

Figure 1D

```
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
Add a new chunk by clicking the Insert Chunk button on the toolbar or by pressing Cmd+Option+I.
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
```

```
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(infected ~ Algae + Time_post_infection + s(Well_ID, bs="re"),data=dat,family=binomial())
```

```
S <- summary(mod)$p.table
```

```
S
```

```
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 2.0492773 0.5655089 3.623776 2.903333e-04
## AlgaeM. gaditana -1.4669002 0.5680177 -2.582490 9.809018e-03
## AlgaeN. oculata -3.9927542 0.6002280 -6.652063 2.890134e-11
## AlgaeC. velia -1.5363069 0.5611932 -2.737572 6.189451e-03
## Time_post_infection2 -0.9271803 0.6327277 -1.465370 1.428199e-01
## Time_post_infection3 -1.3535870 0.6397114 -2.115934 3.435044e-02
## Time_post_infection6 -1.7000981 0.6409976 -2.652269 7.995285e-03
## Time_post_infection10 -2.7061541 0.6591102 -4.105769 4.029718e-05
```

```
#model pairwise comparison (Tukey)
```

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

```
## NOTE: A nesting structure was detected in the fitted model:
## Well_ID %in% (Algae*Time_post_infection)

pairwise <- data.frame(pairs(mod.emm.s))
pairwise$label <- ifelse(pairwise$p.value < 0.001, "***",ifelse(pairwise$p.value < 0.01, "***",ifelse(pairwise$p.value < 0.05, "**",ifelse(pairwise$p.value < 0.1, "*",ifelse(pairwise$p.value < 0.5, "ns", "ns")))))
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      df    t.ratio
## 1   SSB01      1 M. gaditana      1 -1.3212501 0.2904962 4512.851 -4.5482525
## 2   SSB01      1 N. oculata      1  1.0145095 0.2173620 4512.851  4.6673731
## 3   SSB01      1 C. velia      1  0.8091256 0.2153873 4512.851  3.7566082
## 4   SSB01      1   SSB01      2 -0.1972534 0.2269853 4512.851 -0.8690142
## 5   SSB01      1 M. gaditana      2  0.3057778 0.2247459 4512.851  1.3605490
## 6   SSB01      1 N. oculata      2  3.3216871 0.3828243 4512.851  8.6767927
##           p.value label
## 1 9.567707e-04   ***
## 2 5.502180e-04   ***
## 3 2.435942e-02    *
## 4 9.99984e-01
## 5 9.985812e-01
## 6 4.341353e-08   ***

write_csv(pairwise, "ld_pairwise.csv")

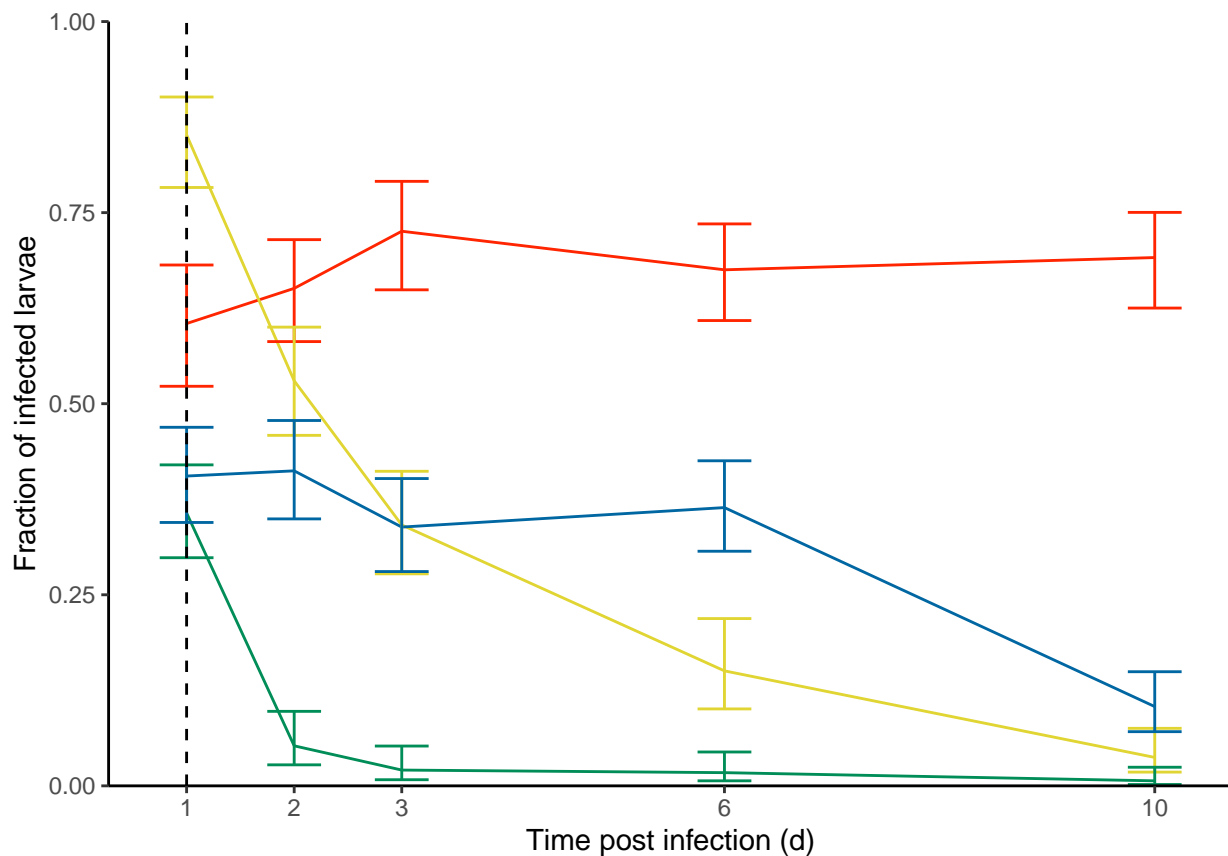
result <- data.frame(mod.emm.s)
summary <- data.frame(Algae=result$Algae)
#Transform data (linkfunction)
summary$Time_post_infection <- as.numeric(as.character(result$Time_post_infection))
summary$mean<- plogis(result$emmean)
summary$down <- plogis(result$lower.CL)
