

Median :0.00	Median :0.0000	Median :0.00000	Median :0.0000	Mode :character	Mode :character	Median :2014	Median :2018
Mean :0.14	Mean :0.3479	Mean :0.08564	Mean :0.2159			Mean :2014	Mean :2018
3rd Qu.:0.00	3rd Qu.:1.0000	3rd Qu.:0.00000	3rd Qu.:0.0000			3rd Qu.:2016	3rd Qu.:2019
Max. :1.00	Max. :1.0000	Max. :1.00000	Max. :1.0000			Max. :2020	Max. :2022

litter_id	axy_age	axy_ageclass	prop_feeding	prop_foraging	prop_nestmoving	prop_nestnotmoving	prop_notmoving
Min. : 37	Min. :2.000	Length:4507	Min. :0.0000	Min. :0.00000	Min. :0.0000	Min. :0.0000	Min. :0.00000
1st Qu.:4891	1st Qu.:2.000	Class :character	1st Qu.:0.0000	1st Qu.:0.00000	1st Qu.:0.0000	1st Qu.:0.0000	1st Qu.:0.00000
Median :5258	Median :3.000	Mode :character	Median :0.0000	Median :0.00000	Median :0.0000	Median :0.0000	Median :0.00000
Mean :5206	Mean :3.428		Mean :0.1654	Mean :0.04129	Mean :0.1390	Mean :0.3479	Mean :0.08601
3rd Qu.:5894	3rd Qu.:4.000		3rd Qu.:0.2857	3rd Qu.:0.07143	3rd Qu.:0.1429	3rd Qu.:0.8571	3rd Qu.:0.00000
Max. :9751	Max. :8.000		Max. :1.0000	Max. :0.64286	Max. :1.0000	Max. :1.0000	Max. :1.00000

prop_travel	PC1	PC2	axy.local.density	axy_avg_fam	grid	grid_yr
Min. :0.0000	Min. :-1.76592	Min. :-3.977248	Min. :0.000	Min. : 0.0	Length:4507	Length:4507
1st Qu.:0.0000	1st Qu.: -1.64767	1st Qu.: -0.035292	1st Qu.:0.000	1st Qu.: 0.0	Class :character	Class :character
Median :0.0000	Median : -0.52416	Median : 0.431994	Median :0.565	Median : 0.0	Mode :character	Mode :character
Mean :0.2213	Mean : -0.09425	Mean : 0.002824	Mean :1.139	Mean :189.1		
3rd Qu.:0.4286	3rd Qu.: 1.42396	3rd Qu.: 0.474153	3rd Qu.:1.883	3rd Qu.:307.9		
Max. :1.0000	Max. : 3.77863	Max. : 2.149915	Max. :5.839	Max. :1140.8		

b.axy.local.density	b.axy_avg_fam
Min. :0.000	Min. : 0.0
1st Qu.:0.000	1st Qu.: 0.0
Median :0.565	Median : 0.0
Mean :1.139	Mean :189.1
3rd Qu.:1.883	3rd Qu.:324.9
Max. :5.839	Max. :1140.8

```

>
> (adult_axy_all) %>% as_tibble() %>% dplyr::count(squirrel_id) %>% nrow() #177 adults
[1] 177
> (adult_axy_all) %>% as_tibble() %>% dplyr::count(squirrel_id, axy_yr, axy_date) %>% nrow() #4507 deployment days
[1] 4507
> nrow(adult_axy_all) #4507 records
[1] 4507
>
> #####
> ##### Adults #####
> ##### n = 177 #####
> #####
>
> #####
> ##### PC1 models #####
> #####
>
> #####
> #non-adjusted repeatability
> #####
>
> m1a<-lmer(PC1 ~ (1|squirrel_id) + (1|grid_yr), data=adult_axy_all)
> summary(m1a)
Linear mixed model fit by REML ['lmerMod']
Formula: PC1 ~ (1 | squirrel_id) + (1 | grid_yr)
Data: adult_axy_all

REML criterion at convergence: 16075.7

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.1230 -0.8383 -0.1673  0.9254  2.5861

Random effects:
Groups      Name      Variance Std.Dev.
