# Reproducible analysis for: Individual flexibility in group foraging behaviour of reef manta rays (Mobula alfredi)

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## Table of contents

## 0.1 Rationale

This is a reproducible script for all statistical models and their outputs presented in our article.

## 0.2 Packages and data import

Make sure to have these packages installed before running the code in this report

```
library(tidyverse); library(here); library(easystats);
library(kableExtra); library(lme4); library(effects)
library(marginaleffects); library(ggeffects); library(rptR)
library(gtsummary); library(ggthemes); library(patchwork)
library(tidybayes)
```

Import complete dataset

```
df = read.csv(here("data/data-clean/Manta Data_Annie.csv"),
              header=TRUE, sep=",", na.strings="NA", dec=".",
              strip.white=TRUE)
df %>%
  select(1:10) %>%
  head() %>%
  kable()
```

| npid | id | day | year | nyear | site | clips | sex | size | maturity |
|------|-----|-----|------|-------|------|-------|-----|------|----------|
| P204 | 204 | 185 | 2016 | year3 | 1 | 10 | 2 | 3 | 2 |
| P204 | 204 | 185 | 2016 | year3 | 1 | 10 | 2 | 3 | 2 |
| P225 | 225 | 259 | 2016 | year3 | 1 | 24 | 1 | 3 | 1 |
| P281 | 281 | 259 | 2016 | year3 | 1 | 24 | 2 | 3 | 2 |
| P281 | 281 | 259 | 2016 | year3 | 1 | 24 | 2 | 3 | 2 |
| P302 | 302 | 259 | 2016 | year3 | 1 | 24 | 1 | 3 | 1 |

Import group foraging dataset

```
df.group = read.csv(here("data/data-clean/group_rp.csv"),
                    header=TRUE, sep=",", na.strings="NA", dec=".",
                    strip.white=TRUE)
df.group$id = as.factor(df.group$id)
df.group$site = as.factor(df.group$site)
df.group$sex_f = as.factor(ifelse(df.group$sex=="1","F","M"))
df.group$size = as.factor(df.group$size)
df.group$maturity = as.factor(df.group$maturity)
df.group$plankton = as.factor(df.group$plankton)
df.group$shark_bite = as.factor(df.group$shark_bite)
df.group$anthropogenic = as.factor(df.group$anthropogenic)
df.group$Id = df.group$id

# Transform Time columns centered aroun 12:00pm expressed in hours
```

```
df.group$time_cen = hm(df.group$time)
df.group$time_cen = as.numeric(df.group$time_cen-hours(12))/3600

# subset with only individuals within groups
df.group = df.group[df.group$group==1,]
df.group=df.group[complete.cases(df.group$position),]
df.group %>%
  select(1:10) %>%
  head() %>%
  kable()
```

| npid | id | obs_nb | rep_tot | day | year | nyear | site | clips | sex |
|------|-----|--------|---------|-----|------|-------|------|-------|-----|
| P19 | 19 | 1 | 2 | 155 | 2016 | year3 | 1 | 46 | 1 |
| P19 | 19 | 2 | 2 | 155 | 2016 | year3 | 1 | 46 | 1 |
| P33 | 33 | 1 | 17 | 153 | 2016 | year3 | 1 | 16 | 2 |
| P33 | 33 | 2 | 17 | 155 | 2016 | year3 | 1 | 46 | 2 |
| P33 | 33 | 3 | 17 | 184 | 2016 | year3 | 1 | 25 | 2 |
| P33 | 33 | 4 | 17 | 184 | 2016 | year3 | 1 | 25 | 2 |

## 0.3 Group vs. solo foraging

## 0.4 What explains variation in group leadership ?

We fit a binomial GLMM on leadership probability with the following covariates:

