Report 3

Malika Ihle

August 22, 2019

Data description

missing values

as per preregistration: if measurements were forgotten and cannot be done (e.g. weight not measure immediately before the test), the group average (e.g. among red averse females or among males with red face and red pedipalps)will be attributed to that individual FID 18401 has no weight (had a typo in the weight of both (before after) that could not be corrected)

FID 18401 has no weight (had a typo in the weight of both (before after) that could not be corrected) MID 18228 (paired with FID 18072) and MID 18390 (paired with FID 18478) have no weight averages as described were given to them

note: companion males were IDed but not weighted (only measured at maturity like all spiders)

dependent variables explanations

CopulateYN: copulation that occur at any time, during the video, or seen after on the shelf (but could also be extrapolated from the fact that spiderlings emerged)
CannibaliseYN: cannibalism that accour during the 2h video or the 46 hours after that (after which male and female were separated)
CopDuringVideo: copulation that occured within the 2h video
EatDuringVideo: cannibalism that occured during the 2h video

decision of dependent variable as preregistered

is frequency of cannibalism within 48h between 15% and 85%?

[1] 36.1991

is frequency of copulation during video between 17% and 83%?

[1] 58.37104

as per preregistration, FTrt and MTrt were recoded as:

Female diet/training

red accustomed/preference group [code (relative to their preference for red) = +0.5]
red averse group [code (relative to their preference for red) = -0.5]

Male color manipulation

AllRed: (face and pedipalps painted red [code (amount of red body parts) = 2]
RedGrey: face painted red and pedipalps painted grey [code (amount of red body parts) = 1]
AllGrey: face and pedipalps painted grey [code (amount of red body parts) = 0]

Covariables or other dependent variables explanations

M and Fcondition were calculated as resid(lm(Mass~CarapaceWidth))
DelayToLay is the difference between the lay date and the trial end date in days **Brood size**: Number of spiderlings emerging from the first clutch following the test (females were allowed to start laying until 22

December 2018)

TrainingDuration: differnece in days between Trial Date and Period Begin Date (which is the start date of training)

Video: time during which we record courtships and attacks

at first we were watching the whole video (2h), unless the male was getting cannibalized
then (soonm maybe after ~30 videos?) we stopped watching videos right after copulation occured (only checking if the male got cannibalized afterwards)
overall, time stopped watching is either the time of attack if she consumed it, the time start of the copulation, or the time at which we stopped watching (after about 2 hours) if none of those two events occured

Sample sizes

this table does not include the *20 trials with unmanipulated males*
Out of 221 females tested with a painted male,
221-54 = 167 females laid clutched

not visible here but looking directly in the DB:
during training: 2 disappeared, 1 died, 9 were killed after 3 months training without maturing
video missing: 254, 497, and 233 with painted males, 149 with unmanipulated male after training: 1
disappeared before getting the opportunity to lay eggs FID 18417 who was tested with an unmanipulated male

Results Raw Data

Sample sizes of tests
as preregistered: We aim at the largest possible sample size, with at least 30 females per FTrt*MTrt

```
##              FTrt AllGrey AllRed RedGrey Unmanipulated
## 1     RedAverse      36     37      36            10
## 2 RedPreference      37     38      37            10
```

Number of tests (and percentages) where copulation was seen during the video

```
##              FTrt AllGrey AllRed RedGrey Unmanipulated
## 1     RedAverse      24     18      25             6
## 2 RedPreference      22     22      18             6
```

```
##              FTrt  AllGrey   AllRed  RedGrey Unmanipulated
## 1     RedAverse 66.66667 48.64865 69.44444            60
## 2 RedPreference 59.45946 57.89474 48.64865            60
```

Number of tests where cannibalism occured during the 48h allocated

```
##              FTrt AllGrey AllRed RedGrey Unmanipulated
## 1     RedAverse      12     15      16             6
## 2 RedPreference      12     10      15             4
```

```
##              FTrt  AllGrey   AllRed  RedGrey Unmanipulated
## 1     RedAverse 33.33333 40.54054 44.44444            60
## 2 RedPreference 32.43243 26.31579 40.54054            40
```

Preregistered Analyses on Copulation and Cannibalism

in preregistration Model 1: glm (CannibalismY/N ~ male treatment * female treatment + female body condition, family = binomial). Model 2: glm (CannibalismY/N ~ female treatment + female body condition, family = binomial Model 3: glm (CopulationY/N ~ male treatment * female treatment + male size + male

body condition, family = binomial). Model 4: glm (CopulationY/N ~ female treatment + male size + male body condition, family = binomial).

