Supplemental Fitness models output

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Variable names and description:

A: count of alternated visits
BreedingYear: year during which the brood was raised
BroodRef: unique identifier for broods
ChickAgeCat: the chick age as a categorical variable (chicks are routinely recorded at 6 and 10 days old, recordings deviating from that were pooled according to whether they were inferior, or superior (or equal) to 10)
DadAge:age of the social male parent (in years)
dam: genetic female parent of a chick
DVDInfoChickNb: the best estimate of the number of chicks at time of recording
DVDRef: nest watch unique identifier
FwillDivorce: Whether or not (1/0) female repaired while her previous partner was still alive, after a specific recorded brood she had with that initial partner ***GenPairID***: combination of the dan and sire IDs
HatchingDayAfter0401: the numbers of day after the first of April of that year
MeanFVisit1RateH: for males, the partner's provisioning rate in number of visits per hour
MeanLogAdev: logarithm of the deviation in alternation [log ((A observed+0.5) / (A random+0.5)], averaged accross all nest watch for that brood
MeanLogSdev: logarithm of the deviation in synchrony, averaged accross all nest watch for that brood
MeanMVisit1RateH: for females, the partner's provisioning rate in number of visits per hour
MeanTotalProRate: the average total provisioning rate for that brood in number of visits per hour
MixedBroodYN: whether or not (1/0) the brood contained cross-fostered chicks
MPriorResidence: whether or not (1/0) a male had nested in this nest box prior to the breeding attempt recorded
MumAge:age of the social female parent (in years)
MwillDivorce: Whether or not (1/0) male repaired while his previous partner was still alive, after a specific recorded brood he had with that initial partner
NbHatched: number of chicks that hatched in that brood
NBRinged:number of chicks ringed in that brood
PairBroodNb: the number of brood a pair already reared together (successfully or unsuccessfully, including the brood of interest)
PairID: combination of the social parents IDs
PairIDYear: combination of the Pair ID and the breeding year
ParentsAge: average of both parents age (in this population, pairs are assortatively mated for age, correlation between male and female age is r= 0.34, p <0.0001)
RearingBrood:the brood where chicks were reared (foster brood for cross-fostered chicks)
RelTimeHrs: the time, relative to sunrise, at which the video was taken
ResMassTarsus_perChick: residuals of the regression of chick mass over its tarsus length
rowID: observation level ID
S: count of synchroneous visits
sdResMassTarsus: standard deviation of the residuals of the regression of chick mass over its tarsus length
sire: genetic male parent of a chick
SocialDadID: unique idenifier for male parent observed caring for a brood
SocialMumID: unique idenifier for female parent observed caring for a brood
TotalProRate: the total number of visits provided by both partners divided by the entire duration of the nest watch in hours

Fitness correlates

Chick Survival

```
summary(modChickSurvival)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## RingedYN ~ scale(MeanTotalProRate) + scale(I(MeanTotalProRate^2)) +
##     scale(NbHatched) + scale(MeanLogAdev) + scale(MeanLogSdev) +
##     scale(HatchingDayAfter0401) + scale(PairBroodNb) + MPriorResidence +
##     (1 | PairID) + (1 | BreedingYear) + (1 | BroodRef) + (1 |
##     NatalBroodID)
##    Data: MY_TABLE_perChick_All
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##   4318.4   4398.8  -2146.2   4292.4     3580
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.1556 -0.9129  0.4827  0.7514  2.9203