squirrel_id (Intercept) 0.07488  0.2736
grid_yr     (Intercept) 0.25419  0.5042
Residual                    1.99547  1.4126
Number of obs: 4507, groups:  squirrel_id, 177; grid_yr, 28

Fixed effects:
              Estimate Std. Error t value
(Intercept) -0.07198    0.10404  -0.692
>
> plot(m1a)
> hist(resid(m1a))
>
> #for axy PC1
> sm1<-arm::sim(m1a,1000)
> smfixef=sm1@fixef
> smranef=sm1@ranef
> smfixef=coda::as.mcmc(smfixef)
> MCMCglmm::posterior.mode(smfixef)
(Intercept)
-0.08647209
> coda::HPDinterval(smfixef)
              lower      upper
(Intercept) -0.2343546  0.1503774
attr(,"Probability")
[1] 0.95
>
> ##among-individual variance
> bID<-sm1@ranef$squirrel_id

```

```

> bvar<-as.vector(apply(bID, 1, var)) ##between individual variance posterior distribution
> bvar<-coda::as.mcmc(bvar)
> MCMCglmm::posterior.mode(bvar) ## mode of the distribution
      var1
0.07266289
> coda::HPDinterval(bvar)
      lower      upper
var1 0.05800851 0.08625261
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
      var1
2.009783
> coda::HPDinterval(rvar)
      lower      upper
var1 1.912797 2.080564
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
      var1
0.03356945
> coda::HPDinterval(rID)
      lower      upper
var1 0.02844267 0.04133965
attr(,"Probability")
[1] 0.95
>
> #####
> #adjusted repeatability
> #####
>
> m1b<-lmer(PC1 ~ sex + b.axy.local.density + b.axy_avg_fam + (1|squirrel_id) + (1|grid_yr), data=adult_axy_all)
> summary(m1b)
Linear mixed model fit by REML ['lmerMod']
Formula: PC1 ~ sex + b.axy.local.density + b.axy_avg_fam + (1 | squirrel_id) + (1 | grid_yr)
Data: adult_axy_all

REML criterion at convergence: 16096.5

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.1126 -0.8409 -0.1676  0.9233  2.5904

Random effects:
    Groups             Name                Variance Std.Dev.
squirrel_id (Intercept) 0.07888      0.2809
grid_yr      (Intercept) 0.23561      0.4854
Residual                                1.99489      1.4124
Number of obs: 4507, groups:  squirrel_id, 177; grid_yr, 28

Fixed effects:
              Estimate Std. Error t value
(Intercept)   -0.1549347   0.1163434   -1.332
sexM           0.0483686   0.0886785    0.545
b.axy.local.density 0.0338760   0.0413184    0.820
b.axy_avg_fam   0.0001609   0.0001643    0.979

Correlation of Fixed Effects:
              (Intr) sexM    b.xy..
