

Delia platyura mating system

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```
```\nknitr::opts_chunk$set(echo = TRUE)\n\nrm(list=ls()) # clear workspace\n\nlibrary(glmmTMB) # glms\n\n## Warning in checkDepPackageVersion(dep_pkg = "TMB"): Package version\ninconsistency detected.\n## glmmTMB was built with TMB version 1.9.2\n## Current TMB version is 1.9.3\n## Please re-install glmmTMB from source or restore original 'TMB' package\n(see '?reinstalling' for more information)\n\nlibrary(DHARMA) # glm diagnostics\n\n## This is DHARMA 0.4.6. For overview type '?DHARMA'. For recent changes,\ntype news(package = 'DHARMA')\n\nlibrary(readxl) # read excel files\nlibrary(ggtext) # plotting\nlibrary(patchwork) # multiple plots\nlibrary(tidyverse)\n\n## — Attaching packages ————— tidyverse\n1.3.2\n## —\n\n## ✓ ggplot2 3.4.2      ✓ purrr  1.0.1\n## ✓ tibble  3.2.1      ✓ dplyr  1.1.0\n## ✓ tidyr   1.3.0      ✓ stringr 1.5.0\n## ✓ readr   2.1.4      ✓ forcats 1.0.0\n\n## Warning: package 'ggplot2' was built under R version 4.2.3\n## Warning: package 'tibble' was built under R version 4.2.3
```

```
— Conflicts —————
tidyverse_conflicts() —
✘ dplyr::filter() masks stats::filter()
✘ dplyr::lag() masks stats::lag()

library(ggribes) # ridge plots
library(survival) # survival analysis
library(survminer) # survival model diagnostics

Loading required package: ggpubr
##
Attaching package: 'survminer'
##
The following object is masked from 'package:survival':
##
myeloma

library(coxed) # predictions for survival analysis

Loading required package: rms
Loading required package: Hmisc
Loading required package: lattice
Loading required package: Formula
##
Attaching package: 'Hmisc'
##
The following objects are masked from 'package:dplyr':
##
src, summarize
##
The following objects are masked from 'package:base':
##
format.pval, units
##
Loading required package: SparseM
##
Attaching package: 'SparseM'
##
The following object is masked from 'package:base':
##
backsolve
##
Loading required package: mgcv

Warning: package 'mgcv' was built under R version 4.2.3

Loading required package: nlme
##
Attaching package: 'nlme'
##
The following object is masked from 'package:dplyr':
```

```
##
collapse
##
This is mgcv 1.8-42. For overview type 'help("mgcv-package")'.

library(nord) # color palette
library(scales) # change scale of y axis

##
Attaching package: 'scales'
##
The following object is masked from 'package:purrr':
##
discard
##
The following object is masked from 'package:readr':
##
col_factor

library(sjPlot) # report model outputs

Load datasets

mating_system <- read_excel("mating.system.xlsx")
dissect <- read_excel("dissect.xlsx")
```

## Define mating system dataset

genotype: 3453 or 2511 (N-line or H-line, respectively) lot: # of lot from which the flies were obtained (relating to fly production) rep: replicate number - some replicates were not kept for analysis due to errors or females dying sex.ratio: proportion of males density: number of flies in group group: group composition; #males:#females day: number of days since the start of trial for a specific group males: # males females: # females laid: number of eggs laid hatched: number of eggs hatched

\*\*\*\*Group 30:3 genotype 3453, rep 8, day 19; eggs were put in freezer before being counted - keep laid and hatched as NA instead of changing to zero when looking at fecundity\*\*\*\*

## Specify variable types & create new variables

```
mating_system <- mating_system %>%
 mutate(laid = as.numeric(laid),
 hatched = as.numeric(hatched),
 unhatched = as.numeric(laid - hatched),
 females = as.numeric(females),
 males = as.numeric(males),
 day = as.numeric(day),
```

```

 genotype = as.character(genotype), #as character so it can be easily
subsetting
 lot = as.character(lot),
 rep = as.character(rep),
 sex.ratio = as.character(sex.ratio),
 density = as.numeric(density),
 group = as.character(group),
 males.replaced = as.numeric(males.replaced),
 dens.fac = as.character(ifelse(density > 20, "High", "Low")) %>%
replace(is.na(.), 0) %>% # change NAs (only present in laid, hatched &
unhatched) to zeros; only works once laid and hatched are set as.numeric
group_by(genotype, rep, lot, group) %>%
mutate(cum.laid = as.numeric(cumsum(laid)),
 cum.hatched = as.numeric(cumsum(hatched)),
 cum.unhatched = as.numeric(cumsum(unhatched)),
 group.id = as.character(cur_group_id()),
 m.status = as.character(ifelse(sum(hatched) == 0, "unmated",
"mated"))) %>%
 ungroup()

Warning: There were 2 warnings in `mutate()`.
The first warning was:
[i] In argument: `laid = as.numeric(laid)`.
Caused by warning:
! NAs introduced by coercion
[i] Run
]8;;ide:run:dplyr::last_dplyr_warnings()dplyr::last_dplyr_warnings()]8;; to
see the 1 remaining warning.

str(mating_system)

tibble [2,080 × 19] (S3: tbl_df/tbl/data.frame)
$ genotype : chr [1:2080] "3453" "3453" "3453" "3453" ...
$ lot : chr [1:2080] "11" "11" "11" "11" ...
$ rep : chr [1:2080] "3" "3" "3" "3" ...
$ sex.ratio : chr [1:2080] "0.5" "0.5" "0.5" "0.5" ...
$ density : num [1:2080] 2 2 2 2 2 2 2 2 2 2 ...
$ group : chr [1:2080] "1:1" "1:1" "1:1" "1:1" ...
$ day : num [1:2080] 0 3 5 7 9 11 13 15 17 19 ...
$ males : num [1:2080] 1 1 1 1 1 1 1 1 1 1 ...
$ females : num [1:2080] 1 1 1 1 1 1 1 1 1 1 ...
$ laid : num [1:2080] 0 0 0 0 0 0 0 0 0 0 ...
$ hatched : num [1:2080] 0 0 0 0 0 0 0 0 0 0 ...
$ males.replaced: num [1:2080] 0 0 0 0 0 0 0 0 0 0 ...
$ unhatched : num [1:2080] 0 0 0 0 0 0 0 0 0 0 ...
$ dens.fac : chr [1:2080] "Low" "Low" "Low" "Low" ...
$ cum.laid : num [1:2080] 0 0 0 0 0 0 0 0 0 0 ...
$ cum.hatched : num [1:2080] 0 0 0 0 0 0 0 0 0 0 ...
$ cum.unhatched : num [1:2080] 0 0 0 0 0 0 0 0 0 0 ...
$ group.id : chr [1:2080] "121" "121" "121" "121" ...