- Sex
- Age class
- Shark injury status
- Anthropogenic injury status
- Individual ID (random effect)

```
glmm.lead=glmer(leader ~
                sex_f + maturity +
                shark_bite + anthropogenic + (1|Id),
            family = "binomial",
            df.group)

summary(glmm.lead)
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: binomial  ( logit )
Formula: leader ~ sex_f + maturity + shark_bite + anthropogenic + (1 |      Id)
   Data: df.group

     AIC      BIC   logLik deviance df.resid
  2152.9   2185.7  -1070.4   2140.9     1754

Scaled residuals:
   Min     1Q Median     3Q    Max
-1.318 -0.650 -0.566  1.217  2.302

Random effects:
 Groups Name        Variance Std.Dev.
 Id     (Intercept) 0.2715   0.521
Number of obs: 1760, groups:  Id, 322

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -0.78194    0.09655  -8.099 5.55e-16 ***
sex_fM        -0.35794    0.14851  -2.410   0.0159 *
maturity2      0.07813    0.13718   0.570   0.5690
shark_bite1    0.12525    0.20364   0.615   0.5385
anthropogenic1 -0.14638    0.17133  -0.854   0.3929
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
           (Intr) sex_fM mtrty2 shrk_1
sex_fM     -0.310
maturity2  -0.377 -0.282
shark_bite1 -0.302 -0.024  0.051
anthropgnc1 -0.305  0.007 -0.078  0.102
```
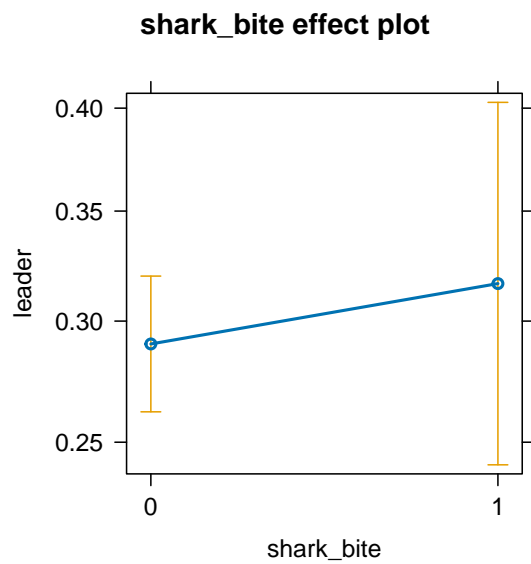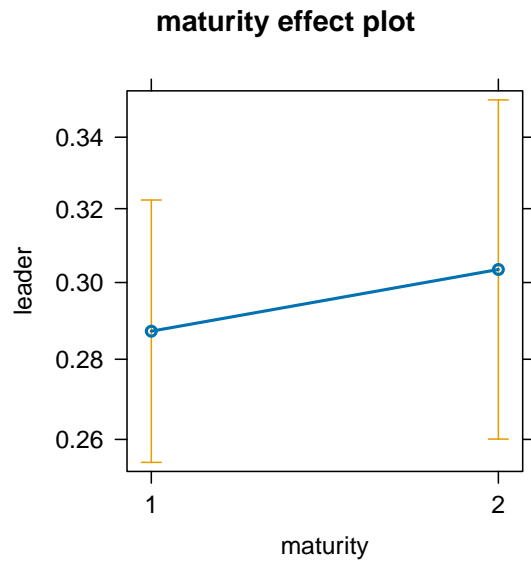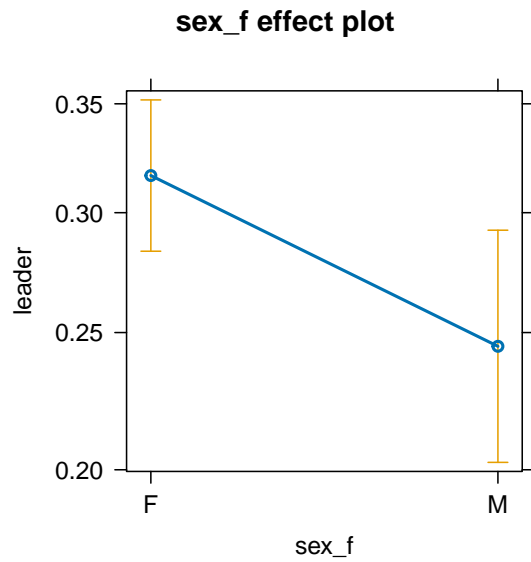
```
plot(allEffects(glmm.lead))
```