sexM          -0.175
b.xy.lcl.dn   -0.383  -0.069
b.axy_vg_fm   -0.151  -0.044  -0.201
>
> plot(m1b)
> hist(resid(m1b))
>
> #for axy PC1
> sm1<-arm::sim(m1b,1000)
> smfixef=sm1@fixef
> smranef=sm1@ranef
> smfixef=coda::as.mcmc(smfixef)
> MCMCglmm::posterior.mode(smfixef)
      (Intercept)      sexM b.axy.local.density      b.axy_avg_fam
-0.1319826081      0.0789459636      0.0208170501      0.0001924642
> coda::HPDinterval(smfixef)
      lower      upper
(Intercept) -0.3825441365 0.0699330651
sexM         -0.1043022919 0.2345023832
b.axy.local.density -0.0399703530 0.1117642643
b.axy_avg_fam  -0.0001704174 0.0004444549
attr(,"Probability")
[1] 0.95
>
> ##among-individual variance
> bID<-sm1@ranef$squirrel_id

```

```

> bvar<-as.vector(apply(bID, 1, var)) ##between individual variance posterior distribution
> bvar<-coda::as.mcmc(bvar)
> MCMCglmm::posterior.mode(bvar) ## mode of the distribution
      var1
0.07481701
> coda::HPDinterval(bvar)
      lower      upper
var1 0.06123364 0.09080989
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
      var1
2.002169
> coda::HPDinterval(rvar)
      lower      upper
var1 1.913888 2.076953
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
      var1
0.03640137
> coda::HPDinterval(rID)
      lower      upper
var1 0.03067361 0.04461125
attr(,"Probability")
[1] 0.95
>
>
> #####
> ##### PC2 models #####
> #####
>
> #####
> #non-adjusted repeatability
> #####
>
> m2a<-lmer(PC2 ~ (1|squirrel_id) + (1|grid_yr), data=adult_axy_all)
> summary(m2a)
Linear mixed model fit by REML ['lmerMod']
Formula: PC2 ~ (1 | squirrel_id) + (1 | grid_yr)
Data: adult_axy_all

REML criterion at convergence: 13249.3

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.0498 -0.1064  0.2854  0.4837  2.0368

Random effects:
 Groups      Name      Variance Std.Dev.
squirrel_id (Intercept) 0.06764  0.2601
grid_yr      (Intercept) 0.06821  0.2612
Residual                        1.05929  1.0292
Number of obs: 4507, groups:  squirrel_id, 177; grid_yr, 28

Fixed effects:
              Estimate Std. Error t value
(Intercept) -0.002423   0.059293  -0.041
>
> plot(m2a)
> hist(resid(m2a))
>
> #for axy PC2
> sm2<-arm::sim(m2a,1000)
> smfixef2=sm2@fixef
> smranef2=sm2@ranef
> smfixef2=coda::as.mcmc(smfixef2)
> MCMCglmm::posterior.mode(smfixef2)
(Intercept)
-0.001539365
> coda::HPDinterval(smfixef2)
      lower      upper
(Intercept) -0.1157172 0.1090618
attr(,"Probability")
[1] 0.95
>
>
> ##among-individual variance
> bID2<-sm2@ranef$squirrel_id
> bvar2<-as.vector(apply(bID2, 1, var)) ##between individual variance posterior distribution
> bvar2<-coda::as.mcmc(bvar2)
> MCMCglmm::posterior.mode(bvar2) ## mode of the distribution
      var1
0.06778137
> coda::HPDinterval(bvar2)

```

```

      lower      upper
var1 0.05502353 0.07887417
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
      var1
1.05974
> coda::HPDinterval(rvar2)
      lower      upper
var1 1.018367 1.105627
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
      var1
0.06015018
> coda::HPDinterval(rID2)
      lower      upper
var1 0.04976309 0.07019037
attr(,"Probability")
[1] 0.95
>
> #####
> #adjusted repeatability
> #####
>
> m2b<-lmer(PC2 ~ sex + b.axy.local.density + b.axy_avg_fam + (1|squirrel_id) + (1|grid_yr), data=adult_axy_all)
> summary(m2b)
Linear mixed model fit by REML ['lmerMod']
Formula: PC2 ~ sex + b.axy.local.density + b.axy_avg_fam + (1 | squirrel_id) + (1 | grid_yr)
Data: adult_axy_all

REML criterion at convergence: 13273.2

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.0465 -0.1094  0.2824  0.4828  2.0113

Random effects:
 Groups      Name      Variance Std.Dev.
