

# Data analyses for Experiment 2

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This code analyzes the data associated with Experiment 2 and produces Figure 3 in the manuscript:

Barnes DK, Burgess SC. Fitness consequences of marine larval dispersal: the role of neighborhood density, spatial arrangement, and genetic relatedness on survival, growth, reproduction, and paternity. *Journal of Evolutionary Biology*

Code finalized September 2024.

Any comments or error reporting, please contact Scott Burgess: sburgess@bio.fsu.edu

## Load required libraries

```
library('tidyverse')
library('glmmTMB')
library('gridExtra')
library('emmeans')
```

```
sessionInfo()
```

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS Sonoma 14.6.1
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib; LAPACK v
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] emmeans_1.10.2  gridExtra_2.3  glmmTMB_1.1.9  lubridate_1.9.3
## [5] forcats_1.0.0   stringr_1.5.1  dplyr_1.1.4    purrr_1.0.2
## [9] readr_2.1.5     tidyr_1.3.1    tibble_3.2.1   ggplot2_3.5.1
## [13] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] utf8_1.2.4      generics_0.1.3  stringi_1.8.4
```

```
## [4] lattice_0.22-6      lme4_1.1-35.3      hms_1.1.3
## [7] digest_0.6.35        magrittr_2.0.3      estimability_1.5.1
## [10] evaluate_0.23         grid_4.4.0          timechange_0.3.0
## [13] mvtnorm_1.2-5         fastmap_1.2.0       Matrix_1.7-0
## [16] mgcv_1.9-1            fansi_1.0.6          scales_1.3.0
## [19] numDeriv_2016.8-1.1  cli_3.6.2           rlang_1.1.3
## [22] munsell_0.5.1         splines_4.4.0        withr_3.0.0
## [25] yaml_2.3.8            tools_4.4.0          tzdb_0.4.0
## [28] coda_0.19-4.1         nloptr_2.0.3         minqa_1.2.7
## [31] colorspace_2.1-0     boot_1.3-30          vctrs_0.6.5
## [34] R6_2.5.1              lifecycle_1.0.4      MASS_7.3-60.2
## [37] pkgconfig_2.0.3       pillar_1.9.0         gtable_0.3.5
## [40] Rcpp_1.0.12           glue_1.7.0           xfun_0.44
## [43] tidyselect_1.2.1      rstudioapi_0.16.0    knitr_1.47
## [46] xtable_1.8-4          htmltools_0.5.8.1    nlme_3.1-164
## [49] rmarkdown_2.28        TMB_1.9.11           compiler_4.4.0
```

## Import data for Experiment 2

```
dat <- read.csv("Data/Experiment_2.csv")
```

Create a new column called “Plate ID” for random effects

```
dat$Plate.ID <- sub("_.*", "", dat$Unique.ID)
```

Create a vector of the ages at which data were recorded. Note that individuals were reared in the lab for 26 days, so age 46 days is 20 days in the field.

```
Age.days.vec <- unique(dat$Age.days)
Age.days.vec
```

```
## [1] 26 46
```

Select the data from when the colonies were retrieved from the field after 20 days (age 46 days)

```
d <- dat %>% filter(Age.days == Age.days.vec[2])
```

## Survival

Generalized linear mixed effects model with a binomial distribution and random effect of plate number (Plate.ID).

```
survival1 <- glmmTMB(Survival ~ Relatedness +
  (1|Plate.ID),
  family = "binomial",
  data = d)

survival2 <- glmmTMB(Survival ~ 1 +
  (1|Plate.ID),
  family = "binomial",
  data = d)
```

Test Relatedness

```
result1 <- round(anova(survival1, survival2, test="Chisq"), 3)
result1
```

```
## Data: d
## Models:
## survival2: Survival ~ 1 + (1 | Plate.ID), zi=~0, disp=~1
## survival1: Survival ~ Relatedness + (1 | Plate.ID), zi=~0, disp=~1
##           Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## survival2  2 187.82 193.84 -91.911   183.82
## survival1  3 189.79 198.82 -91.893   183.79 0.036    1    0.849
```

There was no evidence that relatedness affected survival ( $\chi^2 = 0.036$ ,  $df = 1$ ,  $p = 0.849$ ).

Calculate fitted values for plotting