```

```

$ m.status : chr [1:2080] "unmated" "unmated" "unmated" "unmated"
...
head(mating_system)

A tibble: 6 × 19
genotype lot rep sex.ratio density group day males females laid
hatched
<chr> <chr> <chr> <chr> <dbl> <chr> <dbl> <dbl> <dbl> <dbl>
<dbl>
1 3453 11 3 0.5 2 1:1 0 1 1 0
0
2 3453 11 3 0.5 2 1:1 3 1 1 0
0
3 3453 11 3 0.5 2 1:1 5 1 1 0
0
4 3453 11 3 0.5 2 1:1 7 1 1 0
0
5 3453 11 3 0.5 2 1:1 9 1 1 0
0
6 3453 11 3 0.5 2 1:1 11 1 1 0
0
[i] 8 more variables: males.replaced <dbl>, unhatched <dbl>, dens.fac
<chr>,
cum.laid <dbl>, cum.hatched <dbl>, cum.unhatched <dbl>, group.id
<chr>,
m.status <chr>

```

### Supplemental Figure 3. number of males replaced as a function of group composition

```

replace.males <- mating_system %>%
 group_by(genotype, group, rep) %>%
 summarise(males.replaced = sum(males.replaced))%>%
 group_by(genotype, group) %>%
 summarise(mean.replaced = mean(males.replaced),
 sd = sd(males.replaced),
 n = length(group),
 se.high = mean.replaced + (sd/sqrt(n)),
 se.low = mean.replaced - (sd/sqrt(n)),
 sd.high = mean.replaced + sd,
 sd.low = mean.replaced - sd) %>%
 ungroup()

`summarise()` has grouped output by 'genotype', 'group'. You can override
using
the `.groups` argument.
`summarise()` has grouped output by 'genotype'. You can override using the
`.groups` argument.

```

## replacing males figure H-line

```
replace.H <- subset(replace.males, genotype == "2511")

replacing.H <- ggplot(data = replace.H, aes(x = factor(group, levels =
c("1:1", "16:16", "5:1", "25:5", "10:1", "30:3", "15:1", "30:2")), y =
mean.replaced)) +

 geom_pointrange(aes(ymin = sd.low, ymax = sd.high),
 size = 0.5) +

 scale_y_continuous(position = "right", breaks =
c(0,1,2,3,4,5,6,7,8,9,10,11)) +

 scale_x_discrete(breaks = c("1:1", "16:16", "5:1", "25:5", "10:1", "30:3",
"15:1", "30:2")) +

 coord_cartesian(ylim = c(0, 12)) +

 theme(
 panel.grid.major = element_line(linetype = "blank"),
 panel.grid.minor = element_line(linetype = "blank"),
 panel.background = element_blank(),
 panel.border = element_blank(),
 axis.line = element_line(),
 axis.title.x = element_text(size = 15, hjust = -5),
 axis.text.x = element_text(size = 9),
 axis.text.y = element_text(size = 9),
 plot.title = element_textbox(hjust = 0.5, size = 20, margin = margin(0,
0, 1, 0)),
 plot.margin = margin(0, 0, 0, 2)
) +

 labs(
 x = "Group Composition (Male : Female)",
 y = "",
 title = "H-line"
)
)
```

## replacing males figure N-line

```
replace.N <- subset(replace.males, genotype == "3453")

replacing.N <- ggplot(data = replace.N, aes(x = factor(group, levels =
c("1:1", "16:16", "5:1", "25:5", "10:1", "30:3", "15:1", "30:2")), y =
mean.replaced)) +

 geom_pointrange(aes(ymin = sd.low, ymax = sd.high),
```

```

 size = 0.5) +

 scale_y_continuous(position = "left", breaks =
c(0,1,2,3,4,5,6,7,8,9,10,11)) +

 scale_x_discrete(breaks = c("1:1", "16:16", "5:1", "25:5", "10:1", "30:3",
"15:1", "30:2")) +

 coord_cartesian(ylim = c(0, 12)) +

 theme(
 panel.grid.major = element_line(linetype = "blank"),
 panel.grid.minor = element_line(linetype = "blank"),
 panel.background = element_blank(),
 panel.border = element_blank(),
 axis.line = element_line(),
 axis.title = element_text(size = 15),
 axis.text.x = element_text(size = 9),
 axis.text.y = element_text(size = 9),
 plot.title = element_textbox(hjust = 0.5, size = 20, margin = margin(0,
0, 1, 0)),
 plot.margin = margin(0, 0, 0, 2)
) +

 labs(
 x = "",
 y = "Number of males replaced",
 title = "N-line"
)
)

```

### patchwork replacing males

```

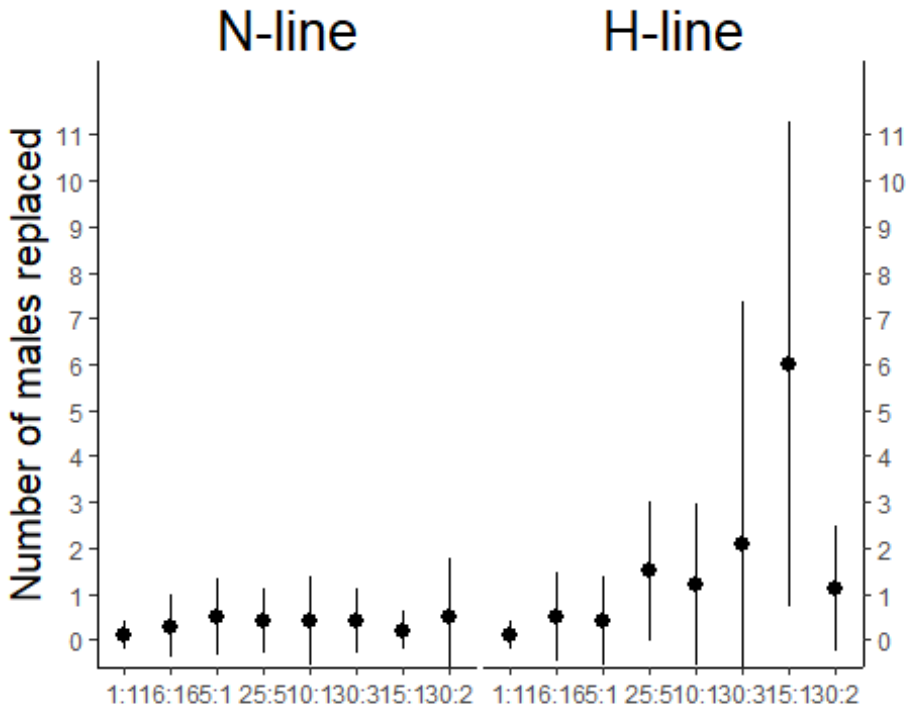
replacing.males <- replacing.N + replacing.H +
 plot_layout(ncol = 2,
 nrow = 1)

```

```

replacing.males

```



```
###Save replacing.males dev.new() replacing.males
jpeg("replacing.males.jpeg",res=600,pointsize=10,height=15,width=21,units="cm")
replacing.males dev.off()
```