squirrel_id (Intercept) 0.07033  0.2652
grid_yr      (Intercept) 0.06858  0.2619
Residual                        1.05897  1.0291
Number of obs: 4507, groups:  squirrel_id, 177; grid_yr, 28

Fixed effects:
              Estimate Std. Error t value
(Intercept)  -0.00789620  0.07442987  -0.106
sexM          0.05780113  0.07038787   0.821
b.axy.local.density -0.01205903  0.03097949  -0.389
b.axy_avg_fam  0.00001779  0.00013526   0.131

Correlation of Fixed Effects:
      (Intr) sexM  b.xy..
sexM      -0.226
b.xy.lcl.dn -0.432 -0.094
b.axy_vg_fm -0.182 -0.041 -0.248
>
> plot(m2b)
> hist(resid(m2b))
>
> #for axy PC2
> sm2<-arm::sim(m2b,1000)
> smfixef2=sm2@fixef
> smranef2=sm2@ranef
> smfixef2=coda::as.mcmc(smfixef2)
> MCMCglmm::posterior.mode(smfixef2)
      (Intercept)      sexM b.axy.local.density      b.axy_avg_fam
0.01007207844      0.05850285522      -0.00498160215      0.00002412125
> coda::HPDinterval(smfixef2)
      lower      upper
(Intercept)  -0.1458311045  0.143507545
sexM          -0.0950075439  0.180519377
b.axy.local.density -0.0629071570  0.056213908
b.axy_avg_fam  -0.0002417164  0.000286184
attr(,"Probability")
[1] 0.95
>
> ##among-individual variance
> bID2<-sm2@ranef$squirrel_id
> bvar2<-as.vector(apply(bID2, 1, var)) ##between individual variance posterior distribution
> bvar2<-coda::as.mcmc(bvar2)
> MCMCglmm::posterior.mode(bvar2) ## mode of the distribution
      var1
0.06945823
> coda::HPDinterval(bvar2)

```

```

      lower      upper
var1 0.05692257 0.08421502
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
      var1
1.062373
> coda::HPDinterval(rvar2)
      lower      upper
var1 1.010586 1.101877
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
      var1
0.06265822
> coda::HPDinterval(rID2)
      lower      upper
var1 0.05088047 0.0736705
attr(,"Probability")
[1] 0.95
> #consecutive seven minute sampling
>
> #repeatabilities for axyl file, yearlings only
> ##KEEP IN MIND: Some squirrels had axy conducted when they were in different ageclasses (A and Y)
> ###these squirrels cause imbalances when looking at ageclass summaries
> #original code by A. R. Martinig
> #last edited April 24, 2024 by A. R. Martinig
>
> #run the following prior to running script:
> start-up code.R
Error: unexpected symbol in "start-up code.R"
> axy data subsets.R
Error: unexpected symbol in "axy data"
> PCA generation code - axy.R
Error: unexpected symbol in "PCA generation"
> local density (global datasets).R
Error: unexpected symbol in "local density"
> familiarity axy (global datasets).R
Error: unexpected symbol in "familiarity axy"
>
> #create working dataframe
> yearling_axy_all<-left_join(axy1, clean_axy, by=c("squirrel_id"="squirrel_id", "axy_yr"="axy_yr"))%>%
+ left_join((tbl(con, "flastall2")) %>% select(squirrel_id, grid=gr) %>% collect()), by="squirrel_id") %>% #to bring in the grid information
+ filter(axy_ageclass=="Y") %>%
+ mutate(
+   grid=ifelse(grid=="SUX", "SU", grid),
+   grid_yr=paste(grid, axy_yr, sep=""),
+   axy_yr=axy_yr-2014) %>%
+ group_by(squirrel_id) %>% #convert these variables to among-ind effects
+ mutate(b.axy.local.density=mean(axy.local.density),