##
## Random effects:
##  Groups       Name        Variance             Std.Dev.
##  NatalBroodID (Intercept) 0.000000000000001155 0.00000003398
##  BroodRef     (Intercept) 0.000000000000000000 0.00000000000
##  PairID       (Intercept) 0.000000000000000000 0.00000000000
##  BreedingYear (Intercept) 0.038637649033835444 0.19656461796
## Number of obs: 3593, groups:
## NatalBroodID, 984; BroodRef, 869; PairID, 441; BreedingYear, 12
##
## Fixed effects:
##                               Estimate Std. Error z value
## (Intercept)                    0.47735    0.07842   6.087
## scale(MeanTotalProRate)        1.53103    0.16212   9.444
## scale(I(MeanTotalProRate^2)) -0.83314    0.16641  -5.006
## scale(NbHatched)               0.04350    0.03943   1.103
## scale(MeanLogAdev)            -0.06842    0.04069  -1.681
## scale(MeanLogSdev)             0.06620    0.04213   1.571
## scale(HatchingDayAfter0401)    0.22778    0.03912   5.822
## scale(PairBroodNb)             0.03731    0.04154   0.898
## MPriorResidenceTRUE            0.07752    0.08135   0.953
##                                          Pr(>|z|)
## (Intercept)                          0.00000000115 ***
## scale(MeanTotalProRate)      < 0.0000000000000002 ***
## scale(I(MeanTotalProRate^2))         0.00000055444 ***
## scale(NbHatched)                             0.2699
## scale(MeanLogAdev)                           0.0927 .
## scale(MeanLogSdev)                           0.1161
## scale(HatchingDayAfter0401)          0.00000000581 ***
## scale(PairBroodNb)                           0.3691
## MPriorResidenceTRUE                          0.3406
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) s(MTPR s(I(MT sc(NH) s(MLA) s(MLS) s(HDA0 s(PBN)
## scl(MnTtPR) -0.027
## s(I(MTPR^2)  0.047 -0.959
## scl(NbHtch)  0.018 -0.108  0.025
## scl(MnLgAd)  0.017 -0.003 -0.001  0.043
## scl(MnLgSd) -0.004 -0.142  0.105 -0.063 -0.430
## sc(HDA0401)  0.042 -0.007  0.014  0.103  0.056 -0.040
## scl(PrBrdN)  0.163 -0.021  0.017 -0.048  0.027  0.053 -0.113
## MPrrRsdTRUE -0.393 -0.003 -0.004 -0.030 -0.021  0.011 -0.120 -0.277
```

```
drop1(modChickSurvival, test="Chisq") # Likelihood ratio test
```

```
## Single term deletions
##
## Model:
## RingedYN ~ scale(MeanTotalProRate) + scale(I(MeanTotalProRate^2)) +
##     scale(NbHatched) + scale(MeanLogAdev) + scale(MeanLogSdev) +
##     scale(HatchingDayAfter0401) + scale(PairBroodNb) + MPriorResidence +
##     (1 | PairID) + (1 | BreedingYear) + (1 | BroodRef) + (1 |
##     NatalBroodID)
##                              Df    AIC    LRT               Pr(Chi)
## <none>                          4318.4
## scale(MeanTotalProRate)       1 4394.7 78.304 < 0.00000000000000022 ***
## scale(I(MeanTotalProRate^2))  1 4337.9 21.432        0.000003666442 ***
## scale(NbHatched)              1 4317.6  1.218               0.26967
## scale(MeanLogAdev)            1 4319.3  2.837               0.09212 .
## scale(MeanLogSdev)            1 4318.9  2.480               0.11531
## scale(HatchingDayAfter0401)   1 4350.7 34.265        0.000000004808 ***
## scale(PairBroodNb)            1 4317.2  0.810               0.36819
## MPriorResidence               1 4317.3  0.909               0.34048
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
dispersion_glmer(modChickSurvival) # from package blmeco
```

```
## [1] 1.091304
```

Divorce correlates

They are 37 polygynous males, for which a total of 67 brood the male divorce (breed with another female), while the female does not (her next brood will be with the same male again). In the first model, the dependent variable 'PairDivorce' is NA (those broods are excluded), in the second, PairDivorce is set to FALSE (female perspective), and in the third model, PairDivorce is set to TRUE (male perspective).