## Time to first fertile egg analysis

```
Subset mating_system dataset to keep only mated groups, summarise to keep
only first fertile-egg-laying day as proxy for time until first mating event
```

```
need to subset the last rep of H-line 1:1 - eleventh rep while the others
have ten
```

```
hline.last.rep <- mating_system %>%
 subset(genotype == "2511" & group == "1:1") %>%
 mutate(rep = as.numeric(rep))
max(hline.last.rep$rep) # rep 17 is the last

[1] 17

timetosurv <- mating_system %>%
 mutate(status = as.numeric(ifelse(mating_system$m.status == "mated", 2,
1))) %>% # 1 = censored, 2 = dead
 group_by(genotype, lot, rep, group, dens.fac, sex.ratio, status, m.status)
%>%
 summarise(maxday = as.numeric(max(day)),
 first.mate = as.numeric(maxday - 6)) %>% #first fertile-egg-
```



*Laying day occurred 6 days before the end (egg hatchability evaluated 6 days after being laid)*

```
ungroup() %>%
mutate(genotype = as.factor(genotype),
 lot = as.factor(lot),
 rep = as.factor(rep),
 sex.ratio = as.factor(sex.ratio),
 group = factor(group, levels = c("1:1", "16:16", "5:1", "25:5",
"10:1", "30:3", "15:1", "30:2")),
 density = as.factor(dens.fac),
 ratio = as.numeric(ifelse(group == "1:1" , 1, ifelse(group == "5:1"
, 5, ifelse(group == "10:1" , 10, ifelse(group == "15:1",15, ifelse(group ==
"16:16", 1, ifelse(group == "25:5", 5, ifelse(group == "30:3", 10,
15))))))),
 females = as.numeric(ifelse(group == "1:1" , 1, ifelse(group ==
"5:1" , 1, ifelse(group == "10:1" , 1, ifelse(group == "15:1",1, ifelse(group
== "16:16", 16, ifelse(group == "25:5", 5, ifelse(group == "30:3", 3,
2))))))),
 males = as.numeric(ifelse(group == "1:1" , 1, ifelse(group == "5:1"
, 5, ifelse(group == "10:1" , 10, ifelse(group == "15:1",15, ifelse(group ==
"16:16", 16, ifelse(group == "25:5", 25, ifelse(group == "30:3", 30,
30))))))))))

`summarise()` has grouped output by 'genotype', 'lot', 'rep', 'group',
'dens.fac', 'sex.ratio', 'status'. You can override using the `.groups`
argument.

str(timetosurv)

tibble [161 × 14] (S3: tbl_df/tbl/data.frame)
$ genotype : Factor w/ 2 levels "2511","3453": 1 1 1 1 1 1 1 1 1 1 ...
$ lot : Factor w/ 25 levels "10","11","12",...: 1 1 1 1 1 3 3 3 3 3
...
$ rep : Factor w/ 19 levels "10","11","12",...: 13 13 13 13 13 14 14
14 14 14 ...
$ group : Factor w/ 8 levels "1:1","16:16",...: 7 2 1 8 3 5 2 1 4 6
...
$ dens.fac : chr [1:161] "Low" "High" "Low" "High" ...
$ sex.ratio : Factor w/ 4 levels "0.5","0.83","0.91",...: 4 1 1 4 2 3 1 1
2 3 ...
$ status : num [1:161] 2 2 1 2 2 2 2 1 2 2 ...
$ m.status : chr [1:161] "mated" "mated" "unmated" "mated" ...
$ maxday : num [1:161] 13 13 63 12 19 16 14 69 15 15 ...
$ first.mate: num [1:161] 7 7 57 6 13 10 8 63 9 9 ...
$ density : Factor w/ 2 levels "High","Low": 2 1 2 1 2 2 1 2 1 1 ...
$ ratio : num [1:161] 15 1 1 15 5 10 1 1 5 10 ...
$ females : num [1:161] 1 16 1 2 1 1 16 1 5 3 ...
$ males : num [1:161] 15 16 1 30 5 10 16 1 25 30 ...

timetosurv <- timetosurv %>%
 subset(genotype != "2511" | group != "1:1" | rep != "17")
```

```
subset genotypes
```

```
hline.surv <- subset(timetosurv, genotype == "2511")
```

```
nline.surv <- subset(timetosurv, genotype == "3453")
```

```
str(hline.surv)
```

```
tibble [80 × 14] (S3: tbl_df/tbl/data.frame)
$ genotype : Factor w/ 2 levels "2511","3453": 1 1 1 1 1 1 1 1 1 1 ...
$ lot : Factor w/ 25 levels "10","11","12",...: 1 1 1 1 1 3 3 3 3 3
...
$ rep : Factor w/ 19 levels "10","11","12",...: 13 13 13 13 13 14 14
14 14 14 ...
$ group : Factor w/ 8 levels "1:1","16:16",...: 7 2 1 8 3 5 2 1 4 6
...
$ dens.fac : chr [1:80] "Low" "High" "Low" "High" ...
$ sex.ratio : Factor w/ 4 levels "0.5","0.83","0.91",...: 4 1 1 4 2 3 1 1
2 3 ...
$ status : num [1:80] 2 2 1 2 2 2 2 1 2 2 ...
$ m.status : chr [1:80] "mated" "mated" "unmated" "mated" ...
$ maxday : num [1:80] 13 13 63 12 19 16 14 69 15 15 ...
$ first.mate: num [1:80] 7 7 57 6 13 10 8 63 9 9 ...
$ density : Factor w/ 2 levels "High","Low": 2 1 2 1 2 2 1 2 1 1 ...
$ ratio : num [1:80] 15 1 1 15 5 10 1 1 5 10 ...
$ females : num [1:80] 1 16 1 2 1 1 16 1 5 3 ...
$ males : num [1:80] 15 16 1 30 5 10 16 1 25 30 ...
```

```
str(nline.surv)
```

```
tibble [80 × 14] (S3: tbl_df/tbl/data.frame)
$ genotype : Factor w/ 2 levels "2511","3453": 2 2 2 2 2 2 2 2 2 2 ...
$ lot : Factor w/ 25 levels "10","11","12",...: 2 2 2 2 4 4 4 4 4 4
...
$ rep : Factor w/ 19 levels "10","11","12",...: 13 13 13 13 14 14 14
14 14 14 ...
$ group : Factor w/ 8 levels "1:1","16:16",...: 2 1 6 3 5 2 1 4 8 3
...
$ dens.fac : chr [1:80] "High" "Low" "High" "Low" ...
$ sex.ratio : Factor w/ 4 levels "0.5","0.83","0.91",...: 1 1 3 2 3 1 1 2
4 2 ...
$ status : num [1:80] 2 1 2 1 2 2 2 2 2 2 ...
$ m.status : chr [1:80] "mated" "unmated" "mated" "unmated" ...
$ maxday : num [1:80] 12 89 14 85 13 14 16 13 19 17 ...
$ first.mate: num [1:80] 6 83 8 79 7 8 10 7 13 11 ...
$ density : Factor w/ 2 levels "High","Low": 1 2 1 2 2 1 2 1 1 2 ...
$ ratio : num [1:80] 1 1 10 5 10 1 1 5 15 5 ...
$ females : num [1:80] 16 1 3 1 1 16 1 5 2 1 ...
$ males : num [1:80] 16 1 30 5 10 16 1 25 30 5 ...
```