```
predictions_survival <- data.frame(Relatedness = unique(dat$Relatedness))

p <- predict(survival1,
             predictions_survival,
             type = "link",
             se.fit = T,
             re.form = NA)

predictions_survival$fit <- plogis(p$fit)
predictions_survival$se.fit <- p$se.fit
# Calculate confidence intervals
predictions_survival$lwr <- plogis(p$fit - 2 * p$se.fit)
predictions_survival$upr <- plogis(p$fit + 2 * p$se.fit)
```

## Relative growth rate

Change data to the wide format

```
dat_wide <- dat %>% pivot_wider(id_cols=Unique.ID:Position,
                               names_from=Age.days,
                               values_from=c(Survival,Bifurcations,Zooids))
```

Calculate relative growth rate

```
dat_wide$relgrowth <- (log(dat_wide$Zooids_46) - log(dat_wide$Zooids_26)) / (46-26)
```

Create a new column called “Plate ID” for random effects

```
dat_wide$Plate.ID <- sub("_.*", "", dat_wide$Unique.ID)
```

Fit generalized linear mixed effects model with a Gaussian distribution and random effect of plate number (Unique.ID).

```
rgr1 <- glmmTMB(relgrowth ~ Relatedness +
                (1|Plate.ID),
                family = "gaussian",
                data = dat_wide)

rgr2 <- glmmTMB(relgrowth ~ 1 +
```

```
(1|Plate.ID),
family = "gaussian",
data = dat_wide)
```

Test Relatedness

```
result1 <- round(anova(rgr1, rgr2, test="Chisq"), 3)
result1
```

```
## Data: dat_wide
## Models:
## rgr2: relgrowth ~ 1 + (1 | Plate.ID), zi=~0, disp=~1
## rgr1: relgrowth ~ Relatedness + (1 | Plate.ID), zi=~0, disp=~1
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## rgr2  3 -288.59 -280.75 147.30 -294.59
## rgr1  4 -286.63 -276.17 147.32 -294.63 0.042    1    0.838
```

There was no evidence that relatedness affected relative growth rate ( $\chi^2 = 0.042$ ,  $df = 1$ ,  $p = 0.838$ ).

Calculate fitted values for plotting

```
predictions_rgr <- data.frame(Relatedness = unique(dat$Relatedness))
```

```
p <- predict(rgr1,
             predictions_rgr,
             type = "link",
             se.fit = T,
             re.form = NA)
```

```
predictions_rgr$fit <- p$fit
predictions_rgr$se.fit <- p$se.fit
# Calculate confidence intervals
predictions_rgr$lwr <- p$fit - 2 * p$se.fit
predictions_rgr$upr <- p$fit + 2 * p$se.fit
```

```
nd <- data.frame(Relatedness = c(rep("Non", 5), rep("Sib", 10)),
                 Plate.ID = rownames(coef(rgr1)$cond$Plate.ID))
```

```
plate_effects_rgr <- data.frame(nd,
                                fit = predict(rgr1,
                                              newdata = nd,
                                              type="response",
                                              se=F))
```

## Reproductive output

Add zero ovicells for colonies that died

```
d$Ovicells.total <- ifelse(is.na(d$Ovicells.total), 0, d$Ovicells.total)
```

Fit zero-inflated generalized linear mixed effects model with a truncated negative binomial distribution and random effect of plate number (Unique.ID).

```
totov1 <- glmmTMB(Ovicells.total ~ Relatedness +
                  (1|Plate.ID),
                  ziformula = ~.,
```

```

        data = d,
        family = truncated_nbinom1)

totov2 <- glmmTMB(Ovicells.total ~ 1 +
                 (1|Plate.ID),
                 ziformula = ~.,
                 data = d,
                 family = truncated_nbinom1)

result1 <- round(anova(totov1, totov2, test="Chisq"), 3)
result1

## Data: d
## Models:
## totov2: Ovicells.total ~ 1 + (1 | Plate.ID), zi=~., disp=~1
## totov1: Ovicells.total ~ Relatedness + (1 | Plate.ID), zi=~., disp=~1
##      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## totov2  5 1387.5 1402.6 -688.77   1377.5
## totov1  7 1391.4 1412.5 -688.71   1377.4 0.121    2    0.942

```

There was no evidence that relatedness affected reproductive output ( $\chi^2 = 0.121$ ,  $df = 2$ ,  $p = 0.942$ ).

### Calculate fitted values for plotting

