```
+   mutate(trialnumber=as.numeric(trialnumber),
+          grid=ifelse(grid=="SUX", "SU", grid),
+       grid_yr=paste(grid, year, sep=""),
+       year=year-2005) %>%
+   ungroup() %>%
+   group_by(squirrel_id) %>% #convert these variables to among-ind effects
+   mutate(b.assay.local.density= mean(assay.local.density),

+       b.assay_avg_fam= mean(assay_avg_fam, na.rm=T)) %>%
+   ungroup()
> m1a<-lmer(OFT1 ~ (1|squirrel_id) + (1| grid_yr), data=adult_assay_all)
> m1b<-lmer(OFT1 ~ trialnumber + sex + b.assay.local.density + b.assay_avg_fam + (1|squirrel_id) + (1|grid_yr), data=adult_assay_all)
> m2a<-lmer(OFT2 ~ (1|squirrel_id) + (1|grid_yr), data= adult_assay_all)
> m2b<-lmer(OFT2 ~ trialnumber + sex + b.assay.local.density + b.assay_avg_fam + (1|squirrel_id) + (1| grid_yr), data=adult_assay_all)
>
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>
> #repeatability estimates for adult squirrels for the assay complete dataset
> #original code by A. R. Martinig
> #last edited April 23, 2024 by A. R. Martinig
>
> #run the following prior to running script:
> #start-up code.R
> #PCA Generation Code - Assays.R
> #local density (global datasets).R
> #familiarity assays (global datasets).R
>
> adult_assay_all<-left_join(personality_all, clean_assay, by=c("squirrel_id"="squirrel_id", "year"="year")) %>%
+   filter(ageclass=="A") %>%
+   mutate(trialnumber=as.numeric(trialnumber),
+          grid=ifelse(grid=="SUX", "SU", grid),
+       grid_yr=paste(grid, year, sep=""),
+       year=year-2005) %>%
+   ungroup() %>%
+   group_by(squirrel_id) %>% #convert these variables to among-ind effects
+   mutate(b.assay.local.density= mean(assay.local.density),

+       b.assay_avg_fam= mean(assay_avg_fam, na.rm=T)) %>%
+   ungroup()
>
> summary(adult_assay_all)
  squirrel_id       sex                OFT1              OFT2             observer           ageclass             cohort           year
 Min.   : 6244   Length:484         Min.   :-3.04881   Min.   :-4.003616   Length:484         Length:484         Min.   :1998   Min.   : 0.000
 1st Qu.: 8008   Class :character   1st Qu.:-1.29546   1st Qu.:-0.486771   Class :character   Class :character   1st Qu.:2003   1st Qu.: 0.000
 Median :10372   Mode  :character   Median :-0.10425   Median : 0.001493   Mode  :character   Mode  :character   Median :2006   Median : 4.000
 Mean   :12066                      Mean   :-0.03433   Mean   :-0.011690                                         Mean   :2007   Mean   : 5.277
 3rd Qu.:13059                      3rd Qu.: 1.13722   3rd Qu.: 0.624574                                         3rd Qu.:2010   3rd Qu.: 8.000
 Max.   :25275                      Max.   : 4.79007   Max.   : 3.565010                                         Max.   :2021   Max.   :18.000
      age           grid            trialnumber      trialdate         assay.local.density assay_avg_fam     grid_yr
 Min.   :2.000   Length:484         Min.   :1.000   Min.   :2005-05-16   Min.   :0.0000      Min.   :   0.0   Length:484
 1st Qu.:2.000   Class :character   1st Qu.:1.000   1st Qu.:2005-08-17   1st Qu.:0.7534      1st Qu.:   0.0   Class :character
 Median :3.000   Mode  :character   Median :1.000   Median :2009-07-05   Median :1.5068     Median : 168.5   Mode  :character
 Mean   :3.023                      Mean   :1.436   Mean   :2010-10-01   Mean   :1.5037      Mean   : 193.6
 3rd Qu.:4.000                      3rd Qu.:2.000   3rd Qu.:2013-06-12   3rd Qu.:2.2602      3rd Qu.: 292.0
 Max.   :7.000                      Max.   :5.000   Max.   :2023-05-25   Max.   :3.9553      Max.   :1096.0