## Model; triple interaction time to event

```
survcurve2 <- coxph(formula = Surv(first.mate, status) ~ genotype*I(ratio-1)*density, data = timetosurv)
summary(survcurve2)
```

```
Call:
coxph(formula = Surv(first.mate, status) ~ genotype * I(ratio -
1) * density, data = timetosurv)
##
n= 160, number of events= 129
##
coef exp(coef) se(coef) z
genotype3453 0.93300 2.54213 0.39762 2.346
I(ratio - 1) -0.03565 0.96498 0.03657 -0.975
densityLow -2.55796 0.07746 0.52817 -4.843
genotype3453:I(ratio - 1) -0.06021 0.94157 0.04735 -1.271
genotype3453:densityLow -0.16952 0.84407 0.66635 -0.254
I(ratio - 1):densityLow 0.11252 1.11910 0.05658 1.989
genotype3453:I(ratio - 1):densityLow 0.08892 1.09299 0.07192 1.236
##
Pr(>|z|)
genotype3453 0.0190 *
I(ratio - 1) 0.3296
densityLow 1.28e-06 ***
genotype3453:I(ratio - 1) 0.2036
genotype3453:densityLow 0.7992
I(ratio - 1):densityLow 0.0467 *
genotype3453:I(ratio - 1):densityLow 0.2163

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
exp(coef) exp(-coef) lower .95 upper
.95
genotype3453 2.54213 0.3934 1.16611
5.5419
I(ratio - 1) 0.96498 1.0363 0.89824
1.0367
densityLow 0.07746 12.9095 0.02751
0.2181
genotype3453:I(ratio - 1) 0.94157 1.0621 0.85811
1.0331
genotype3453:densityLow 0.84407 1.1847 0.22866
3.1158
I(ratio - 1):densityLow 1.11910 0.8936 1.00163
1.2503
genotype3453:I(ratio - 1):densityLow 1.09299 0.9149 0.94928
1.2585
##
Concordance= 0.75 (se = 0.024)
Likelihood ratio test= 89 on 7 df, p=<2e-16
```

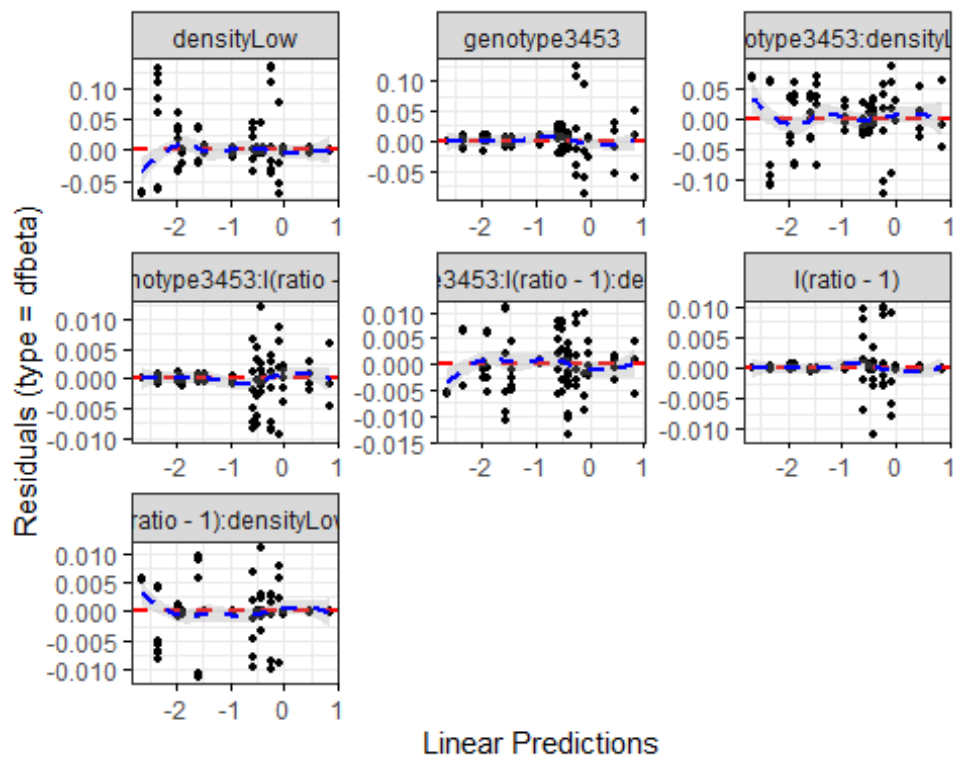


```

Warning: `gather_()` was deprecated in tidyr 1.2.0.
[i] Please use `gather()` instead.
[i] The deprecated feature was likely used in the survminer package.
Please report the issue at
<]8;;https://github.com/kassambara/survminer/issueshttps://github.com/kassamb
ara/survminer/issues]8;;>.
This warning is displayed once every 8 hours.
Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
generated.

`geom_smooth()` using formula = 'y ~ x'

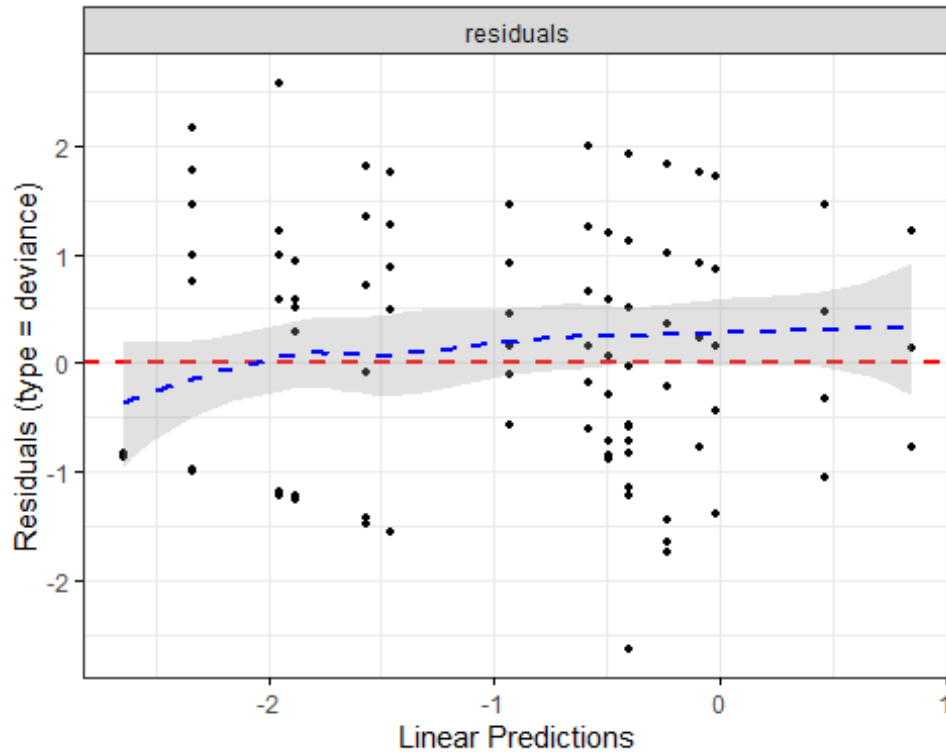
```



```

ggcoxdiagnostics(survcurve2, type = "deviance", linear.predictions = TRUE)
`geom_smooth()` using formula = 'y ~ x'