We also preregistered that if Fcondition is significantly leading to more cannibalism this should be removed FCondition was positively significant in the cannibalism model so it is silenced in the models below

```r
# Model 1
modCannibalism <- glm (CannibalizeYN ~ FTrtCode* MTrtCode
                        #+ Fcondition
                      , family = "binomial", data = MY_TABLE)

summary(modCannibalism)
```

```
##
## Call:
## glm(formula = CannibalizeYN ~ FTrtCode * MTrtCode, family = "binomial",
##     data = MY_TABLE)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.0604  -0.9480  -0.8952   1.3652   1.5522
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -0.57403    0.22255  -2.579   0.0099 **
## FTrtCode           0.01430    0.44511   0.032   0.9744
## MTrtCode           0.00454    0.17197   0.026   0.9789
## FTrtCode:MTrtCode -0.29045    0.34393  -0.844   0.3984
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 289.31  on 220  degrees of freedom
## Residual deviance: 287.61  on 217  degrees of freedom
## AIC: 295.61
##
## Number of Fisher Scoring iterations: 4
```

```r
# Model 2
modCannibalism2 <- glm (CannibalizeYN ~ FTrtCode
                        #+  Fcondition
                      , family = "binomial", data = MY_TABLE[MY_TABLE$MTrt == "AllRed",])

summary(modCannibalism2)
```

```
##
## Call:
## glm(formula = CannibalizeYN ~ FTrtCode, family = "binomial",
##     data = MY_TABLE[MY_TABLE$MTrt == "AllRed", ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.0197  -1.0197  -0.7815   1.3438   1.6340
##
## Coefficients:
```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.7063     0.2489  -2.838  0.00455 **
## FTrtCode     -0.6466     0.4978  -1.299  0.19398
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 95.477  on 74  degrees of freedom
## Residual deviance: 93.762  on 73  degrees of freedom
## AIC: 97.762
##
## Number of Fisher Scoring iterations: 4
```

```r
# Model 3
modCop <- glm (CopDuringVideo ~ FTrtCode* MTrtCode + MCarapaceWidth + Mcondition
              , family = "binomial", data = MY_TABLE)
summary(modCop)
```

```
##
## Call:
## glm(formula = CopDuringVideo ~ FTrtCode * MTrtCode + MCarapaceWidth +
##     Mcondition, family = "binomial", data = MY_TABLE)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.667  -1.251   0.863   1.064   1.378
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -2.6707     2.6696  -1.000    0.317
## FTrtCode          -0.6627     0.4506  -1.471    0.141
## MTrtCode          -0.2135     0.1703  -1.253    0.210
## MCarapaceWidth     2.4294     2.0026   1.213    0.225
## Mcondition        -7.3388    33.3506  -0.220    0.826
## FTrtCode:MTrtCode  0.3843     0.3402   1.130    0.259
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 300.15  on 220  degrees of freedom
## Residual deviance: 295.21  on 215  degrees of freedom
## AIC: 307.21
##
## Number of Fisher Scoring iterations: 4
```

```r
# Model 4
modCop2 <- glm (CopDuringVideo ~ FTrtCode + MCarapaceWidth + Mcondition
               , family = "binomial", data = MY_TABLE[MY_TABLE$MTrt == "AllRed",])
summary(modCop2)
```

```
##
## Call:
## glm(formula = CopDuringVideo ~ FTrtCode + MCarapaceWidth + Mcondition,
##     family = "binomial", data = MY_TABLE[MY_TABLE$MTrt == "AllRed",
##         ])
##
```

