Report 2

Malika Ihle

June 27, 2019

Trial data structure

Remarks

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, seen after on the shelf, or 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] 57.91855
```

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]

Covariablesor 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)

Table structure

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, of which

not visible here but looking directly in the DB: during training: 2 disappeared, one died, 9 were killed after 3 months training without maturing ; after training: one disappeared before getting the opportunity to lay eggs FID 18417 who was tested with an unmanipulated male

```
##       FID                    FTrt       PeriodBeginDate      TrialDate
##  Min.   :18064   RedAverse    :109   2018-05-09: 36    2018-06-10:  9
##  1st Qu.:18127   RedPreference:112   2018-05-11: 31    2018-06-24:  8
##  Median :18327                       2018-05-18: 18    2018-07-10:  8
##  Mean   :18306                       2018-06-11:  9    2018-06-04:  6
##  3rd Qu.:18474                       2018-06-20:  9    2018-06-29:  6
##  Max.   :18577                       2018-06-18:  8    2018-07-11:  6
##                                      (Other)   :110    (Other)   :178
##    CopulateYN     CopDuringVideo   CannibalizeYN   EatDuringVideo
##  Min.   :0.0000   Min.   :0.0000   Min.   :0.000   Min.   :0.0000
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.000   1st Qu.:0.0000
##  Median :1.0000   Median :1.0000   Median :0.000   Median :0.0000
##  Mean   :0.6199   Mean   :0.5792   Mean   :0.362   Mean   :0.1176
##  3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.000   3rd Qu.:0.0000
##  Max.   :1.0000   Max.   :1.0000   Max.   :1.000   Max.   :1.0000
##
##             CannibalismTime   CannibalismDate
##  1899-12-30 08:00:00:  8    2018-06-11:  4
##  1899-12-30 08:30:00:  7    2018-07-10:  4
##  1899-12-30 08:15:00:  4    2018-06-05:  3
##  1899-12-30 09:30:00:  3    2018-06-29:  3
##  1899-12-30 16:00:00:  3    2018-07-01:  3
##  (Other)            : 48    (Other)   : 57
##  NA's               :148    NA's      :147
##                                        TestRemarks      FMass
##  copulation right after 2h video              :  2   Min.   :0.00970
##  24h < cannibalism < 48h                      :  1   1st Qu.:0.01660
##  6/26 copulation 8:45AM                       :  1   Median :0.01830
##  camera died for one min between 8:30 and 8:31:  1   Mean   :0.01878
##  camera tilted up                             :  1   3rd Qu.:0.02110
##  (Other)                                      : 27   Max.   :0.03390
##  NA's                                         :188
##  FCarapaceWidth       MID                   MTrt
##  Min.   :1.209   Min.   :18140   AllGrey      :73
##  1st Qu.:1.501   1st Qu.:18221   AllRed       :75
```

```
##  Median :1.548   Median :18295   RedGrey      :73
##  Mean   :1.556   Mean   :18320   Unmanipulated: 0
##  3rd Qu.:1.616   3rd Qu.:18408
##  Max.   :1.847   Max.   :18584
##
##                                  MalePaintingRemarks MCarapaceWidth
##  picture with scale                         : 54      Min.   :1.072
##  put to sleep twice                         :  9      1st Qu.:1.282
##  clean eye with thinner                     :  2      Median :1.339
##  put to sleep twice, clean eye with thinner:  2      Mean   :1.332
##   a tiny bit of paint on top one chelicerae:  1      3rd Qu.:1.375
##  (Other)                                    : 26      Max.   :1.580
##  NA's                                       :127
##      MMass         CompanionID        TrialDateEnd    EmergenceDate
##  Min.   :0.0056   Min.   :18140   2018-06-12:  8   2018-09-09:  8
##  1st Qu.:0.0111   1st Qu.:18245   2018-06-24:  7   2018-07-13:  5
##  Median :0.0121   Median :18364   2018-07-01:  7   2018-07-26:  5
##  Mean   :0.0125   Mean   :18354   2018-07-10:  6   2018-08-06:  5
##  3rd Qu.:0.0131   3rd Qu.:18439   2018-07-19:  6   2018-08-14:  5
##  Max.   :0.0651   Max.   :18584   2018-07-30:  6   (Other)   :115
##                                   (Other)   :181   NA's      : 78
##    BroodSize       DelaytoLay
##  Min.   : 0.00   Min.   :  8.00
##  1st Qu.: 0.00   1st Qu.: 12.00
##  Median :16.00   Median : 15.00
##  Mean   :15.62   Mean   : 21.44
##  3rd Qu.:25.00   3rd Qu.: 18.00
##  Max.   :62.00   Max.   :194.00
##                  NA's   :54
##                                          BroodRemarks   Fcondition
##  unsure of hatch date                           :  5   Min.   :-1.166e-02
##  end date ealier                                :  4   1st Qu.:-1.282e-03
##  end date earlier                               :  3   Median :-2.292e-04
##  a lot of dried out eggs                        :  1   Mean   :-6.833e-05
##  about two weeks prior to 7/2. end date ealier:  1   3rd Qu.: 1.063e-03
##  (Other)                                        : 10   Max.   : 1.629e-02
##  NA's                                           :197
##    Mcondition            FTrtCode            MTrtCode     TrainingDuration
##  Min.   :-4.861e-03   Min.   :-0.500000   Min.   :0.000   Min.   :10.00
##  1st Qu.:-1.127e-03   1st Qu.:-0.500000   1st Qu.:0.000   1st Qu.:11.00
##  Median :-4.316e-04   Median : 0.500000   Median :1.000   Median :24.00
##  Mean   : 1.878e-05   Mean   : 0.006787   Mean   :1.009   Mean   :27.84
##  3rd Qu.: 3.694e-04   3rd Qu.: 0.500000   3rd Qu.:2.000   3rd Qu.:34.00
##  Max.   : 4.848e-02   Max.   : 0.500000   Max.   :2.000   Max.   :97.00
##
```

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 (note that this may change sligthly as we havent finish watching them so we may have misidentified a copulation when watching live or missed one - both these events are rare)