```



### Predictions; time to event triple interaction

```
newdata3 <- expand.grid(genotype = as.factor(c("3453", "2511")), ratio =
c(1,5,10,15), density = c("High", "Low"))
```

```
pred3 <- predict(survcurve2, newdata = newdata3, Full = T, se.fit = T, type =
"risk")
```

```
pred3
```

```
$fit
```

```
1 2 3 4 5 6
```

```
7
```

```
2.33270611 0.91761857 1.58977718 0.79567005 0.98442254 0.66576588
0.60957456
```

```
8 9 10 11 12 13
```

```
14
```

```
0.55707037 0.15251992 0.07108081 0.23267111 0.09667048 0.39446849
0.14197790
```

```
15 16
```

```
0.66877828 0.20851996
```

```
##
```

```
$se.fit
```

```
1 2 3 4 5 6 7
```

```
8
```

```
0.6176823 0.1162814 0.4261836 0.1193121 0.3044460 0.2336528 0.2706981
0.3444340
```

```
9 10 11 12 13 14 15
```

```

16
0.1749286 0.1500822 0.1770421 0.1374304 0.1979210 0.1345013 0.2786542
0.1784511

predictions3 <- cbind(newdata3,data.frame(pred3)) %>%
 mutate(CI.up = fit + 1.96*(se.fit),
 CI.low = fit - 1.96*(se.fit))

hline.pred.timeto <- subset(predictions3, genotype == "2511")
nline.pred.timeto <- subset(predictions3, genotype == "3453")

```

## Figure 1B.

### H-line time to event predictions for publication

```

color <- c("#E69F00", "#009E73")

hline.time.to <- ggplot(hline.pred.timeto,aes(ratio,fit, fill = density))+
 geom_line(aes(color = density))+
 geom_ribbon(aes(ymin = CI.low,ymax = CI.up),alpha=0.2)+
 geom_pointrange(data = hline.pred.timeto,
 aes(x = ratio, y = fit, ymin = CI.low, ymax = CI.up, color
= density),
 size = 0.5) +

 scale_x_continuous(breaks = c(1,5,10,15)) +

 scale_y_continuous(position = "right", breaks = c(0, 0.5, 1.0, 1.5, 2.0,
2.5, 3.0, 3.5), limits = c(-0.3,3.6)) +

 scale_color_manual(guide = "none", values = color) +
 scale_fill_manual(guide = "none", values = color)+

 theme(
 panel.grid.major = element_line(linetype = "blank"),
 panel.grid.minor = element_line(linetype = "blank"),
 panel.background = element_blank(),
 panel.border = element_blank(),

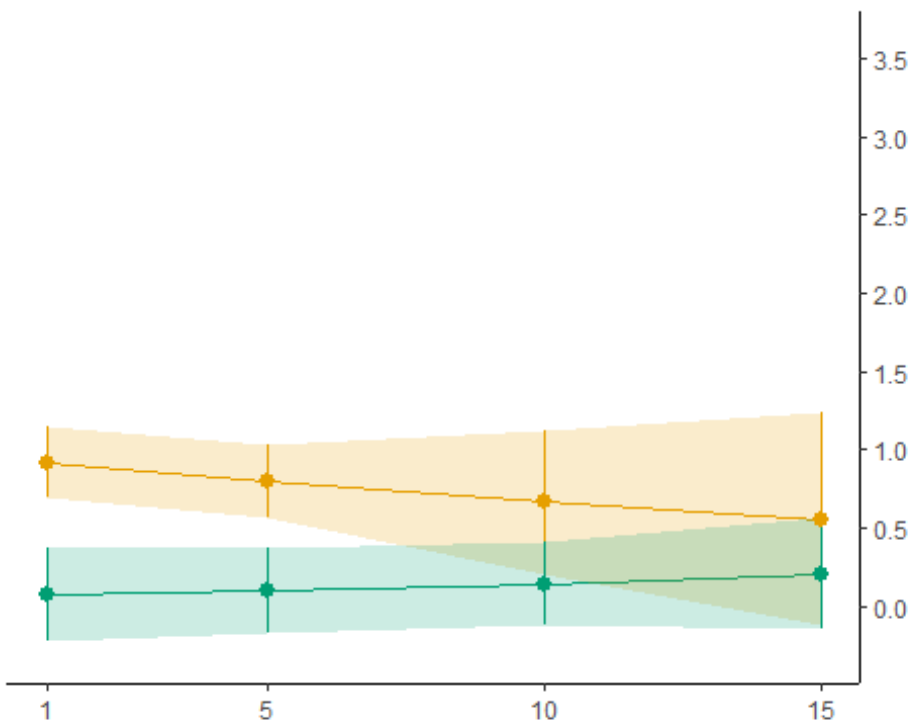
```

```

axis.line = element_line(),
axis.title = element_text(size = 10, hjust = -0.7),
axis.text.x = element_text(size = 9),
axis.text.y = element_text(size = 9),
plot.title = element_textbox(hjust = 0.5, size = 15, margin = margin(0,
0, 1, 0)),
plot.margin = margin(0, 0, 0, 2),
legend.key = element_rect(fill = NA, color = NA),
legend.position = c(0.1,1),
) +
plot_layout(tag_level = 'new')+
labs(
 x = "Sex Ratio (Males/Female)",
 y = "",
 title = ""
)
)

```

hline.time.to



### N-line time to event predictions for publication

```

nline.time.to <- ggplot(nline.pred.timeto,aes(ratio,fit, fill = density))+
 geom_line(aes(color = density))+