```
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4301  -1.2341   0.9328   1.1197   1.2874
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)      3.5662     4.3885   0.813    0.416
## FTrtCode         0.4061     0.4734   0.858    0.391
## MCarapaceWidth  -2.6047     3.3098  -0.787    0.431
## Mcondition     -83.0930   195.7720  -0.424    0.671
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 103.64  on 74  degrees of freedom
## Residual deviance: 102.34  on 71  degrees of freedom
## AIC: 110.34
##
## Number of Fisher Scoring iterations: 4
```

Exploratory analyses

Are effect sizes stronger when subsetting to females that had more than 2 weeks training (which may increase the strength of learning the color biases)?

```
# Model 1sub
modCannibalismSub <- glm (CannibalizeYN ~ FTrtCode* MTrtCode
                          #+ Fcondition
                          , family = "binomial", data = MY_TABLE[MY_TABLE$TrainingDuration > 14,])
summary(modCannibalismSub)
```

```
##
## Call:
## glm(formula = CannibalizeYN ~ FTrtCode * MTrtCode, family = "binomial",
##     data = MY_TABLE[MY_TABLE$TrainingDuration > 14, ])
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.097  -1.028  -0.952   1.335   1.421
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -0.4596     0.2639  -1.742   0.0816 .
## FTrtCode           0.1934     0.5278   0.366   0.7140
## MTrtCode           0.0910     0.2002   0.454   0.6495
## FTrtCode:MTrtCode -0.1820     0.4004  -0.454   0.6495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 211.21  on 155  degrees of freedom
## Residual deviance: 210.78  on 152  degrees of freedom
## AIC: 218.78
##
```

```
## Number of Fisher Scoring iterations: 4
# Model 2sub
modCannibalism2Sub <- glm (CannibalizeYN ~ FTrtCode
                           #+  Fcondition
                           , family = "binomial"
                           , data = MY_TABLE[MY_TABLE$MTrt == "AllRed" & MY_TABLE$TrainingDuration > 14,])
summary(modCannibalism2Sub)


##
## Call:
## glm(formula = CannibalizeYN ~ FTrtCode, family = "binomial",
##     data = MY_TABLE[MY_TABLE$MTrt == "AllRed" & MY_TABLE$TrainingDuration >
##         14, ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.0906  -1.0906  -0.9448   1.2668   1.4294
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.3915     0.2797  -1.399    0.162
## FTrtCode     -0.3677     0.5595  -0.657    0.511
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 72.997  on 53  degrees of freedom
## Residual deviance: 72.563  on 52  degrees of freedom
## AIC: 76.563
##
## Number of Fisher Scoring iterations: 4
# Model 3sub

modCopSub <- glm (CopDuringVideo ~ FTrtCode * MTrtCode + MCarapaceWidth + Mcondition
                 , family = "binomial", data = MY_TABLE[MY_TABLE$TrainingDuration > 14,])
summary(modCopSub) # trend, the more red the less copulations


##
## Call:
## glm(formula = CopDuringVideo ~ FTrtCode * MTrtCode + MCarapaceWidth +
##     Mcondition, family = "binomial", data = MY_TABLE[MY_TABLE$TrainingDuration >
##     14, ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5954  -1.2442   0.8487   1.0502   1.4052
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -1.5857     3.2630  -0.486   0.6270
## FTrtCode           0.1125     0.5528   0.204   0.8387
## MTrtCode          -0.4171     0.2047  -2.038   0.0416 *
## MCarapaceWidth     1.7479     2.4417   0.716   0.4741
## Mcondition        -1.6318    36.7785  -0.044   0.9646
## FTrtCode:MTrtCode -0.1466     0.4100  -0.358   0.7207
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 212.55  on 155  degrees of freedom
## Residual deviance: 207.64  on 150  degrees of freedom
## AIC: 219.64
##
## Number of Fisher Scoring iterations: 4
```

```r
# Model 4sub

modCop2Sub <- glm (CopDuringVideo ~ FTrtCode + MCarapaceWidth + Mcondition
                 , family = "binomial"
                 , data = MY_TABLE[MY_TABLE$MTrt == "AllRed" & MY_TABLE$TrainingDuration > 14,])
summary(modCop2Sub)
```