```
summary(mod_Divorce)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## PairDivorce ~ scale(MeanLogSdev) + scale(MeanLogAdev) + scale(MumAge) +
##     scale(DadAge) + scale(PairBroodNb) + scale(MeanMVisit1RateH) +
```

```
##     scale(MeanFVisit1RateH) + scale(NbRinged) + (1 | SocialMumID) +
##     (1 | SocialDadID) + (1 | BreedingYear)
##    Data: MY_TABLE_perBrood
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##    528.4    580.2   -252.2    504.4      541
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.0269 -0.4569 -0.3586 -0.2299  3.4514
##
## Random effects:
##  Groups       Name        Variance Std.Dev.
##  SocialDadID  (Intercept) 0.0000   0.0000
##  SocialMumID  (Intercept) 0.7786   0.8824
##  BreedingYear (Intercept) 0.0000   0.0000
## Number of obs: 553, groups:
## SocialDadID, 222; SocialMumID, 218; BreedingYear, 12
##
## Fixed effects:
##                           Estimate Std. Error z value            Pr(>|z|)
## (Intercept)              -1.727052   0.174814  -9.879 <0.0000000000000002
## scale(MeanLogSdev)       -0.009213   0.150579  -0.061              0.9512
## scale(MeanLogAdev)        0.054973   0.137092   0.401              0.6884
## scale(MumAge)            -0.090166   0.158380  -0.569              0.5692
## scale(DadAge)            -0.472227   0.188989  -2.499              0.0125
## scale(PairBroodNb)       -0.068961   0.205416  -0.336              0.7371
## scale(MeanMVisit1RateH) -0.145258   0.160888  -0.903              0.3666
## scale(MeanFVisit1RateH) -0.135565   0.158321  -0.856              0.3919
## scale(NbRinged)           0.163177   0.176703   0.923              0.3558
##
## (Intercept)              ***
## scale(MeanLogSdev)
## scale(MeanLogAdev)
## scale(MumAge)
## scale(DadAge)            *
## scale(PairBroodNb)
## scale(MeanMVisit1RateH)
## scale(MeanFVisit1RateH)
## scale(NbRinged)
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) s(MLS) s(MLA) sc(MA) sc(DA) s(PBN) s(MMV1 s(MFV1
## scl(MnLgSd)  0.060
## scl(MnLgAd) -0.082 -0.428
## scale(MmAg)  0.093  0.067 -0.058
## scale(DdAg)  0.187  0.045  0.002 -0.093
## scl(PrBrdN) -0.052 -0.060  0.052 -0.350 -0.469
## scl(MMV1RH)  0.010  0.042 -0.091  0.098  0.044 -0.021
## scl(MFV1RH)  0.023 -0.104  0.023  0.013 -0.035 -0.023 -0.033
## scl(NbRngd) -0.060 -0.116  0.117 -0.083  0.000 -0.004 -0.491 -0.478
```

```
drop1(mod_Divorce, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## PairDivorce ~ scale(MeanLogSdev) + scale(MeanLogAdev) + scale(MumAge) +
##     scale(DadAge) + scale(PairBroodNb) + scale(MeanMVisit1RateH) +
##     scale(MeanFVisit1RateH) + scale(NbRinged) + (1 | SocialMumID) +
##     (1 | SocialDadID) + (1 | BreedingYear)
##                         Df    AIC    LRT  Pr(Chi)
## <none>                     528.39
## scale(MeanLogSdev)       1 526.39 0.0037 0.951211
## scale(MeanLogAdev)       1 526.55 0.1616 0.687696
## scale(MumAge)            1 526.72 0.3295 0.565926
## scale(DadAge)            1 533.41 7.0242 0.008041 **
## scale(PairBroodNb)       1 526.50 0.1123 0.737545
## scale(MeanMVisit1RateH)  1 527.22 0.8302 0.362214
## scale(MeanFVisit1RateH)  1 527.14 0.7489 0.386810
## scale(NbRinged)          1 527.25 0.8609 0.353480
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
dispersion_glmer(mod_Divorce)
```

```
## [1] 0.9087477
```

```
summary(mod_Divorce_PolygynousDontDivorce)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## PairDivorce ~ scale(MeanLogSdev) + scale(MeanLogAdev) + scale(MumAge) +
##     scale(DadAge) + scale(PairBroodNb) + scale(MeanMVisit1RateH) +
##     scale(MeanFVisit1RateH) + scale(NbRinged) + (1 | SocialMumID) +
##     (1 | SocialDadID) + (1 | BreedingYear)
##    Data: MY_TABLE_perBrood_PolygynousDontDivorce
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##    554.2    607.4   -265.1    530.2      608
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.9454 -0.4339 -0.3387 -0.2302  3.9329