+   b.axy_avg_fam=mean(axy_avg_fam, na.rm=T)) %>%
+ ungroup()
>
> summary(yearling_axy_all)
squirrel_id    axy_date      axy_yr      axy_month    axy_season      tod      feed      forage
Min.   :19537   Min.   :2014-08-26   Min.   :0.000   Min.   :5.000   Length:1764   Length:1764   Min.   :0.0000   Min.   :0.00000
1st Qu.:21473   1st Qu.:2015-09-18   1st Qu.:1.000   1st Qu.:7.000   Class :character   Class :character   1st Qu.:0.0000   1st Qu.:0.00000
Median :23261   Median :2017-09-22   Median :3.000   Median :8.000   Mode  :character   Mode  :character   Median :0.0000   Median :0.00000
Mean   :22789   Mean   :2017-11-20   Mean   :3.277   Mean   :7.836                                     Mean :0.1882   Mean :0.05215
3rd Qu.:23869   3rd Qu.:2019-06-15   3rd Qu.:5.000   3rd Qu.:9.000                                     3rd Qu.:0.0000   3rd Qu.:0.00000
Max.   :25314   Max.   :2022-09-15   Max.   :8.000   Max.   :9.000                                     Max.   :1.0000   Max.   :1.00000

nestmove      nestnotmove      notmoving      travel      axy_id      sex      byear      dyear
Min.   :0.00000   Min.   :0.000   Min.   :0.00000   Min.   :0.0000   Length:1764   Length:1764   Min.   :2013   Min.   :2014
1st Qu.:0.00000   1st Qu.:0.000   1st Qu.:0.00000   1st Qu.:0.0000   Class :character   Class :character   1st Qu.:2014   1st Qu.:2018
Median :0.00000   Median :0.000   Median :0.00000   Median :0.0000   Mode  :character   Mode  :character   Median :2016   Median :2019
Mean   :0.09524   Mean   :0.292   Mean   :0.09014   Mean   :0.2823                                     Mean :2016   Mean :2018
3rd Qu.:0.00000   3rd Qu.:1.000   3rd Qu.:0.00000   3rd Qu.:1.0000                                     3rd Qu.:2018   3rd Qu.:2019
Max.   :1.00000   Max.   :1.000   Max.   :1.00000   Max.   :1.0000                                     Max.   :2021   Max.   :2022

litter_id      axy_age      axy_ageclass      prop_feeding      prop_foraging      prop_nestmoving      prop_nestnotmoving      prop_notmoving
Min.   : 77   Min.   :1   Length:1764   Min.   :0.00000   Min.   :0.00000   Min.   :0.00000   Min.   :0.0000   Min.   :0.00000
1st Qu.:5801   1st Qu.:1   Class :character   1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000
Median :5982   Median :1   Mode  :character   Median :0.07143   Median :0.00000   Median :0.00000   Median :0.0000   Median :0.00000
Mean   :6323   Mean   :1   Mean   :0.20517   Mean :0.04993   Mean :0.09674   Mean :0.2915   Mean :0.08293
3rd Qu.:7779   3rd Qu.:1   3rd Qu.:0.35714   3rd Qu.:0.07143   3rd Qu.:0.07143   3rd Qu.:0.7857   3rd Qu.:0.00000
Max.   :9878   Max.   :1   Max.   :1.00000   Max.   :0.78571   Max.   :1.00000   Max.   :1.4286   Max.   :1.00000
NA's   :1165

prop_travel      PC1      PC2      axy.local.density      axy_avg_fam      grid      grid_yr
Min.   :0.0000   Min.   :-2.7616   Min.   :-3.977248   Min.   :0.0000   Min.   : 0.00   Length:1764   Length:1764
1st Qu.:0.0000   1st Qu.:-1.6264   1st Qu.:0.122480   1st Qu.:0.0000   1st Qu.: 0.00   Class :character   Class :character
Median :0.2143   Median : 0.9459   Median : 0.431994   Median :0.1883   Median : 0.00   Mode  :character   Mode  :character