## sex_f effect plot



## maturity effect plot



## shark_bite effect plot
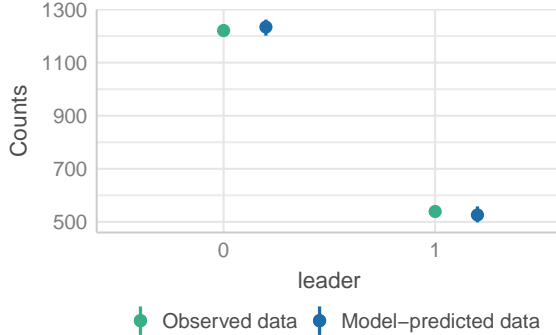


## anthropogenic effect plot
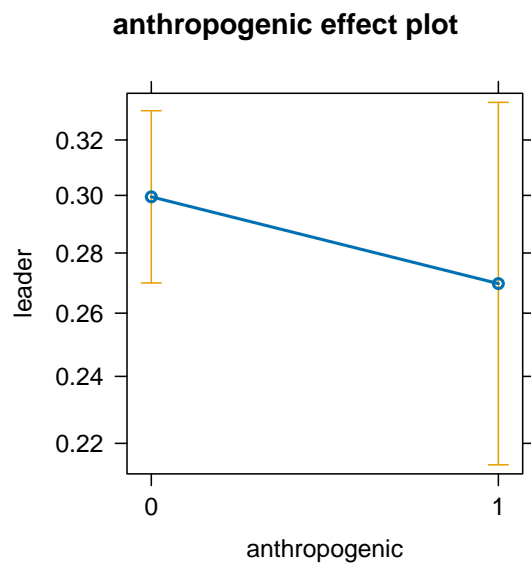


```
# Save model file
saveRDS(glmm.lead, file = here("outputs/mods/glmm.lead.rds"))
```

Inspect the model

```
check_model(glmm.lead)
```

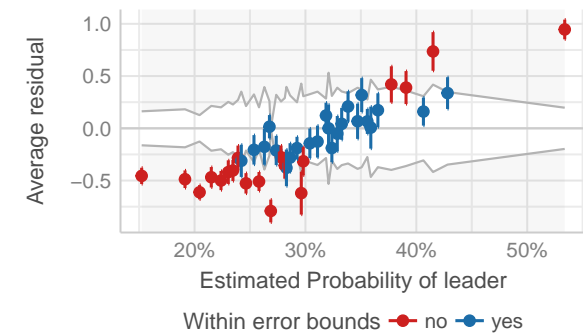## Posterior Predictive Check
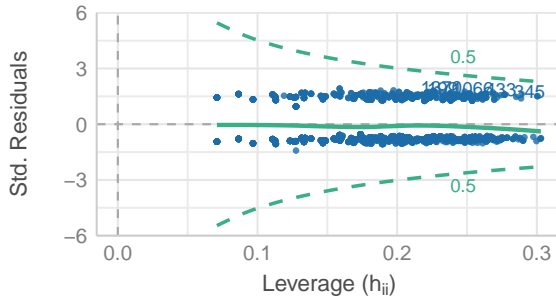Model−predicted intervals should include observed data points