 b.assay.local.density b.assay_avg_fam
 Min.   :0.0000        Min.   :   0.0
 1st Qu.:0.7534        1st Qu.:   0.0
 Median :1.5068        Median :165.6
 Mean   :1.5037        Mean   :193.6
 3rd Qu.:2.2602        3rd Qu.:306.3
 Max.   :3.9553        Max.   :997.6
>
> (adult_assay_all) %>% as_tibble() %>% dplyr::count(squirrel_id) %>% nrow() #367 individuals
[1] 367
> summary(adult_assay_all$trialnumber)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.000   1.000   1.000   1.436   2.000   5.000
> nrow(adult_assay_all) #484
[1] 484
>
>
>
>
> #######################################
> #############       Adults       #############
> #############       n = 367      #############
> #######################################
```

```
> 
> ############################
> ######## OFT1 models ########
> ############################
> 
> ############################
> #non-adjusted repeatability
> ############################
> 
> m1a<-lmer(OFT1 ~ (1|squirrel_id) + (1| grid_yr), data=adult_assay_all)
> summary(m1a)
Linear mixed model fit by REML ['lmerMod']
Formula: OFT1 ~ (1 | squirrel_id) + (1 | grid_yr)
   Data: adult_assay_all

REML criterion at convergence: 1715

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.55461 -0.60023 -0.05276  0.65290  2.25241

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.6894   0.8303
 grid_yr     (Intercept) 0.5190   0.7204
 Residual                1.2493   1.1177
Number of obs: 484, groups:  squirrel_id, 367; grid_yr, 25

Fixed effects:
            Estimate Std. Error t value
(Intercept)  0.04059    0.17584   0.231
> 
> plot(m1a)
> hist(resid(m1a))
> 
> #for OFT PC1 (i.e. OFT1)
> sm1<-arm::sim(m1a,1000)
> smfixef=sm1@fixef
> smranef=sm1@ranef
> smfixef=coda::as.mcmc(smfixef)
> MCMCglmm::posterior.mode(smfixef)
(Intercept)
0.005969833
> coda::HPDinterval(smfixef)
                 lower     upper
(Intercept) -0.2962815 0.3642354
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
0.6822426
> coda::HPDinterval(bvar)
         lower    upper
var1 0.5753138 0.781515
attr(,"Probability")
[1] 0.95
> 
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
    var1
1.244799
> coda::HPDinterval(rvar)
        lower    upper
var1 1.098206 1.429716
attr(,"Probability")
[1] 0.95
> 
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
     var1
0.3507237
> coda::HPDinterval(rID)
        lower    upper
var1 0.319942 0.3838772
attr(,"Probability")
[1] 0.95
> 
> 
> 
> 
> ############################
> #adjusted repeatability
> ############################
> 
```

```
> m1b<-lmer(OFT1 ~ trialnumber + sex + b.assay.local.density + b.assay_avg_fam + (1|squirrel_id) + (1|grid_yr), data=adult_assay_all)
> summary(m1b)
Linear mixed model fit by REML ['lmerMod']
Formula: OFT1 ~ trialnumber + sex + b.assay.local.density + b.assay_avg_fam +      (1 | squirrel_id) + (1 | grid_yr)
   Data: adult_assay_all

REML criterion at convergence: 1705.6

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.43157 -0.58301 -0.00141  0.60766  1.98237

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.7371   0.8586
 grid_yr     (Intercept) 0.4423   0.6650
 Residual                1.1207   1.0586
Number of obs: 484, groups:  squirrel_id, 367; grid_yr, 25

Fixed effects:
                       Estimate Std. Error t value
(Intercept)           1.0276125  0.2548418   4.032
trialnumber          -0.4940993  0.0972383  -5.081
sexM                 -0.0621295  0.1582575  -0.393
b.assay.local.density -0.2036817  0.0906913  -2.246
b.assay_avg_fam        0.0001002  0.0004335   0.231

Correlation of Fixed Effects:
           (Intr) trlnmb sexM   b.ss..