Mean   :0.2794   Mean : 0.2408   Mean :-0.007215   Mean :1.2580   Mean : 24.27                                     Mean :24.27
3rd Qu.:0.5714   3rd Qu.: 1.5922   3rd Qu.: 0.474153   3rd Qu.:2.2602   3rd Qu.: 30.67                                     3rd Qu.:30.67
Max.   :1.0714   Max.   : 4.1645   Max.   : 2.529580   Max.   :5.8388   Max.   :241.94

```

```

b.axy.local.density b.axy_avg_fam
Min. :0.0000 Min. : 0.00
1st Qu.:0.0000 1st Qu.: 0.00
Median :0.1883 Median : 0.00
Mean :1.2580 Mean : 24.27
3rd Qu.:2.2602 3rd Qu.: 30.67
Max. :5.8388 Max. :241.94

>
> (yearling_axy_all) %>% as_tibble() %>% dplyr::count(squirrel_id) %>% nrow() #86 individuals
[1] 86
> (yearling_axy_all) %>% as_tibble() %>% dplyr::count(squirrel_id, axy_yr, axy_date) %>% nrow() #1764 deployment days
[1] 1764
> nrow(yearling_axy_all) #1792 records
[1] 1764
>
> #####
> ##### Yearlings #####
> ##### n = 86 #####
> #####
>
> #####
> ##### PC1 models #####
> #####
>
> #####
> #non-adjusted repeatability
> #####
>
> m1a<-lmer(PC1 ~ (1|squirrel_id) + (1|grid_yr), data=yearling_axy_all)
> summary(m1a)
Linear mixed model fit by REML ['lmerMod']
Formula: PC1 ~ (1 | squirrel_id) + (1 | grid_yr)
Data: yearling_axy_all

REML criterion at convergence: 6341.9

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.4224 -0.9173  0.2880  0.8362  2.2568

Random effects:
Groups      Name      Variance Std.Dev.
squirrel_id (Intercept) 0.1453   0.3812
grid_yr     (Intercept) 0.2688   0.5185
Residual    2.0121   1.4185
Number of obs: 1764, groups: squirrel_id, 86; grid_yr, 21

Fixed effects:
              Estimate Std. Error t value
(Intercept)   0.2251     0.1359   1.656
>
> plot(m1a)
> hist(resid(m1a))
>
> #for axy PC1
> sm1<-arm::sim(m1a,1000)
> smfixef=sm1@fixef
> smranef=sm1@ranef
> smfixef=coda::as.mcmc(smfixef)
> MCMCglmm::posterior.mode(smfixef)
(Intercept)
0.2391794
> coda::HPDinterval(smfixef)
              lower      upper
(Intercept) -0.03876061 0.4997017
attr(,"Probability")
[1] 0.95
>
> ##among-individual variance
> bID<-sm1@ranef$squirrel_id
> bvar<-as.vector(apply(bID, 1, var)) ##between individual variance posterior distribution
> bvar<-coda::as.mcmc(bvar)
> MCMCglmm::posterior.mode(bvar) ## mode of the distribution
var1
0.130332
> coda::HPDinterval(bvar)
              lower      upper
var1 0.1014705 0.1839754
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
var1
2.059537
> coda::HPDinterval(rvar)
              lower      upper
var1 1.884034 2.149255

```

```

attr("Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
var1
0.06390204
> coda::HPDinterval(rID)
lower upper
var1 0.0488568 0.08407763
attr("Probability")
[1] 0.95
>
> #####
> #adjusted repeatability
> #####
>
> m1b<-lmer(PC1 ~ sex + b.axy.local.density + b.axy_avg_fam + (1|squirrel_id) + (1|grid_yr), data=yearling_axy_all)
> summary(m1b)
Linear mixed model fit by REML ['lmerMod']
Formula: PC1 ~ sex + b.axy.local.density + b.axy_avg_fam + (1 | squirrel_id) + (1 | grid_yr)
Data: yearling_axy_all

REML criterion at convergence: 6352.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.4196 -0.9049  0.3000  0.8306  2.2628

Random effects:
 Groups      Name      Variance Std.Dev.