```

predictions_totov <- data.frame(Relatedness = unique(dat$Relatedness))

# p <- predict(totov1,
#              predictions_totov,
#              type = "link",
#              se.fit = T,
#              re.form = NA)
#
# predictions_totov$fit <- exp(p$fit)
# predictions_totov$se.fit <- p$se.fit
# # Calculate confidence intervals
# predictions_totov$lwr <- exp(p$fit - 2 * p$se.fit)
# predictions_totov$upr <- exp(p$fit + 2 * p$se.fit)

p <- emmeans(totov1, ~ Relatedness,
              component = "cond",
              type = "response")

predictions_totov$fit <- summary(p)$response
predictions_totov$lwr <- summary(p)$asympt.LCL
predictions_totov$upr <- summary(p)$asympt.UCL

nd <- data.frame(Relatedness = c(rep("Non", 5), rep("Sib", 10)),
                 Plate.ID = rownames(coef(totov1)$cond$Plate.ID))

plate_effects_totov <- data.frame(nd,
                                  fit = predict(totov1,
                                                  newdata = nd,
                                                  type="response",
                                                  se=F))

plate_effects_totov <- d %>%

```

```

group_by(Plate.ID) %>%
summarize(fit = mean(Ovicells.total))

plate_effects_totov$Relatedness <- ifelse(
  grepl("non", plate_effects_totov$Plate.ID),
  "Non",
  "Sib")

```

## Make Figure 3

```

panel_A <- ggplot(data = predictions_survival,
  aes(x = Relatedness,
      y = fit)) +
  geom_linerange(aes(min = lwr,
                    max = upr)) +
  geom_point() +
  ylim(0,1) +
  labs(y = "Probability of survival",
       title = "a") +
  scale_x_discrete(labels = c("Unrelated", "Siblings")) +
  theme_classic()

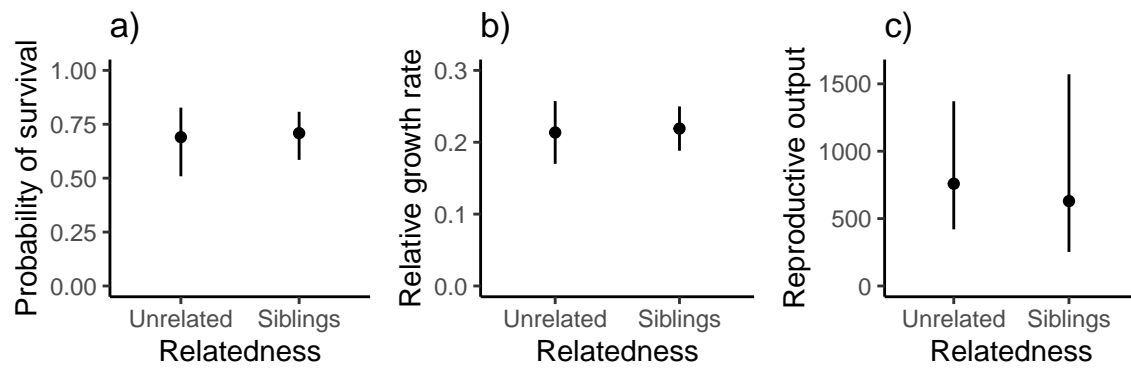
panel_B <- ggplot(data = predictions_rgr,
  aes(x = Relatedness,
      y = fit)) +
  # geom_jitter(data = plate_effects_rgr,
  #             aes(x = Relatedness,
  #                 y = fit),
  #             alpha = 0.4,
  #             width = 0.05) +
  geom_linerange(aes(min = lwr,
                    max = upr)) +
  geom_point() +
  ylim(0,0.3) +
  labs(y = "Relative growth rate",
       title = "b") +
  scale_x_discrete(labels = c("Unrelated", "Siblings")) +
  theme_classic()

panel_C <- ggplot(data = predictions_totov,
  aes(x = Relatedness,
      y = fit)) +
  geom_linerange(aes(min = lwr,
                    max = upr)) +
  geom_point() +
  ylim(0,1600) +
  labs(y = "Reproductive output",
       title = "c") +
  scale_x_discrete(labels = c("Unrelated", "Siblings")) +
  theme_classic()

grid.arrange(panel_A, panel_B, panel_C,

```

```
nrow = 1,  
ncol = 3)
```



```
## pdf  
## 2
```