## Binned Residuals
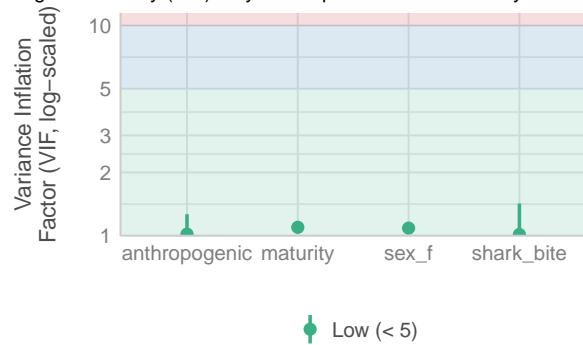Points should be within error bounds



## Influential Observations
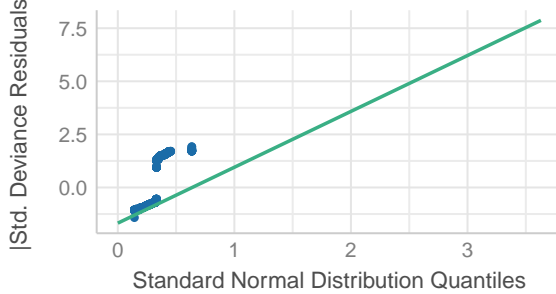Points should be inside the contour lines



## Collinearity
High collinearity (VIF) may inflate parameter uncertainty



## Normality of Residuals
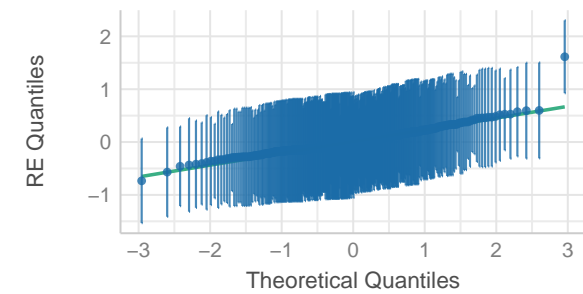Dots should fall along the line



## Normality of Random Effects (Id)
Dots should be plotted along the line



Check R2 and repeatability

```r
r2.lead = r2_nakagawa(glmm.lead, ci = T)
icc.lead = icc(glmm.lead, ci = T)
r2.lead; icc.lead

# Save files to avoid reloading
saveRDS(r2.lead, file = here("outputs/mods/r2.lead.rds"))
saveRDS(icc.lead, file = here("outputs/mods/icc.lead.rds"))
```

Get model summary in table format

```r
tbl.glmm.lead = glmm.lead %>%
  tbl_regression(
    intercept = T,
    exponentiate = TRUE,
    pvalue_fun = ~ style_pvalue(.x, digits = 2)) %>%
  add_global_p() %>%
  bold_p(t = .05) %>%
  bold_labels() %>%
  italicize_levels() %>%
  add_nevent(location = "level")
tbl.glmm.lead
```

| Characteristic | Event N | OR | 95% CI | p-value |
|---|---|---|---|---|
| **(Intercept)** | 539 | 0.46 | 0.38, 0.55 | **<0.001** |
| **sex_f** | | | | **0.016** |
| *F* | 395 | — | — | |
| *M* | 144 | 0.70 | 0.52, 0.94 | |
| **maturity** | | | | 0.57 |
| *1* | 344 | — | — | |
| *2* | 195 | 1.08 | 0.83, 1.41 | |
| **shark_bite** | | | | 0.54 |
| *0* | 473 | — | — | |
| *1* | 66 | 1.13 | 0.76, 1.69 | |
| **anthropogenic** | | | | 0.39 |
| *0* | 435 | — | — | |
| *1* | 104 | 0.86 | 0.62, 1.21 | |

We can now export the table in both word and html format

```r
tbl.glmm.lead %>%
  as_gt() %>%
  gt::gtsave(filename = here("outputs/tables/tbl.glmm.lead.html"))

tbl.glmm.lead %>%
  as_gt() %>%
  gt::gtsave(filename = here("outputs/tables/tbl.glmm.lead.docx"))
```