squirrel_id (Intercept) 0.1358   0.3685
grid_yr     (Intercept) 0.2293   0.4789
Residual    2.0136   1.4190
Number of obs: 1764, groups:  squirrel_id, 86; grid_yr, 21

Fixed effects:
              Estimate Std. Error t value
(Intercept)    0.127911   0.168631   0.759
sexM            0.362593   0.148892   2.435
b.axy.local.density 0.009468   0.062495   0.151
b.axy_avg_fam   -0.001398   0.001377  -1.015

Correlation of Fixed Effects:
              (Intr) sexM   b.xy..
sexM          -0.335
b.xy.lcl.dn   -0.530  0.079
b.axy_vg_fm   -0.024 -0.087 -0.352
>
> plot(m1b)
> hist(resid(m1b))
>
> #for axy PC1
> sm1<-arm::sim(m1b,1000)
> smfixef=sm1@fixef
> smranef=sm1@ranef
> smfixef=coda::as.mcmc(smfixef)
> MCMCglmm::posterior.mode(smfixef)
              (Intercept)      sexM b.axy.local.density      b.axy_avg_fam
0.080757398      0.297568581    -0.002201154    -0.000805555
> coda::HPDinterval(smfixef)
lower upper
(Intercept) -0.198445829 0.448060182
sexM         0.093904113 0.650408953
b.axy.local.density -0.115591938 0.116311635
b.axy_avg_fam   -0.004059435 0.001026786
attr("Probability")
[1] 0.95
>
> ##among-individual variance
> bID<-sm1@ranef$squirrel_id
> bvar<-as.vector(apply(bID, 1, var)) ##between individual variance posterior distribution
> bvar<-coda::as.mcmc(bvar)
> MCMCglmm::posterior.mode(bvar) ## mode of the distribution
var1
0.1229288
> coda::HPDinterval(bvar)
lower upper
var1 0.09515482 0.1668929
attr("Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
var1
1.98596
> coda::HPDinterval(rvar)
lower upper

```

```

var1 1.872943 2.144388
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
      var1
0.05630104
> coda::HPDinterval(rID)
      lower      upper
var1 0.04488694 0.07698903
attr(,"Probability")
[1] 0.95
>
> #####
> ##### PC2 models #####
> #####
> #####
> #####non-adjusted repeatability#####
>
> m2a<-lmer(PC2 ~ (1|squirrel_id) + (1|grid_yr), data=yearling_axy_all)
> summary(m2a)
Linear mixed model fit by REML ['lmerMod']
Formula: PC2 ~ (1 | squirrel_id) + (1 | grid_yr)
Data: yearling_axy_all

REML criterion at convergence: 5176.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.0730 -0.1576  0.2987  0.5184  2.4748

Random effects:
 Groups      Name      Variance Std.Dev.