trialnumber -0.493
sexM        -0.207 -0.070
b.ssy.lcl.d -0.432 -0.001  0.024
b.ssy_vg_fm -0.127 -0.039 -0.103 -0.300
>
> plot(m1b)
> hist(resid(m1b))
>
> #for OFT PC1 (i.e. OFT1)
> sm1<-arm::sim(m1b,1000)
> smfixef=sm1@fixef
> smranef=sm1@ranef
> smfixef=coda::as.mcmc(smfixef)
> MCMCglmm::posterior.mode(smfixef)
        (Intercept)           trialnumber                 sexM b.assay.local.density        b.assay_avg_fam
       1.0950088774         -0.4852542080         -0.1109374425          -0.2293824220           0.0001189606
> coda::HPDinterval(smfixef)
                           lower         upper
(Intercept)            0.5638584169  1.5444213371
trialnumber           -0.7025936163 -0.3110552409
sexM                  -0.3888937637  0.2494301307
b.assay.local.density -0.3922538410 -0.0381642613
b.assay_avg_fam       -0.0007238169  0.0008980569
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
0.7368306
> coda::HPDinterval(bvar)
        lower     upper
var1 0.6210897 0.8439081
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
   var1
1.12114
> coda::HPDinterval(rvar)
        lower     upper
var1 0.9807687 1.261099
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
     var1
0.395265
> coda::HPDinterval(rID)
        lower     upper
var1 0.358766 0.4268113
attr(,"Probability")
[1] 0.95
>
>
```

```
> 
> ###########################
> ######## OFT2 models ########
> ###########################
> 
> ###########################
> #non-adjusted repeatability
> ###########################
> 
> m2a<-lmer(OFT2 ~ (1|squirrel_id) + (1|grid_yr), data= adult_assay_all)
> summary(m2a)
Linear mixed model fit by REML ['lmerMod']
Formula: OFT2 ~ (1 | squirrel_id) + (1 | grid_yr)
   Data: adult_assay_all

REML criterion at convergence: 1441.5

Scaled residuals:
     Min       1Q   Median       3Q      Max
-3.15384 -0.33337  0.01616  0.43448  2.78207

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.3867   0.6218
 grid_yr     (Intercept) 0.4125   0.6423
 Residual                0.7005   0.8370
Number of obs: 484, groups:  squirrel_id, 367; grid_yr, 25

Fixed effects:
            Estimate Std. Error t value
(Intercept)  -0.1069     0.1512  -0.707
> 
> plot(m2a)
> hist(resid(m2a))
> 
> #for OFT PC2 (i.e. OFT2)
> sm2<-arm::sim(m2a,1000)
> smfixef2=sm2@fixef
> smranef2=sm2@ranef
> smfixef2=coda::as.mcmc(smfixef2)
> MCMCglmm::posterior.mode(smfixef2)
(Intercept)
-0.09979941
> coda::HPDinterval(smfixef2) #potential issues with trialnumber; gridJO
                lower    upper
(Intercept) -0.4065787 0.200181
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
0.3773333
> coda::HPDinterval(bvar2)
       lower     upper
var1 0.31889 0.4353281
attr(,"Probability")
[1] 0.95
> 
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
     var1
0.6706178
> coda::HPDinterval(rvar2)
         lower     upper
var1 0.6119491 0.7844804
attr(,"Probability")
[1] 0.95
> 
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
     var1
0.3410976
> coda::HPDinterval(rID2)
         lower     upper
var1 0.3208434 0.3837283
attr(,"Probability")
[1] 0.95
> 
> 
> 
> ###########################
> #adjusted repeatability
> ###########################
> 
> m2b<-lmer(OFT2 ~ trialnumber + sex + b.assay.local.density + b.assay_avg_fam + (1|squirrel_id) + (1| grid_yr), data=adult_assay_all)
```

```
> summary(m2b)
Linear mixed model fit by REML ['lmerMod']
Formula: OFT2 ~ trialnumber + sex + b.assay.local.density + b.assay_avg_fam +      (1 | squirrel_id) + (1 | grid_yr)
   Data: adult_assay_all

REML criterion at convergence: 1447

Scaled residuals:
     Min       1Q   Median       3Q      Max
-3.12831 -0.30216  0.01702  0.42524  2.63548

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.4017   0.6338
 grid_yr     (Intercept) 0.3882   0.6231
 Residual                0.6609   0.8130
Number of obs: 484, groups:  squirrel_id, 367; grid_yr, 25

Fixed effects:
                       Estimate Std. Error t value
(Intercept)           -0.3517382  0.2088795  -1.684
trialnumber            0.2594788  0.0744092   3.487
sexM                  -0.0368011  0.1209347  -0.304
b.assay.local.density  0.0500543  0.0694762   0.720
b.assay_avg_fam       -0.0008585  0.0003299  -2.602

Correlation of Fixed Effects:
            (Intr) trlnmb sexM   b.ss..