```



```

geom_ribbon(aes(ymin = CI.low,ymax = CI.up),alpha=0.2)+
geom_pointrange(data = nline.pred.timeto,
 aes(x = ratio, y = fit, ymin = CI.low, ymax = CI.up, color
= density),
 size = 0.5) +

scale_x_continuous(breaks = c(1,5,10,15)) +

scale_y_continuous(position = "left", breaks = c(0, 0.5, 1.0, 1.5, 2.0,
2.5, 3.0, 3.5), limits = c(-0.3,3.6)) +

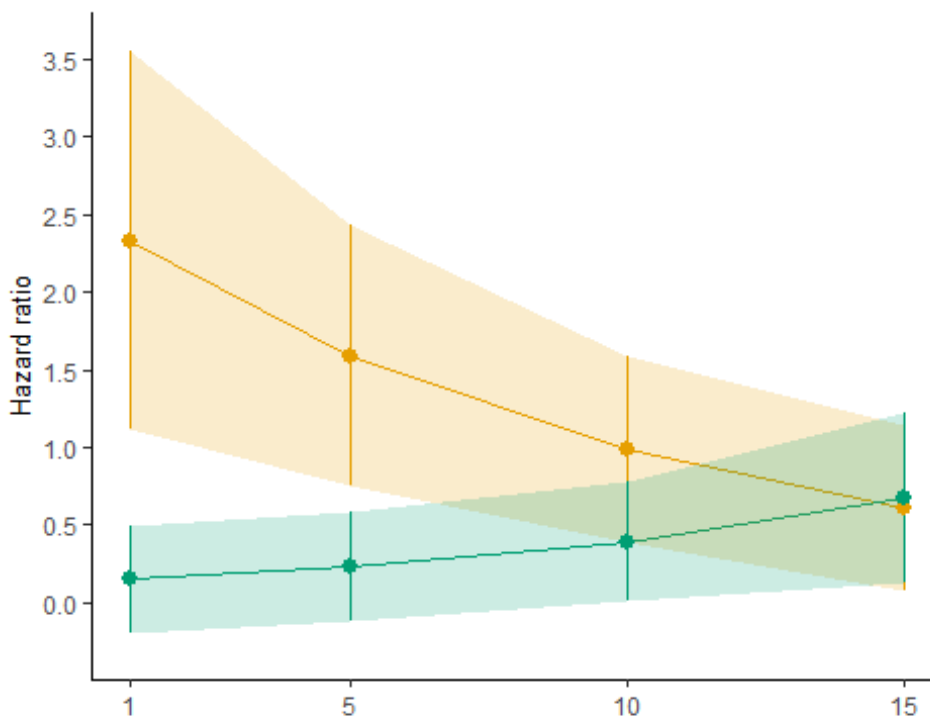
scale_color_manual(guide = "none", values = color) +

scale_fill_manual(guide = "none", values = color)+

theme(
 panel.grid.major = element_line(linetype = "blank"),
 panel.grid.minor = element_line(linetype = "blank"),
 panel.background = element_blank(),
 panel.border = element_blank(),
 axis.line = element_line(),
 axis.title = element_text(size = 12),
 axis.text.x = element_text(size = 9),
 axis.text.y = element_text(size = 9),
 plot.title = element_textbox(hjust = 0.5, size = 15, margin = margin(0,
0, 1, 0)),
 plot.margin = margin(0, 0, 0, 2),
 axis.title.y = element_text(size = 10),
 plot.tag.position = c(0.1,1.05)
) +
plot_layout(tag_level = 'new')+
labs(
 x = "",
 y = "Hazard ratio",
 title = "",
 tag = "B")
)

nline.time.to

```



## Dissections (Proportion Mated females)

Defining Variables: totfemale: total number of females in group mated: number of females mated unmated: number of females unmated femeggs: number of females with eggs present in abdomen rep: replicate number group: group composition (male:female) genotype: genotype (H or N line; 2511 or 3453 respectively)

some females from the same rep/group were stored individually - need to sum mated, unmated, totfemale, and femeggs

```
dissect <- dissect %>%
 mutate(totfemale = as.numeric(totfemale),
 mated = as.numeric(mated),
 unmated = as.numeric(unmated),
 femeggs = as.numeric(femeggs),
 genotype = as.factor(genotype),
 rep = as.factor(rep),
 group = as.factor(group)) %>%
 group_by(genotype, group, rep) %>%
 summarise(totfemale = as.numeric(sum(totfemale)),
 mated = as.numeric(sum(mated)),
 unmated = as.numeric(sum(unmated)),
 femeggs = as.numeric(sum(femeggs))) %>%
 ungroup() %>%
 mutate(binommated = cbind(mated, unmated),
```

```

 propmated = as.numeric(mated/totfemale),
 m.status = as.factor(ifelse(mated == 0, "unmated", "mated")),
 density = as.factor(ifelse(totfemale == 1, "Low", "High")),
 ratio = as.numeric(ifelse(group == "1:1" , 1, ifelse(group == "5:1"
, 5, ifelse(group == "10:1" , 10, ifelse(group == "15:1",15, ifelse(group ==
"16:16", 1, ifelse(group == "25:5", 5, ifelse(group == "30:3", 10,
15))))))))) ,
 n_males = as.numeric(ifelse(group == "1:1" , 1, ifelse(group ==
"5:1" , 5, ifelse(group == "10:1" , 10, ifelse(group == "15:1",15,
ifelse(group == "16:16", 16, ifelse(group == "25:5", 25, ifelse(group ==
"30:3", 30, 30)))))))))

Warning: There was 1 warning in `mutate()`.
[i] In argument: `femeggs = as.numeric(femeggs)`.
Caused by warning:
! NAs introduced by coercion

`summarise()` has grouped output by 'genotype', 'group'. You can override
using
the `.groups` argument.

str(dissect)

tibble [161 × 13] (S3: tbl_df/tbl/data.frame)
$ genotype : Factor w/ 2 levels "2511","3453": 1 1 1 1 1 1 1 1 1 1 ...
$ group : Factor w/ 8 levels "1:1","10:1","15:1",...: 1 1 1 1 1 1 1 1
1 1 ...
$ rep : Factor w/ 19 levels "3","4","5","6",...: 1 2 3 4 5 6 8 12 13
14 ...
$ totfemale : num [1:161] 1 1 1 1 1 1 1 1 1 1 ...
$ mated : num [1:161] 0 0 0 0 0 0 0 0 0 0 ...
$ unmated : num [1:161] 1 1 1 1 1 1 1 1 1 1 ...
$ femeggs : num [1:161] NA 1 1 1 1 1 1 1 1 1 ...
$ binommated: num [1:161, 1:2] 0 0 0 0 0 0 0 0 0 0 ...
.. attr(*, "dimnames")=List of 2
.. ..$: NULL
.. ..$: chr [1:2] "mated" "unmated"
$ propmated : num [1:161] 0 0 0 0 0 0 0 0 0 0 ...
$ m.status : Factor w/ 2 levels "mated","unmated": 2 2 2 2 2 2 2 2 2 2
...
$ density : Factor w/ 2 levels "High","Low": 2 2 2 2 2 2 2 2 2 2 ...
$ ratio : num [1:161] 1 1 1 1 1 1 1 1 1 1 ...
$ n_males : num [1:161] 1 1 1 1 1 1 1 1 1 1 ...

dissect <- dissect %>% subset(genotype != "2511" | group != "1:1" | rep !=
"17") # remove additional hline 1:1 group rep

hline.dissect <- subset(dissect, genotype == "2511")
nline.dissect <- subset(dissect, genotype == "3453")

```

```
##Function for model diagnostics
```

```

sim.check<-function(mod){
mods<-list(mod)
par(mfrow=c(length(mods),4))
lapply(mods,function(i){
 x<-simulateResiduals(fittedModel = i,n=250)
 testUniformity(x)
 plotResiduals(x,rank=T)
 testDispersion(x)
 testZeroInflation(x)
})
}