```
##
## Call:
## glm(formula = CopDuringVideo ~ FTrtCode + MCarapaceWidth + Mcondition,
##     family = "binomial", data = MY_TABLE[MY_TABLE$MTrt == "AllRed" &
##         MY_TABLE$TrainingDuration > 14, ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3013  -1.0840  -0.8712   1.2376   1.4175
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)      6.4937     5.9546   1.091    0.275
## FTrtCode         0.1721     0.5567   0.309    0.757
## MCarapaceWidth  -5.0032     4.4835  -1.116    0.264
## Mcondition     -88.7425   227.0321  -0.391    0.696
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 74.563  on 53  degrees of freedom
## Residual deviance: 73.218  on 50  degrees of freedom
## AIC: 81.218
##
## Number of Fisher Scoring iterations: 4
```

Do females on the two diet treatments differ in final adult size or condition (in ways that might suggest that the presence of aversive prey reduces overall feeding rate)?

```r
wilcox.test(MY_TABLE$Fcondition[MY_TABLE$FTrt == "RedPreference"],
            MY_TABLE$Fcondition[MY_TABLE$FTrt == "RedAverse"])
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  MY_TABLE$Fcondition[MY_TABLE$FTrt == "RedPreference"] and MY_TABLE$Fcondition[MY_TABLE$FTrt ==
## W = 6181, p-value = 0.8721
## alternative hypothesis: true location shift is not equal to 0
```

Is the number of spiderlings different for any of the categories Ftrt*MTrt?

74 females had a brood size of 0 221-74 = 147 had spiderlings

20 females had spiderlings but were not seen copulated out of 147 females with spiderlings
11 females were seen copulated but had no spiderlings out of 138 females that were seen copulating (9 of which were seen after the two hours videos, by chance)

```
##             FTrt AllGrey AllRed RedGrey
## 1    RedAverse    543    501     547
## 2 RedPreference   628    638     596
```

because this is a wero inflated poisson distribution, and that zeros comes from a different phenomenon, I split this analysis in two: first model explains whether females have spiderlings or not (if not: did not copulate, or did nor lay, or laid infertile eggs, or laid non hatching eggs)
second model explains the number of spiderlings for those where at least one spiderling emerged

```r
summary(glm(BroodYN ~ FTrtCode* MTrtCode
            , data = MY_TABLE, family = 'binomial'))
```

```
##
## Call:
## glm(formula = BroodYN ~ FTrtCode * MTrtCode, family = "binomial",
##     data = MY_TABLE)
##
## Deviance Residuals:
##     Min      1Q   Median      3Q      Max
## -1.5747  -1.4523   0.8663   0.9079   0.9938
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)         0.7622     0.2293   3.325 0.000885 ***
## FTrtCode           -0.2717     0.4585  -0.593 0.553466
## MTrtCode           -0.0723     0.1749  -0.413 0.679379
## FTrtCode:MTrtCode   0.3050     0.3498   0.872 0.383232
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 281.80  on 220  degrees of freedom
## Residual deviance: 280.85  on 217  degrees of freedom
## AIC: 288.85
##
## Number of Fisher Scoring iterations: 4
```

```r
summary(glmer(BroodSize ~ FTrtCode* MTrtCode + (1|FID)
              , data = MY_TABLE[MY_TABLE$BroodSize >0,], family = 'poisson'))
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: BroodSize ~ FTrtCode * MTrtCode + (1 | FID)
##    Data: MY_TABLE[MY_TABLE$BroodSize > 0, ]
##
##      AIC      BIC   logLik deviance df.resid
##   1106.4   1121.3   -548.2   1096.4      142
```