## 0.5 Individual differences in group leadership compared between sexes, age and injury status

### 0.5.1 Male - female differences

#### 0.5.1.1 Fit glmer models

```
glmm.lead.f = glmer(leader ~
                      maturity +
                      shark_bite + anthropogenic + (1|id),
                    family = "binomial",
                    subset(df.group, sex_f == "F"))
glmm.lead.m = glmer(leader ~
                      maturity +
                      shark_bite + anthropogenic + (1|id),
                    family = "binomial",
                    subset(df.group, sex_f == "M"))

summary(glmm.lead.f); summary(glmm.lead.m)
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: binomial  ( logit )
Formula: leader ~ maturity + shark_bite + anthropogenic + (1 | id)
   Data: subset(df.group, sex_f == "F")

     AIC      BIC   logLik deviance df.resid
  1538.9   1564.4   -764.5   1528.9     1210

Scaled residuals:
    Min      1Q  Median      3Q     Max
-0.8534 -0.6976 -0.6550  1.3714  1.5921

Random effects:
 Groups Name        Variance Std.Dev.
 id     (Intercept) 0.05108  0.226
Number of obs: 1215, groups:  id, 205

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -0.81548    0.08899  -9.164   <2e-16 ***
maturity2     0.15263    0.14658   1.041    0.298
```

```
shark_bite1      0.28231     0.20398    1.384     0.166
anthropogenic1  0.01023     0.16630    0.062     0.951
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Correlation of Fixed Effects:
          (Intr) mtrty2 shrk_1
maturity2   -0.448
shark_bite1 -0.345  0.030
anthropgnc1 -0.378 -0.010  0.088


Generalized linear mixed model fit by maximum likelihood (Laplace
  Approximation) [glmerMod]
 Family: binomial  ( logit )
Formula: leader ~ maturity + shark_bite + anthropogenic + (1 | id)
   Data: subset(df.group, sex_f == "M")

     AIC       BIC    logLik deviance df.resid
   609.3     630.8    -299.7    599.3      540


Scaled residuals:
    Min      1Q  Median      3Q      Max
-1.7946 -0.5537 -0.4665  0.5572  2.7748


Random effects:
 Groups Name        Variance Std.Dev.
 id     (Intercept) 0.6399   0.8
Number of obs: 545, groups:  id, 119


Fixed effects:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)   -1.001829   0.001641 -610.64   <2e-16 ***
maturity2     -0.069563   0.001640  -42.41   <2e-16 ***
shark_bite1   -0.476913   0.001640 -290.88   <2e-16 ***
anthropogenic1 -0.482348  0.001640 -294.18   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Correlation of Fixed Effects:
          (Intr) mtrty2 shrk_1
maturity2   0.000
shark_bite1 0.000  0.000
```
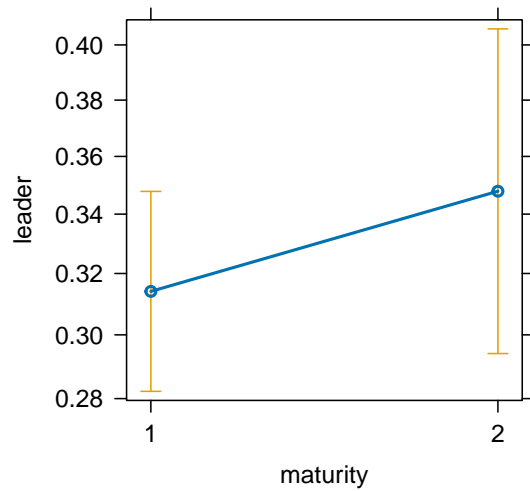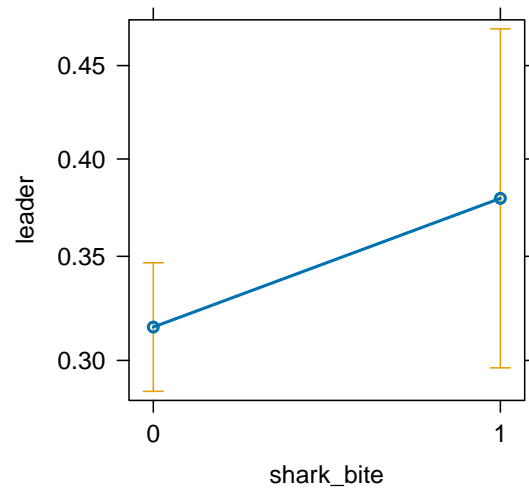
```
anthropgnc1 0.000   0.000   0.000
optimizer (Nelder_Mead) convergence code: 0 (OK)
Model failed to converge with max|grad| = 0.0430752 (tol = 0.002, component 1)
```

```
plot(allEffects(glmm.lead.f)); plot(allEffects(glmm.lead.f))
```
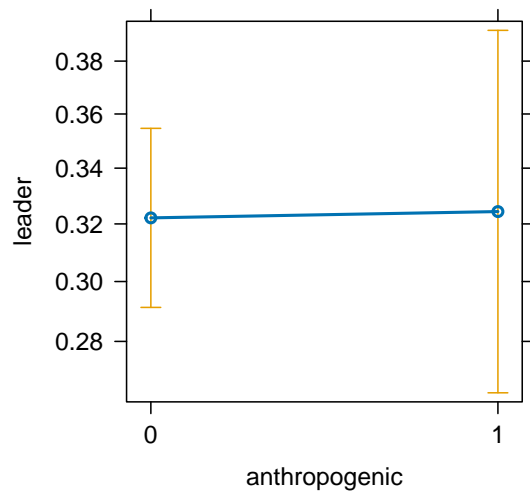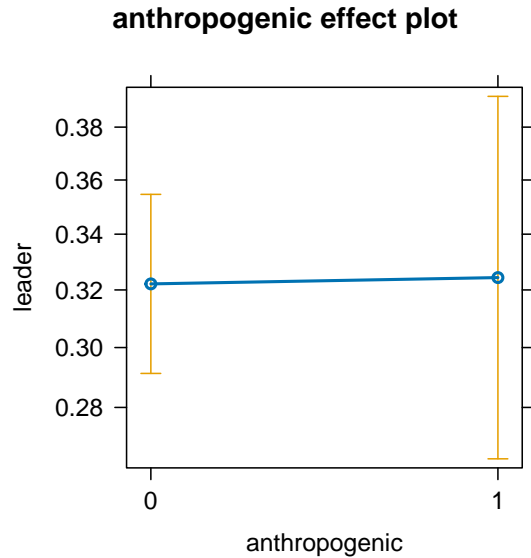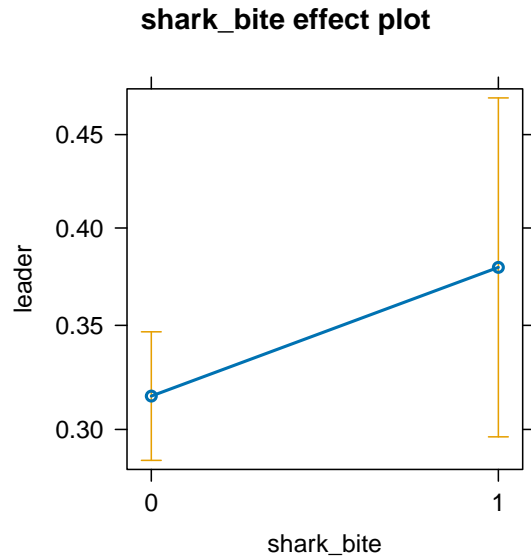
**maturity effect plot**