```

##Model & predictions; triple interaction

```

full.m2 <- glmmTMB(binomated ~ genotype*I(ratio-1)*density +
offset(log(n_males)),
 family = binomial(link = "cloglog"),
 data = dissect)

summary(full.m2)

Family: binomial (cloglog)
Formula:
binomated ~ genotype * I(ratio - 1) * density + offset(log(n_males))
Data: dissect
##
AIC BIC logLik deviance df.resid
306.7 331.3 -145.3 290.7 152
##
Conditional model:
Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.92412 0.13760 -28.519 < 2e-16

genotype3453 1.16282 0.16823 6.912 4.78e-12

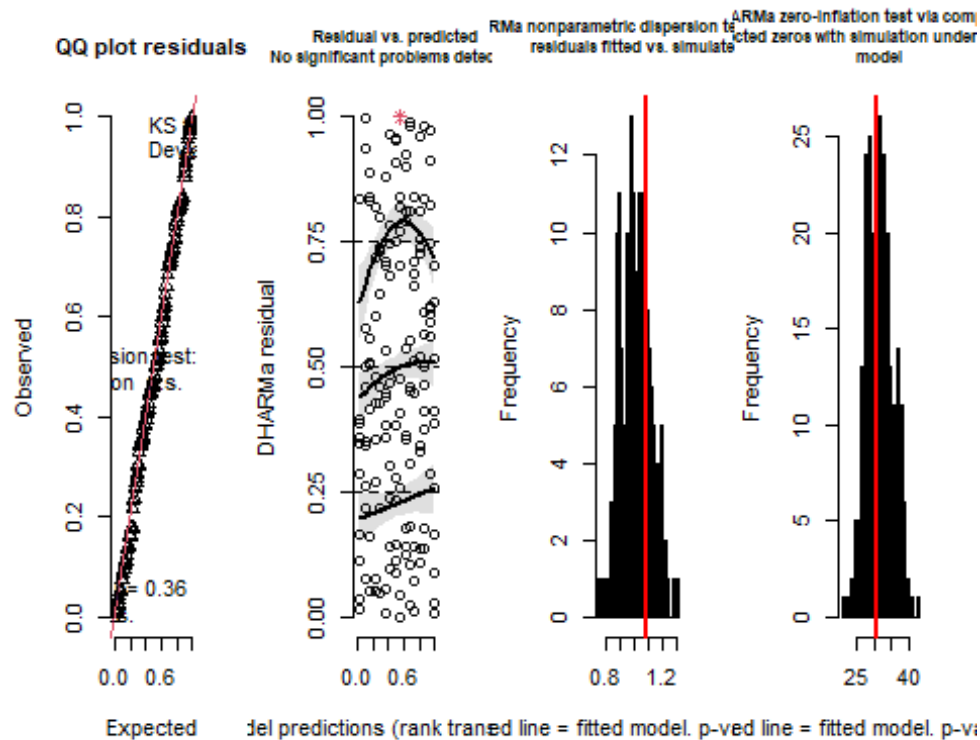
I(ratio - 1) 0.04562 0.02095 2.178 0.0294
*
densityLow 2.33086 0.50461 4.619 3.85e-06

genotype3453:I(ratio - 1) -0.03725 0.02789 -1.336 0.1817
genotype3453:densityLow -0.51336 0.68222 -0.752 0.4518
I(ratio - 1):densityLow -0.13875 0.05422 -2.559 0.0105
*
genotype3453:I(ratio - 1):densityLow 0.14117 0.10157 1.390 0.1646

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

sim.check(full.m2)

```



```

[[1]]
##
DHARMA zero-inflation test via comparison to expected zeros with
simulation under H0 = fitted model
##
data: simulationOutput
ratioObsSim = 0.97374, p-value = 0.968
alternative hypothesis: two.sided

newdata2 <- expand.grid(genotype = as.factor(c("3453", "2511")),
 ratio = c(1,5,10,15),
 density = c("High", "Low")) %>%
 mutate(n_males = ifelse(ratio == 1 & density == "Low", 1, ifelse(ratio == 1
& density == "High", 16, ifelse(ratio == 5 & density == "Low", 5,
ifelse(ratio == 5 & density == "High", 25, ifelse(ratio == 10 & density ==
"Low", 10, ifelse(ratio == 10 & density == "High", 30, ifelse(ratio == 15
& density == "Low", 15, 30))))))))))

pred2 <- predict(full.m2, newdata = newdata2, se.fit = T, type = "link")

ilink<- family(full.m2)$linkinv
predictions2 <- cbind(newdata2,data.frame(pred2)) %>%
 mutate(CI.up = ilink(fit + (1.96*se.fit)),

```

```

 CI.low = ilink(fit - (1.96*se.fit)),
 Pred=ilink(fit))

hline.pred <- subset(predictions2, genotype == "2511")
nline.pred <- subset(predictions2, genotype == "3453")

##Figure 1A. # H-line predictions for publication

color <- c("#E69F00", "#009E73")

hline.prop.mated <- ggplot(hline.pred,aes(ratio,Pred, fill = density))+
 geom_line(aes(color = density))+
 geom_ribbon(aes(ymin = CI.low,ymax = CI.up),alpha=0.2)+
 geom_pointrange(data = hline.pred,
 aes(x = ratio, y = Pred, ymin = CI.low, ymax = CI.up, color
= density),
 size = 0.5) +
 geom_jitter(data = hline.dissect,
 aes(x = ratio, y = propmated, color = density),
 width = 0.2, height = 0.001,
 alpha = 0.1) +

 scale_x_continuous(breaks = c(1,5,10,15)) +

 scale_y_continuous(position = "right", breaks = c(0, 0.20, 0.40, 0.60,
0.80, 1.00), labels = percent) +

 #scale_color_manual(paste(""), values = color, labels = c("High density",
"Low density")) +

 scale_color_manual(values = color, guide = "none")+
 scale_fill_manual(values = color, guide = "none")+

 theme(
 panel.grid.major = element_line(linetype = "blank"),
 panel.grid.minor = element_line(linetype = "blank"),
 panel.background = element_blank(),
 panel.border = element_blank(),
 axis.line = element_line(),

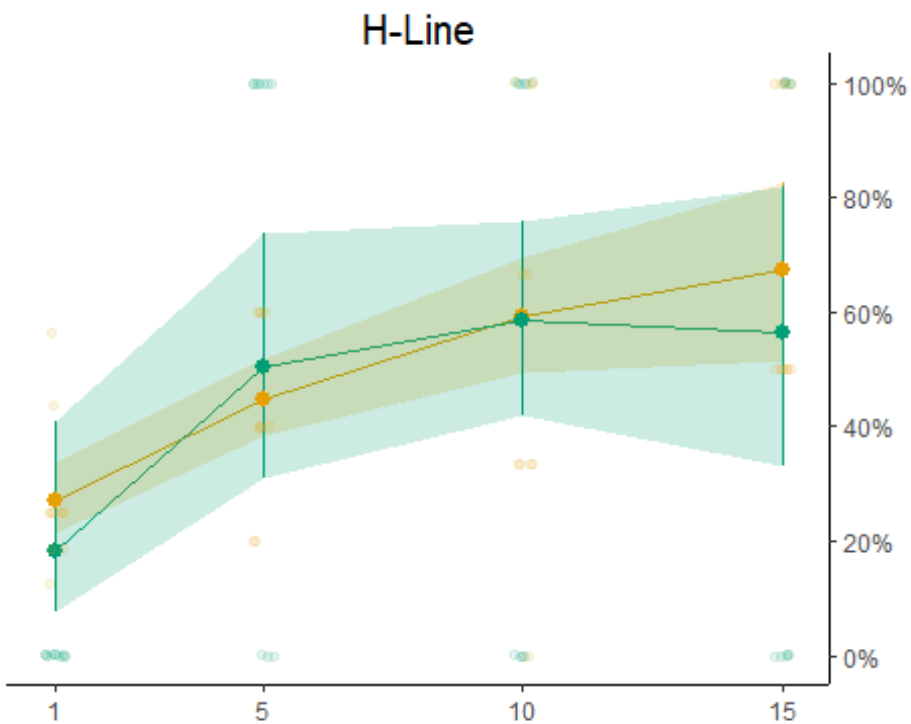
```

```

axis.title = element_text(size = 10, hjust = -0.5),
axis.text.x = element_text(size = 9),
axis.text.y = element_text(size = 9),
plot.title = element_textbox(hjust = 0.5, size = 15, margin = margin(0,
0, 1, 0)),
plot.margin = margin(0, 0, 0, 2),
legend.key = element_rect(fill = NA, color = NA),
legend.position = c(0.1,1),
) +
plot_layout(tag_level = 'new')+
labs(
 x = "",
 y = "",
 title = "H-Line"
)

