunction)
summary$Time_post_infection <- factor(result$Time_post_infection,levels= c("1","2","3","6","10"))</pre>
summary$mean<- exp(result$emmean)</pre>
summary$down <- exp(result$lower.CL)</pre>
summary$up <- exp(result$upper.CL)</pre>
head(summary)
##
           Algae Time_post_infection
                                                    down
                                          mean
## 1
           SSB01
                                   1 2.4790726 1.9862722 3.0941384
                                   1 3.0985284 2.5637618 3.7448402
## 2 M. gaditana
## 3 N. oculata
                                   1 0.6914674 0.5495087 0.8700993
                                   1 1.7299206 1.4254932 2.0993613
## 4
       C. velia
## 5
           SSB01
                                   2 3.1919233 2.6380917 3.8620244
                                   2 1.5005067 1.2051352 1.8682719
## 6 M. gaditana
write_csv(summary, "1e_summary.csv")
#Plot graph
P1<-ggplot(data = summary) +
  geom_bar(aes(x = Time_post_infection, y = mean, color = Algae, fill = Algae), stat = "identity", show.1
  facet_wrap(~ Algae, nrow = 1)+
  geom_errorbar(aes(x = Time_post_infection, group=Algae, y = mean, ymin=down, ymax=up), width=.5, show
  theme_classic() +
  theme(strip.background = element_blank(), strip.text = element_blank())+
  scale_color_manual(breaks = c("SSB01", "M. gaditana", "N. oculata", "C. velia"),
                     values=c("#FF2500","#E0D532","#008D58","#0067A2")) +
```

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scale_fill_manual(breaks = c("SSB01", "M. gaditana", "N. oculata", "C. velia"),
                      values=c("#FF2500","#E0D532","#008D58","#0067A2")) +
  labs(x = "Time post infection (d)", y = "Algae per larvae") +
  scale_y_continuous(expand = c(0, 0), limits = c(0,6))
plot(P1)
   6
   5
   4
Algae per larvae
   2
   1
               3
                   6
                       10
                                  2
                                      3
                                              10
                                                                    10
                                      Time post infection (d)
ggsave("Figure_1e.pdf", width=16, height=11, units="cm")
# get n count per treatment
ndata <- ddply(dat, c("Algae", "Time_post_infection", "Repeat.Date."), summarise, N = length("Larvae"))</pre>
head(ndata)
     Algae Time_post_infection Repeat.Date. N
## 1 SSB01
                               1
                                             I 1
## 2 SSB01
                               1
                                            II 1
## 3 SSB01
                               1
                                          III 1
## 4 SSB01
                                            IV 1
                               1
## 5 SSB01
                               1
                                            V 1
## 6 SSB01
                               2
                                             I 1
n_Figure <- ddply(ndata, c("Algae", "Time_post_infection"), summarise, N = length(Repeat.Date.))
n_Figure
             Algae Time_post_infection N
##
```

4

1 5

2 5

3 5

6 5

## 1

## 2

## 3 ## 4 SSB01

SSB01

SSB01

SSB01

```
SSB01
## 5
                                 10 5
## 6 M. gaditana
                                  1 5
## 7 M. gaditana
                                  2 5
## 8 M. gaditana
                                  3 5
## 9 M. gaditana
                                  6 5
## 10 M. gaditana
                                10 5
## 11 N. oculata
                                  1 5
## 12 N. oculata
                                  2 5
                                  3 5
## 13 N. oculata
## 14 N. oculata
                                  6 5
## 15 N. oculata
                                 10 5
       C. velia
## 16
                                  1 5
## 17
        C. velia
                                   2 5
## 18
        C. velia
                                   3 5
## 19
        C. velia
                                  6 5
## 20
        C. velia
                                  10 5
write_csv(n_Figure, "1e_n.csv")
```