##
## Random effects:
##  Groups       Name        Variance Std.Dev.
##  SocialMumID  (Intercept) 0.6769   0.8228
##  SocialDadID  (Intercept) 0.0000   0.0000
##  BreedingYear (Intercept) 0.0000   0.0000
## Number of obs: 620, groups:
## SocialMumID, 230; SocialDadID, 227; BreedingYear, 12
##
## Fixed effects:
```

```
##                          Estimate Std. Error z value            Pr(>|z|)
## (Intercept)              -1.86136    0.17272 -10.777 <0.0000000000000002
## scale(MeanLogSdev)       -0.03077    0.13239  -0.232              0.8162
## scale(MeanLogAdev)        0.09439    0.13073   0.722              0.4703
## scale(MumAge)            -0.15386    0.15224  -1.011              0.3122
## scale(DadAge)            -0.50977    0.18403  -2.770              0.0056
## scale(PairBroodNb)        0.02970    0.19967   0.149              0.8818
## scale(MeanMVisit1RateH) -0.09666    0.15363  -0.629              0.5292
## scale(MeanFVisit1RateH) -0.20235    0.15255  -1.326              0.1847
## scale(NbRinged)           0.20645    0.17167   1.203              0.2291
##
## (Intercept)              ***
## scale(MeanLogSdev)
## scale(MeanLogAdev)
## scale(MumAge)
## scale(DadAge)            **
## scale(PairBroodNb)
## scale(MeanMVisit1RateH)
## scale(MeanFVisit1RateH)
## scale(NbRinged)
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) s(MLS) s(MLA) sc(MA) sc(DA) s(PBN) s(MMV1 s(MFV1
## scl(MnLgSd)  0.048
## scl(MnLgAd) -0.079 -0.375
## scale(MmAg)  0.121  0.072 -0.062
## scale(DdAg)  0.189  0.070  0.006 -0.102
## scl(PrBrdN) -0.073 -0.066  0.049 -0.343 -0.461
## scl(MMV1RH)  0.029  0.035 -0.104  0.105  0.064 -0.044
## scl(MFV1RH)  0.051 -0.131  0.016 -0.002 -0.014 -0.016 -0.026
## scl(NbRngd) -0.093 -0.086  0.119 -0.080 -0.016  0.002 -0.501 -0.468
```

```
drop1(mod_Divorce_PolygynousDontDivorce, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## PairDivorce ~ scale(MeanLogSdev) + scale(MeanLogAdev) + scale(MumAge) +
##     scale(DadAge) + scale(PairBroodNb) + scale(MeanMVisit1RateH) +
##     scale(MeanFVisit1RateH) + scale(NbRinged) + (1 | SocialMumID) +
##     (1 | SocialDadID) + (1 | BreedingYear)
##                          Df    AIC    LRT  Pr(Chi)
## <none>                      554.24
## scale(MeanLogSdev)        1 552.29 0.0539 0.816400
## scale(MeanLogAdev)        1 552.76 0.5249 0.468759
## scale(MumAge)             1 553.30 1.0610 0.302994
## scale(DadAge)             1 560.95 8.7111 0.003163 **
## scale(PairBroodNb)        1 552.26 0.0222 0.881674
## scale(MeanMVisit1RateH)   1 552.64 0.4013 0.526429
## scale(MeanFVisit1RateH)   1 554.06 1.8288 0.176271
## scale(NbRinged)           1 553.71 1.4702 0.225306
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
dispersion_glmer(mod_Divorce_PolygynousDontDivorce)
```

```
## [1] 0.8859993
```

```
summary(mod_Divorce_PolygynousDivorce)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula:
## PairDivorce ~ scale(MeanLogSdev) + scale(MeanLogAdev) + scale(MumAge) +
##     scale(DadAge) + scale(PairBroodNb) + scale(MeanMVisit1RateH) +
##     scale(MeanFVisit1RateH) + scale(NbRinged) + (1 | SocialMumID) +
##     (1 | SocialDadID) + (1 | BreedingYear)
##    Data: MY_TABLE_perBrood_PolygynousDivorce
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
##    697.8    751.0   -336.9    673.8      608
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.2703 -0.5116 -0.3759  0.7376  3.1157
