

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"))

##
## -- 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 0 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 5 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)
dat$Time_post_infection <- factor(as.double(dat$Time_post_infection))
dat$Repeat.Date. <- factor(as.character(dat$Repeat.Date.))
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 0 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 5 4 1
## 6 I SSB01 SI1 6 4 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())
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)
```

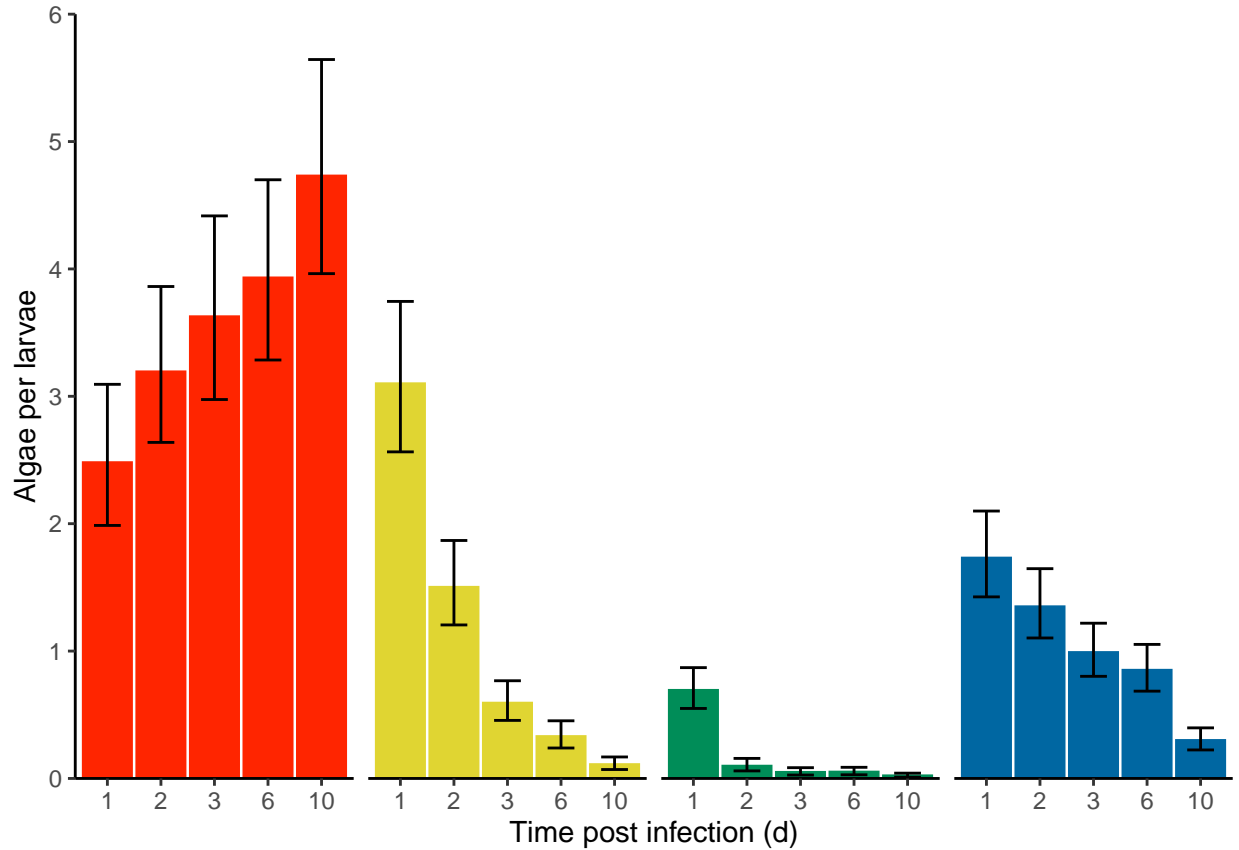
```
mod.emm.s <- emmeans(mod, c("Algae","Time_post_infection"))
```



```

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)

```



```

ggsave("Figure_1e.pdf",width=16,height=11,units="cm")

```

```

# get n count per treatment
ndata <- ddpoly(dat, c("Algae", "Time_post_infection", "Repeat.Date."), summarise, N = length("Larvae"))
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                    1          IV 1
## 5 SSB01                    1           V 1
## 6 SSB01                    2           I 1

```

```

n_Figure <- ddpoly(ndata, c("Algae", "Time_post_infection"), summarise, N = length(Repeat.Date.))
n_Figure

```

```

##      Algae Time_post_infection N
## 1     SSB01                    1 5
## 2     SSB01                    2 5
## 3     SSB01                    3 5
## 4     SSB01                    6 5

```

```

## 5      SSB01      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
## 13 N. oculata     3 5
## 14 N. oculata     6 5
## 15 N. oculata    10 5
## 16 C. velia      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")

```