**shark_bite effect plot**

**anthropogenic effect plot**
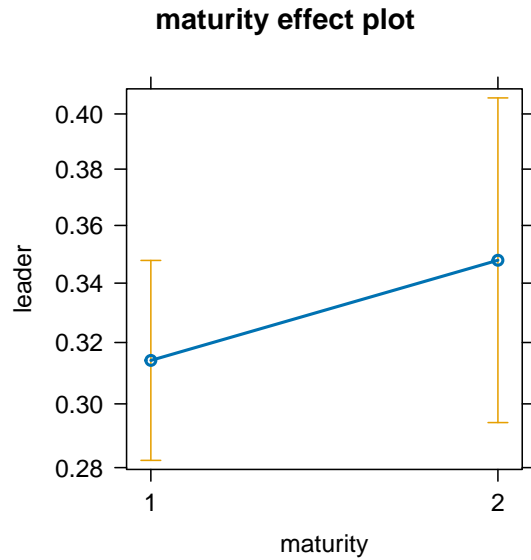
## maturity effect plot



## shark_bite effect plot



## anthropogenic effect plot



```
# Save model file
saveRDS(glmm.lead.f, file = here("outputs/mods/glmm.lead.f.rds"))
saveRDS(glmm.lead.m, file = here("outputs/mods/glmm.lead.m.rds"))
```

The model does not converges properly with the male dataset. This comes from that fact that there are few adult males in the population. Because our question is now related to variance component, we keep the fixed effect structure the same regardless for consistency.