trialnumber -0.457
sexM        -0.194 -0.067
b.ssy.lcl.d -0.401 -0.002  0.025
b.ssy_vg_fm -0.121 -0.043 -0.109 -0.287
>
> plot(m2b)
> hist(resid(m2b))
>
> #for OFT PC2 (i.e. OFT2)
> sm2<-arm::sim(m2b,1000)
> smfixef2=sm2@fixef
> smranef2=sm2@ranef
> smfixef2=coda::as.mcmc(smfixef2)
> MCMCglmm::posterior.mode(smfixef2)
        (Intercept)             trialnumber                 sexM b.assay.local.density       b.assay_avg_fam
       -0.4241993642           0.2307000745           0.0335351575           0.0085664209           -0.0009625079
> coda::HPDinterval(smfixef2) #potential issues with trialnumber; gridJO
                          lower        upper
(Intercept)          -0.755516469  0.0878365969
trialnumber           0.119269314  0.4005504608
sexM                 -0.281841200  0.2075490368
b.assay.local.density -0.088247770  0.1828325314
b.assay_avg_fam      -0.001496303 -0.0002121551
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
0.3803306
> coda::HPDinterval(bvar2)
        lower     upper
var1 0.3387166 0.4584188
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
     var1
0.6585302
> coda::HPDinterval(rvar2)
       lower     upper
var1 0.580594 0.7482966
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
     var1
0.371252
> coda::HPDinterval(rID2)
        lower     upper
var1 0.3383822 0.4052874
attr(,"Probability")
[1] 0.95
> #repeatability estimates for yearling squirrels for the assay complete dataset
> #original code by A. R. Martinig
> #last edited April 23, 2024 by A. R. Martinig
```

```
>
>
> #run the following prior to running script:
> #start-up code.R
> #PCA Generation Code - Assays.R
> #local density (global datasets).R
> #familiarity assays (global datasets).R
>
> yearling_assay_all<-left_join(personality_all, clean_assay, by=c("squirrel_id"="squirrel_id", "year"="year")) %>%
+   filter(ageclass=="Y") %>%
+   mutate(trialnumber=as.numeric(trialnumber),
+          grid=ifelse(grid=="SUX", "SU", grid),
+      grid_yr=paste(grid, year, sep=""),
+      year=year-2005) %>%
+   group_by(squirrel_id) %>% #convert these variables to among-ind effects
+   mutate(b.assay.local.density= mean(assay.local.density),
+
+      b.assay_avg_fam= mean(assay_avg_fam, na.rm=T)) %>%
+   ungroup()
>
> summary(yearling_assay_all)
   squirrel_id        sex                OFT1               OFT2             observer           ageclass            cohort          year
 Min.   : 6313   Length:257         Min.   :-2.97025   Min.   :-3.81614   Length:257         Length:257         Min.   :2004   Min.   : 0.000
 1st Qu.: 7818   Class :character   1st Qu.:-1.10023   1st Qu.:-0.41213   Class :character   Class :character   1st Qu.:2004   1st Qu.: 0.000
 Median :10403   Mode  :character   Median :-0.02053   Median : 0.04009   Mode  :character   Mode  :character   Median :2007   Median : 3.000
 Mean   :11825                      Mean   : 0.06465   Mean   : 0.02202                                         Mean   :2008   Mean   : 4.401