```
##            FTrt AllGrey AllRed RedGrey Unmanipulated
## 1     RedAverse      23     18      25             6
## 2 RedPreference      22     22      18             6
```

```
##            FTrt  AllGrey   AllRed  RedGrey Unmanipulated
## 1     RedAverse 63.88889 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).

If Fcondition is significantly leading to more cannibalism this should be removed (Preregistered)

FCondition was positively significant in the cannibalism model so it is silenced in the models below

```
# 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
```

```
# 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
```

```
# 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
## -1.651  -1.251   0.915   1.070   1.296
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        -1.7654     2.6427  -0.668    0.504
## FTrtCode           -0.5422     0.4455  -1.217    0.224
## MTrtCode           -0.1809     0.1691  -1.070    0.285
## MCarapaceWidth      1.7080     1.9806   0.862    0.388
## Mcondition         -7.2680    33.2151  -0.219    0.827
## FTrtCode:MTrtCode   0.3122     0.3376   0.925    0.355
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 300.80  on 220  degrees of freedom
## Residual deviance: 297.58  on 215  degrees of freedom
## AIC: 309.58
##
## 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$MTrt == "AllRed" & MY_TABLE$Tra
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
## -1.5631  -1.2270   0.8537   1.0546   1.3131
##
## Coefficients:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)        -0.2265     3.2310  -0.070   0.9441
## FTrtCode            0.2869     0.5474   0.524   0.6002
## MTrtCode           -0.3750     0.2034  -1.844   0.0652 .
## MCarapaceWidth      0.6744     2.4136   0.279   0.7799
## Mcondition         -1.6470    36.0701  -0.046   0.9636
## FTrtCode:MTrtCode  -0.2458     0.4074  -0.603   0.5464
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 213.15  on 155  degrees of freedom
## Residual deviance: 209.26  on 150  degrees of freedom
## AIC: 221.26
##
## Number of Fisher Scoring iterations: 4
```

```
# Model 4sub

modCop2Sub <- glm (CopDuringVideo ~ FTrtCode + MCarapaceWidth + Mcondition
               , family = "binomial", data = MY_TABLE[MY_TABLE$MTrt == "AllRed" & MY_TABLE$TrainingDura
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
```

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

74 females had a brood size of 0 221-74 = 147 led to spiderlings (for 4 of them the emergence date is not known precisely)

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

Not sure this would be the right model:

```
summary(lm(BroodSize ~ FTrtCode* MTrtCode  , data = MY_TABLE))
```

```
##
## Call:
## lm(formula = BroodSize ~ FTrtCode * MTrtCode, data = MY_TABLE)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -16.714 -14.603  -0.537   8.463  45.286
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        16.0465     1.5104  10.624   <2e-16 ***
## FTrtCode            1.3353     3.0209   0.442    0.659
## MTrtCode           -0.4319     1.1626  -0.371    0.711
## FTrtCode:MTrtCode   0.6870     2.3253   0.295    0.768
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.14 on 217 degrees of freedom
## Multiple R-squared:  0.006224,   Adjusted R-squared:  -0.007515
## F-statistic: 0.453 on 3 and 217 DF,  p-value: 0.7154
```

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)?

```
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
```