### 0.5.1.2 Fit rptR models

Adjusted repeatability

```r
rpt.R.f = rpt(leader ~ maturity +
                shark_bite + anthropogenic + (1|id),
            grname = "id",
            datatype = "Binary",
            data = subset(df.group, sex_f == "F"))
rpt.R.m = rpt(leader ~ maturity +
                shark_bite + anthropogenic + (1|id),
            grname = "id",
            datatype = "Binary",
            data = subset(df.group, sex_f == "M"))


saveRDS(rpt.R.f, here("outputs/mods/rpt.R.f.rds"))
saveRDS(rpt.R.m, here("outputs/mods/rpt.R.m.rds"))
```

All variance components

```r
rpt.V.f = rpt(leader ~ maturity +
                shark_bite + anthropogenic + (1|id),
            grname = c("id", "Fixed", "Residual"),
            datatype = c("Binary"),
            data = subset(df.group, sex_f == "F"),
            ratio = FALSE)
rpt.V.m = rpt(leader ~ maturity +
                shark_bite + anthropogenic + (1|id),
            grname = c("id", "Fixed", "Residual"),
            datatype = "Binary",
            data = subset(df.group, sex_f == "M"),
            ratio = FALSE)
saveRDS(rpt.V.f, here("outputs/mods/rpt.V.f.rds"))
saveRDS(rpt.V.m, here("outputs/mods/rpt.V.m.rds"))
```

All variance ratios

```r
rpt.r2.f = rpt(leader ~ maturity +
                shark_bite + anthropogenic + (1|id),
            grname = c("id", "Fixed", "Residual"),
            datatype = c("Binary"),
            data = subset(df.group, sex_f == "F"),
```

```
                 ratio = T)
rpt.r2.m = rpt(leader ~ maturity +
                  shark_bite + anthropogenic + (1|id),
               grname = c("id", "Fixed", "Residual"),
               datatype = "Binary",
               data = subset(df.group, sex_f == "M"),
               ratio = T)
saveRDS(rpt.r2.f, here("outputs/mods/rpt.r2.f.rds"))
saveRDS(rpt.r2.m, here("outputs/mods/rpt.r2.m.rds"))
```

### 0.5.1.3 Plot the model estimates

Store all variance components

```
Vi_f = rpt.V.f$R_boot_link$id
Vi_m = rpt.V.m$R_boot_link$id
Vfe_f = rpt.V.f$R_boot_link$Fixed
Vfe_m = rpt.V.m$R_boot_link$Fixed
VR_f = rpt.V.f$R_boot_link$Residual
VR_m = rpt.V.m$R_boot_link$Residual
R_f = rpt.R.f$R_boot_link$id
R_m = rpt.R.m$R_boot_link$id
```

Put into formated table

```
# Variance ratio difference figure
r2_Vi_f = rpt.r2.f$R_boot_link$id
r2_Vi_m = rpt.r2.m$R_boot_link$id
r2_Vfe_f = rpt.r2.f$R_boot_link$Fixed
r2_Vfe_m = rpt.r2.m$R_boot_link$Fixed
r2_VR_f = rpt.r2.f$R_boot_link$Residual
r2_VR_m = rpt.r2.m$R_boot_link$Residual

df = data.frame(r2_Vi = c(r2_Vi_f, r2_Vi_m),
                r2_Vfe = c(r2_Vfe_f, r2_Vfe_m),
                r2_VR = c(r2_VR_f, r2_VR_m),
                Sex = c(rep("F", length(r2_Vi_f)),
                        rep("M", length(r2_Vi_m)))) %>%
  pivot_longer(cols = r2_Vi:r2_VR,
               names_to = "v.compo",
               values_to = "var")
```

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```
# Store effect sizes
df.2  = data.frame(delta_r2_Vi = r2_Vi_f - r2_Vi_m,
                   delta_r2_Vfe = r2_Vfe_f - r2_Vfe_m,
                   delta_r2_VR = r2_VR_f - r2_VR_m)
```

Plot

```
p1 = df %>%
  group_by(v.compo, Sex) %>%
  summarise(var = mean(var)) %>%
  ggplot(aes(y = var, x = Sex, fill = v.compo)) +
  geom_bar(position = "fill",
           stat = "identity", width = .2) +
  scale_fill_wsj(labels = c(
    bquote(V[fe]),
    bquote(V[i]),
    bquote(V[R]))) +
  ylab("Variance explained") +
  theme_bw(18) +
  labs(fill = "") +
  theme(legend.position = c(.9, .5))

delta.vi.r = df.2 %>%
  ggplot(aes(x = delta_r2_Vi * 100)) +
  stat_halfeye(alpha = .6) +
  geom_vline(xintercept = 0,
             linetype = "dashed") +
  xlab(bquote(Delta[V[i]])) +
  ylab("Density") +
  theme_bw(18) +
  ggtitle("Difference in variance explained (%)")