```
## 
## Scaled residuals:
##      Min      1Q  Median      3Q     Max
## -2.44788 -0.36186  0.00457  0.29795  0.75665
## 
## Random effects:
##  Groups Name        Variance Std.Dev.
##  FID    (Intercept) 0.1557   0.3946
## Number of obs: 147, groups:  FID, 147
## 
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       3.074823   0.058841  52.257   <2e-16 ***
## FTrtCode          0.144483   0.117190   1.233    0.218
## MTrtCode          0.003204   0.045664   0.070    0.944
## FTrtCode:MTrtCode -0.038281   0.091329  -0.419    0.675
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Correlation of Fixed Effects:
##            (Intr) FTrtCd MTrtCd
## FTrtCode    0.002
## MTrtCode   -0.771  0.008
## FTrtCd:MTrC 0.007 -0.773 -0.043
```

Does copulation duration (when observed (i.e. excluding zeros here)) explain number of spiderlings?

```
summary(lm(BroodSize~ CopDur , data=MY_TABLE[ MY_TABLE$CopDur > 0 ,]))
```

```
## 
## Call:
## lm(formula = BroodSize ~ CopDur, data = MY_TABLE[MY_TABLE$CopDur >
##     0, ])
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -25.483  -7.736  -1.154   7.007  31.931
## 
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 14.628704   2.391604   6.117 9.68e-09 ***
## CopDur       0.005051   0.001367   3.694 0.000319 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 11.54 on 135 degrees of freedom
##   (8 observations deleted due to missingness)
## Multiple R-squared:  0.09182,	Adjusted R-squared:  0.08509
## F-statistic: 13.65 on 1 and 135 DF,  p-value: 0.0003191
```

is male courtship effort correlated to female body condition?

observation length vary greatly between videos, depending on when the copulation occured (the shorter TotalWatch, the earlier the copulation occured)
here I use the total sum of courtship seconds with an offset of the total duration during which courtships were recorded, in a Poisson model

```r
summary(glm(TotalCourtDur~ Fcondition
            , offset = log(TotalWatch)
            , family = 'poisson'
            , data = MY_TABLE_Videos))
```

```
##
## Call:
## glm(formula = TotalCourtDur ~ Fcondition, family = "poisson",
##     data = MY_TABLE_Videos, offset = log(TotalWatch))
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -69.62  -10.49    4.52   15.20   43.28
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.842394   0.001558 -540.75   <2e-16 ***
## Fcondition  21.885966   0.565675   38.69   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 120082  on 232  degrees of freedom
## Residual deviance: 118611  on 231  degrees of freedom
##   (4 observations deleted due to missingness)
## AIC: 120702
##
## Number of Fisher Scoring iterations: 4
```

does male courtship effort predict copulation likelihood?

again, observation length vary greatly between videos, depending on when the copulation or cannibalism occured I think one cannot just do CopulateYN~TotalCourtDur or even CopulateYN~CourtshipRate
one would probably need to use STAN as in https://ecoevorxiv.org/jq9n6/ with https://osf.io/kv3uc/ part S6.3 (although the dependent variable in the example provided was a continuous trait not a binomial trait like here) or maybe give weights (inversely proportional to the variance) for each rate?

!!this is probably not a correct model!!

```r
summary(glm(CopulateYN~ CourtshipRate
            , family = 'binomial'
            , data = MY_TABLE_Videos))
```

```
##
## Call:
## glm(formula = CopulateYN ~ CourtshipRate, family = "binomial",
##     data = MY_TABLE_Videos)
##
## Deviance Residuals:
```

```
##     Min       1Q   Median       3Q      Max
## -2.0923  -1.0263   0.5822   0.9169   1.6034
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.24104    0.34773  -3.569 0.000358 ***
## CourtshipRate  0.06675    0.01207   5.532 3.17e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 303.47  on 232  degrees of freedom
## Residual deviance: 266.73  on 231  degrees of freedom
##   (4 observations deleted due to missingness)
## AIC: 270.73
##
## Number of Fisher Scoring iterations: 3
```

Are copulation and attacks negatively correlated (while controlling for male courtship effort)?

Similar problem as above but even more complex as two variables are depending on the duration of observation Here, I use attack rate and courtship rate (which doesn't weight for the fact that some were watch 1 min while some were watched 2 hours)

!!this is not a correct model!!