squirrel_id (Intercept) 0.02848  0.1688
grid_yr      (Intercept) 0.04283  0.2070
Residual                    1.06618  1.0326
Number of obs: 1764, groups: squirrel_id, 86; grid_yr, 21

Fixed effects:
              Estimate Std. Error t value
(Intercept) 0.001122    0.061105  0.018
>
> plot(m2a)
> hist(resid(m2a))
>
> #for axy PC2
> sm2<-arm::sim(m2a,1000)
> smfixef2=sm2@fixef
> smranef2=sm2@ranef
> smfixef2=coda::as.mcmc(smfixef2)
> MCMCglmm::posterior.mode(smfixef2)
(Intercept)
0.003066947
> coda::HPDinterval(smfixef2)
      lower      upper
(Intercept) -0.1108204 0.1243262
attr(,"Probability")
[1] 0.95
>
> ##among-individual variance
> bID2<-sm2@ranef$squirrel_id
> bvar2<-as.vector(apply(bID2, 1, var)) ##between individual variance posterior distribution
> bvar2<-coda::as.mcmc(bvar2)
> MCMCglmm::posterior.mode(bvar2) ## mode of the distribution
      var1
0.02626174
> coda::HPDinterval(bvar2)
      lower      upper
var1 0.01904003 0.03561669
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
      var1
1.036547
> coda::HPDinterval(rvar2)
      lower      upper
var1 1.004938 1.147753
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)

```



```

      var1
0.02412265
> coda::HPDinterval(rID2)
      lower      upper
var1 0.01792588 0.03219275
attr(,"Probability")
[1] 0.95
>
>
> #####
> #adjusted repeatability
> #####
>
> m2b<-lmer(PC2 ~ sex + b.axy.local.density + b.axy_avg_fam + (1|squirrel_id) + (1|grid_yr), data=yearling_axy_all)
> summary(m2b)
Linear mixed model fit by REML ['lmerMod']
Formula: PC2 ~ sex + b.axy.local.density + b.axy_avg_fam + (1 | squirrel_id) + (1 | grid_yr)
Data: yearling_axy_all

REML criterion at convergence: 5192.8

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.1088 -0.1576  0.2939  0.5361  2.5070

Random effects:
 Groups      Name      Variance Std.Dev.
squirrel_id (Intercept) 0.02859  0.1691
grid_yr     (Intercept) 0.03079  0.1755
Residual                    1.06723  1.0331
Number of obs: 1764, groups:  squirrel_id, 86; grid_yr, 21

Fixed effects:
              Estimate Std. Error t value
(Intercept)   -0.0458696   0.0759349   -0.604
sexM           0.1719114   0.0844715    2.035
b.axy.local.density -0.0170572  0.0319168   -0.534
b.axy_avg_fam   0.0005169   0.0008423    0.614

Correlation of Fixed Effects:
      (Intr) sexM   b.xy..
sexM      -0.332
b.xy.lcl.dn -0.507 -0.009
b.axy_vg_fm  0.003 -0.108 -0.470
>
> plot(m2b)
> hist(resid(m2b))
>
> #for axy PC2
> sm2<-arm::sim(m2b,1000)
> smfixef2=sm2@fixef
> smranef2=sm2@ranef
> smfixef2=coda::as.mcmc(smfixef2)
> MCMCglmm::posterior.mode(smfixef2)
      (Intercept)      sexM b.axy.local.density      b.axy_avg_fam
-0.0462556125      0.1433801707      -0.0118077751      0.0008651256
> coda::HPDinterval(smfixef2)
      lower      upper
(Intercept) -0.195321231 0.098632090
sexM         0.017196379 0.334920293
b.axy.local.density -0.081217861 0.040369032
b.axy_avg_fam -0.001136087 0.002058615
attr(,"Probability")
[1] 0.95
>
> ##among-individual variance
> bID2<-sm2@ranef$squirrel_id
> bvar2<-as.vector(apply(bID2, 1, var)) ##between individual variance posterior distribution
> bvar2<-coda::as.mcmc(bvar2)
> MCMCglmm::posterior.mode(bvar2) ## mode of the distribution
      var1
0.02719354
> coda::HPDinterval(bvar2)
      lower      upper
var1 0.02000741 0.03680305
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
      var1
1.070241
> coda::HPDinterval(rvar2)
      lower      upper
var1 1.009443 1.150583
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)

```

```
> MCMCglmm::posterior.mode(rID2)
      var1
0.02454906
> coda::HPDinterval(rID2)
      lower      upper
var1 0.01759755 0.03235325
attr(,"Probability")
[1] 0.95
2024-05-09 13:30:02.180 R[25768:596427] allowedContentTypes : UTType pdf does not have a valid preferredFilenameExtension and will be ignored when
validating the file name
>
```