delta.vfe.r = df.2 %>%
  ggplot(aes(x = delta_r2_Vfe * 100)) +
  stat_halfeye(alpha = .6) +
  geom_vline(xintercept = 0,
             linetype = "dashed") +
  xlab(bquote(Delta[V[fe]])) +
  ylab("Density") +
  theme_bw(18)
```
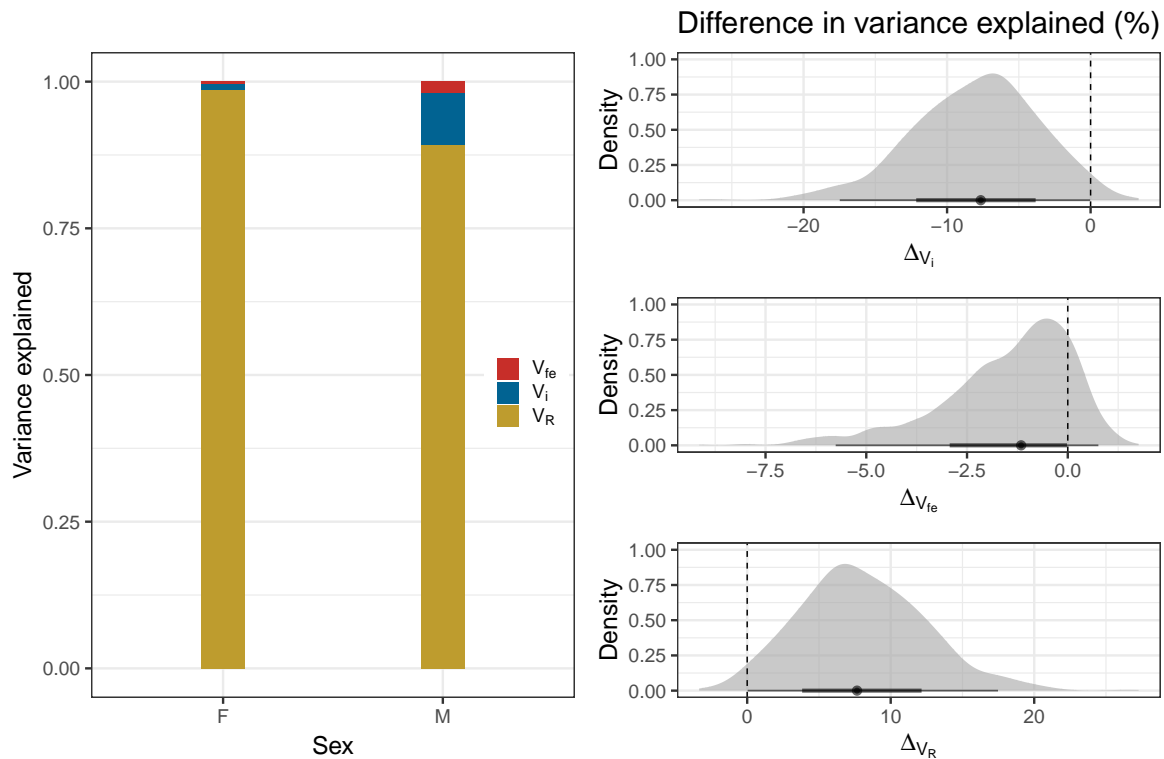
```
delta.vr.r = df.2 %>%
  ggplot(aes(x = delta_r2_VR * 100)) +
  stat_halfeye(alpha = .6) +
  geom_vline(xintercept = 0,
             linetype = "dashed") +
  xlab(bquote(Delta[V[R]])) +
  ylab("Density") +
  theme_bw(18)

delta.v.r = delta.vi.r / delta.vfe.r / delta.vr.r

delta.v.r = p1 + (delta.vi.r / delta.vfe.r / delta.vr.r)
delta.v.r
```



```
ggsave(filename = "outputs/figs/delta.v.r.jpeg", delta.v.r,
       width = 12, height = 8)
ggsave(filename = "outputs/figs/delta.v.r.pdf", delta.v.r,
       width = 12, height = 8)
```

### 0.5.2 Juvenile - adult differences

### 0.5.3