summary$up <- plogis(result$upper.CL)
summary

##      Algae Time_post_infection      mean      down      up
## 1   SSB01                    1 0.604890211 0.522798524 0.68146428
## 2 M. gaditana                    1 0.851590870 0.782906285 0.90128484
## 3 N. oculata                    1 0.356950120 0.298503877 0.41998864
## 4 C. velia                    1 0.405345140 0.344601799 0.46913153
## 5   SSB01                    2 0.650931609 0.581286110 0.71467891
## 6 M. gaditana                    2 0.529990335 0.458593173 0.60018081
## 7 N. oculata                    2 0.052361385 0.027489880 0.09747987
## 8 C. velia                    2 0.412167681 0.349292859 0.47804563
## 9   SSB01                    3 0.725650204 0.649015441 0.79094219
## 10 M. gaditana                   3 0.341334823 0.277417142 0.41159077
## 11 N. oculata                    3 0.020656919 0.008029030 0.05210251
## 12 C. velia                    3 0.338568305 0.280375016 0.40209114
## 13   SSB01                   6 0.675198611 0.608791679 0.73523549
## 14 M. gaditana                   6 0.150445162 0.100660292 0.21886066
## 15 N. oculata                    6 0.017255422 0.006607804 0.04429525
## 16 C. velia                    6 0.364079712 0.306959161 0.42530655
## 17   SSB01                   10 0.691233013 0.625128298 0.75033637
## 18 M. gaditana                   10 0.037186744 0.017999617 0.07525936
## 19 N. oculata                    10 0.006568242 0.001748194 0.02435372
```

```
## 20      C. velia                10 0.103722389 0.070887175 0.14932262
```

```
write_csv(summary, "1d_summary.csv")
```

```
P1 <- ggplot(data = summary) +
  geom_line(aes(x = Time_post_infection, y = mean, color = Algae), show.legend = FALSE) +
  geom_errorbar(aes(x = Time_post_infection, group = Algae, y = mean, ymin = down, ymax = up, color = Algae),
    theme_classic() +
    scale_color_manual(breaks = c("SSB01", "M. gaditana", "N. oculata", "C. velia"),
      values = c("#FF2500", "#E0D532", "#008D58", "#0067A2")) +
    labs(x = "Time post infection (d)", y = "Fraction of infected larvae") +
    scale_y_continuous(expand = c(0, 0), limits = c(0, 1)) +
    scale_x_continuous(breaks = c(1, 2, 3, 6, 10)) +
    geom_vline(xintercept = 1, linetype = 2)
plot(P1)
```



```
ggsave("Figure_1d.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"))
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 <- ddply(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, "1d_n.csv")
```