```

hline.prop.mated



## N-line predictions for publication

```

nline.prop.mated <- ggplot(nline.pred,aes(ratio,Pred, fill = density))+
 geom_line(aes(color = density))+

```

```

geom_ribbon(aes(ymin = CI.low,ymax = CI.up),alpha=0.2)+

geom_pointrange(data = nline.pred,
 aes(x = ratio, y = Pred, ymin = CI.low, ymax = CI.up, color
= density),
 size = 0.5) +

geom_jitter(data = nline.dissect,
 aes(x = ratio, y = propmated, color = density),
 width = 0.2, height = 0.001,
 alpha = 0.1) +

scale_x_continuous(breaks = c(1,5,10,15)) +

scale_y_continuous(position = "left", breaks = c(0, 0.20, 0.40, 0.60,
0.80, 1.00), labels = percent) +

scale_color_manual(paste(""), values = color, labels = c("High density",
"Low density"))+

#scale_color_manual(guide = "none", values = color) +

scale_fill_manual(guide = "none", values = color)+

theme(
 panel.grid.major = element_line(linetype = "blank"),
 panel.grid.minor = element_line(linetype = "blank"),
 panel.background = element_blank(),
 panel.border = element_blank(),
 axis.line = element_line(),
 axis.title = element_text(size = 12),
 axis.text.x = element_text(size = 9),
 axis.text.y = element_text(size = 9),
 plot.title = element_textbox(hjust = 0.5, size = 15, margin = margin(0,
0, 1, 0)),
 plot.margin = margin(0, 0, 0, 2),
 axis.title.y = element_text(size = 10),
 plot.tag.position = c(0.1,0.95),
 legend.key = element_rect(fill = NA, color = NA),
 legend.position = c(0.6,0.4)
) +
plot_layout(tag_level = 'new')+
labs(
 x = "",
 y = "Proportion mated females",

```

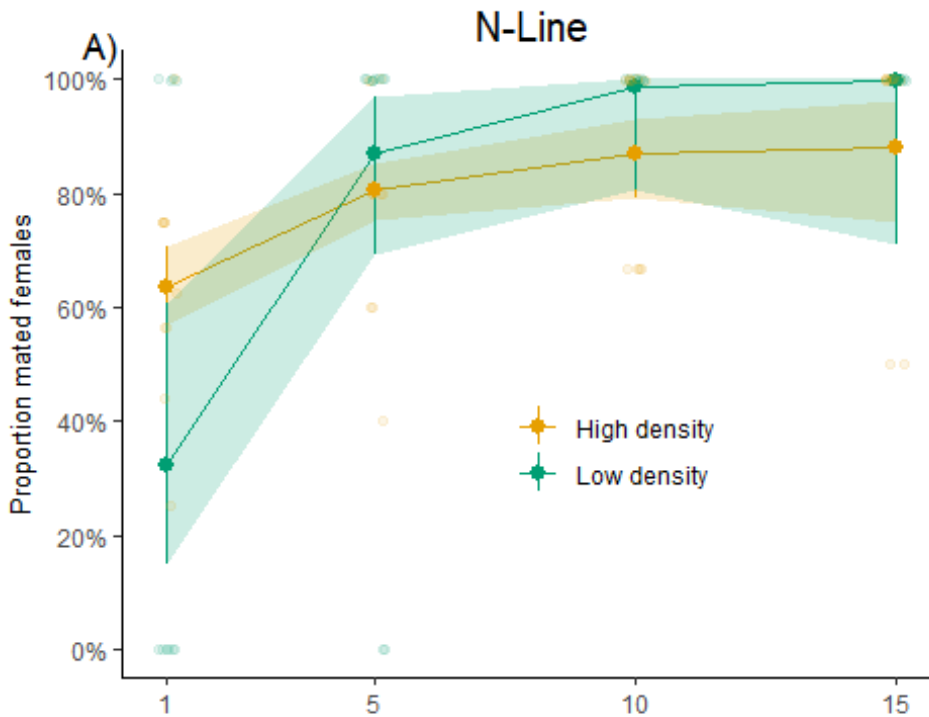


```

title = "N-Line",
tag = "A")
)

```

nline.prop.mated



#Table 2

```

tab_model(full.m2,survcurve2 , transform = NULL, show.p = FALSE, string.ci =
"95% CI", string.pred = "Covariates", show.obs = FALSE, dv.labels = c("Female
Mating Probability", "Time to First Fertile Egg"), pred.labels =
c("Intercept", "Line [N]", "Sex Ratio", "Density [Low]", "Line [N] : Sex
Ratio", "Line [N] : Density [Low]", "Sex Ratio : Density [Low]", "Line [N] :
Sex Ratio : Density [Low]"),file = "result_table.html")

```

## Random effect variances not available. Returned R2 does not account for random effects.

Female Mating Probability

Time to First Fertile Egg

Covariates

Log-Odds

95% CI

Estimates

95% CI

Intercept

-3.92

-4.19 – -3.65

Line [N]

1.16

0.83 – 1.49

0.93

0.15 – 1.71

Sex Ratio

0.05

0.00 – 0.09

-0.04

-0.11 – 0.04

Density [Low]

2.33

1.34 – 3.32

-2.56

-3.59 – -1.52

Line [N] : Sex Ratio

-0.04

-0.09 – 0.02

-0.06

-0.15 – 0.03

Line [N] : Density [Low]

-0.51

-1.85 – 0.82

-0.17

-1.48 – 1.14

Sex Ratio : Density [Low]

-0.14

-0.25 – -0.03

0.11

0.00 – 0.22

Line [N] : Sex Ratio : Density [Low]

0.14

-0.06 – 0.34

0.09

-0.05 – 0.23

R2 conditional / R2 marginal

NA / 0.393

0.427

#Figure 1. PATCHWORK plots for publication

```
patchworkV15<- nline.prop.mated + hline.prop.mated +
 nline.time.to + hline.time.to +
 plot_layout(
 ncol = 2,
 nrow = 2,
 heights = c(4,4),
 widths = c(2,2)
)
```

```
##Save patchworkV15 dev.new() patchworkV15
```

```
jpeg("patchworkV15.jpeg",res=800,pointsize=10,height=15,width=17,units="cm")
```

```
patchworkV15 dev.off()
```