##
## Random effects:
##  Groups       Name        Variance Std.Dev.
##  SocialMumID  (Intercept) 0.6004   0.7749
##  SocialDadID  (Intercept) 0.7757   0.8807
##  BreedingYear (Intercept) 0.0000   0.0000
## Number of obs: 620, groups:
## SocialMumID, 230; SocialDadID, 227; BreedingYear, 12
##
## Fixed effects:
##                          Estimate Std. Error z value            Pr(>|z|)
## (Intercept)              -1.35086    0.17055  -7.921 0.00000000000000236
## scale(MeanLogSdev)        0.09581    0.12380   0.774              0.4390
## scale(MeanLogAdev)       -0.10343    0.12095  -0.855              0.3925
## scale(MumAge)             0.08335    0.14138   0.590              0.5555
## scale(DadAge)            -0.18807    0.16472  -1.142              0.2536
## scale(PairBroodNb)       -0.40884    0.17897  -2.284              0.0224
## scale(MeanMVisit1RateH) -0.30209    0.14986  -2.016              0.0438
## scale(MeanFVisit1RateH)  0.03940    0.13830   0.285              0.7758
## scale(NbRinged)           0.06830    0.15837   0.431              0.6663
##
## (Intercept)              ***
## scale(MeanLogSdev)
## scale(MeanLogAdev)
## scale(MumAge)
## scale(DadAge)
## scale(PairBroodNb)       *
## scale(MeanMVisit1RateH) *
## scale(MeanFVisit1RateH)
## scale(NbRinged)
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) s(MLS) s(MLA) sc(MA) sc(DA) s(PBN) s(MMV1 s(MFV1
## scl(MnLgSd) -0.029
## scl(MnLgAd)  0.025 -0.371
## scale(MmAg)  0.041  0.058 -0.042
## scale(DdAg)  0.064  0.046  0.034 -0.142
## scl(PrBrdN)  0.112 -0.041  0.032 -0.328 -0.406
## scl(MMV1RH)  0.066  0.050 -0.107  0.084  0.069 -0.024
## scl(MFV1RH) -0.019 -0.126  0.034 -0.004 -0.067  0.018 -0.048
## scl(NbRngd) -0.010 -0.081  0.090 -0.044  0.028 -0.049 -0.505 -0.433
```

```
drop1(mod_Divorce_PolygynousDivorce, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## PairDivorce ~ scale(MeanLogSdev) + scale(MeanLogAdev) + scale(MumAge) +
##     scale(DadAge) + scale(PairBroodNb) + scale(MeanMVisit1RateH) +
##     scale(MeanFVisit1RateH) + scale(NbRinged) + (1 | SocialMumID) +
##     (1 | SocialDadID) + (1 | BreedingYear)
##                         Df    AIC    LRT Pr(Chi)
## <none>                     697.81
## scale(MeanLogSdev)       1 696.41 0.6019 0.43787
## scale(MeanLogAdev)       1 696.54 0.7318 0.39230
## scale(MumAge)            1 696.15 0.3439 0.55759
## scale(DadAge)            1 697.14 1.3346 0.24799
## scale(PairBroodNb)       1 700.94 5.1359 0.02344 *
## scale(MeanMVisit1RateH)  1 700.01 4.2033 0.04035 *
## scale(MeanFVisit1RateH)  1 695.89 0.0809 0.77613
## scale(NbRinged)          1 695.99 0.1867 0.66567
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
dispersion_glmer(mod_Divorce_PolygynousDivorce)
```

```
## [1] 0.9576187
```