```r
summary(glm(CopulateYN~ IntendedFAttacksNotFatalRate + CourtshipRate
            , family = 'binomial'
            , data = MY_TABLE_Videos))
```

```
##
## Call:
## glm(formula = CopulateYN ~ IntendedFAttacksNotFatalRate + CourtshipRate,
##     family = "binomial", data = MY_TABLE_Videos)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.1013  -1.0248   0.5926   0.9196   1.6046
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  -1.234861   0.348737  -3.541 0.000399 ***
## IntendedFAttacksNotFatalRate -0.004138   0.019439  -0.213 0.831417
## CourtshipRate                 0.067096   0.012190   5.504 3.71e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 303.47  on 232  degrees of freedom
## Residual deviance: 266.68  on 230  degrees of freedom
##   (4 observations deleted due to missingness)
## AIC: 272.68
##
## Number of Fisher Scoring iterations: 3
```

While here I use whether or not they attacked the male at least one (see distribution of the Nb of attacks below). I am suprised the results are so different.

!!this is not a correct model!!

```
summary(glm(CopulateYN~ IntendedFAttacksNotFatalYN + CourtshipRate
            , family = 'binomial'
            , data = MY_TABLE_Videos))
```

```
##
## Call:
## glm(formula = CopulateYN ~ IntendedFAttacksNotFatalYN + CourtshipRate,
##     family = "binomial", data = MY_TABLE_Videos)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.4521  -0.9990   0.5401   0.8470   1.7716
##
## Coefficients:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -0.51839    0.42721  -1.213  0.22497
## IntendedFAttacksNotFatalYN -1.11521    0.37399  -2.982  0.00286 **
## CourtshipRate               0.07121    0.01268   5.614 1.97e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 303.47  on 232  degrees of freedom
## Residual deviance: 256.92  on 230  degrees of freedom
##   (4 observations deleted due to missingness)
## AIC: 262.92
##
## Number of Fisher Scoring iterations: 4
```

Is cannibalism predicted by attacks ?

similar problem as above, here I use attack rate as a predictor

!!this is not a correct model!!

```
summary(glm(CannibalizeYN~ IntendedFAttacksNotFatalRate
            , family = 'binomial'
            , data = MY_TABLE_Videos))
```

```
##
## Call:
## glm(formula = CannibalizeYN ~ IntendedFAttacksNotFatalRate, family = "binomial",
##     data = MY_TABLE_Videos)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.1292  -0.9470  -0.9284   1.3827   1.4488
##
## Coefficients:
##                              Estimate Std. Error z value Pr(>|z|)
## (Intercept)                  -0.61867    0.15410  -4.015 5.95e-05 ***
```

```
## IntendedFAttacksNotFatalRate  0.02827    0.01989   1.421     0.155
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 313.71  on 236  degrees of freedom
## Residual deviance: 311.13  on 235  degrees of freedom
## AIC: 315.13
##
## Number of Fisher Scoring iterations: 4
```

besdides, the distribution of Nb of attacks should probably be assimilated to a binomial one

```
summary(MY_TABLE_Videos$NbIntendedFAttacksNotFatal)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   0.000   2.000   3.283   4.000  27.000
```

so maybe this model is cleaner?

```
summary(glm(CannibalizeYN~ IntendedFAttacksNotFatalYN
            , family = 'binomial'
            , data = MY_TABLE_Videos))
```

```
##
## Call:
## glm(formula = CannibalizeYN ~ IntendedFAttacksNotFatalYN, family = "binomial",
##     data = MY_TABLE_Videos)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.9914  -0.9914  -0.9171   1.3756   1.4623
##
## Coefficients:
##                            Estimate Std. Error z value Pr(>|z|)
## (Intercept)                 -0.6487     0.2573  -2.521   0.0117 *
## IntendedFAttacksNotFatalYN   0.1940     0.3016   0.643   0.5202
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 313.71  on 236  degrees of freedom
## Residual deviance: 313.29  on 235  degrees of freedom
## AIC: 317.29
##
## Number of Fisher Scoring iterations: 4
```