 3rd Qu.:12703                      3rd Qu.: 1.33115   3rd Qu.: 0.63363                                         3rd Qu.:2011   3rd Qu.: 7.000
 Max.   :26017                      Max.   : 3.45457   Max.   : 2.99803                                         Max.   :2022   Max.   :18.000
      age          grid            trialnumber       trialdate          assay.local.density assay_avg_fam       grid_yr           b.assay.local.density
 Min.   :1    Length:257         Min.   :1.000   Min.   :2005-05-17   Min.   :0.0000      Min.   :  0.00   Length:257         Min.   :0.0000
 1st Qu.:1    Class :character   1st Qu.:1.000   1st Qu.:2005-07-24   1st Qu.:0.7534      1st Qu.:  0.00   Class :character   1st Qu.:0.7534
 Median :1    Mode  :character   Median :1.000   Median :2008-07-08   Median :1.3184      Median :  0.00   Mode  :character   Median :1.3184
 Mean   :1                       Mean   :1.444   Mean   :2009-11-19   Mean   :1.4269      Mean   : 56.67                      Mean   :1.4269
 3rd Qu.:1                       3rd Qu.:2.000   3rd Qu.:2012-07-21   3rd Qu.:2.0718      3rd Qu.: 84.46                      3rd Qu.:2.0718
 Max.   :1                       Max.   :7.000   Max.   :2023-05-24   Max.   :5.8388      Max.   :365.00                      Max.   :5.8388
 b.assay_avg_fam
 Min.   :  0.00
 1st Qu.:  0.00
 Median :  0.00
 Mean   : 56.67
 3rd Qu.: 84.46
 Max.   :365.00
>
> (yearling_assay_all) %>% as_tibble() %>% dplyr::count(squirrel_id) %>% nrow() #209 individuals
[1] 209
> summary(yearling_assay_all$trialnumber)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  1.000   1.000   1.000   1.444   2.000   7.000
> nrow(yearling_assay_all) #257
[1] 257
>
>
> ##########################################
> ############     Yearlings      ###########
> ############      n = 209          ###########
> ##########################################
>
> ###########################
> ######## OFT1 models ########
> ###########################
>
> ###########################
> #non-adjusted repeatability
> ###########################
>
> m3a<-lmer(OFT1 ~ (1|squirrel_id) + (1| grid_yr), data= yearling_assay_all)
> summary(m3a)
Linear mixed model fit by REML ['lmerMod']
Formula: OFT1 ~ (1 | squirrel_id) + (1 | grid_yr)
   Data: yearling_assay_all

REML criterion at convergence: 921.9

Scaled residuals:
     Min       1Q   Median       3Q      Max
-1.97879 -0.62084 -0.01792  0.65786  1.96964

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.7753   0.8805
 grid_yr     (Intercept) 0.2735   0.5230
 Residual                1.2537   1.1197
Number of obs: 257, groups:  squirrel_id, 209; grid_yr, 27

Fixed effects:
            Estimate Std. Error t value
(Intercept)   0.1425     0.1551   0.919
>
> plot(m3a)
> hist(resid(m3a))
>
> #for OFT PC1 (i.e. OFT1)
```

```
> sm1<-arm::sim(m3a,1000)
> smfixef=sm1@fixef
> smranef=sm1@ranef
> smfixef=coda::as.mcmc(smfixef)
> MCMCglmm::posterior.mode(smfixef)
(Intercept)
  0.1353377
> coda::HPDinterval(smfixef) #potential issue w/grid RR, SU, SUX
                lower     upper
(Intercept) -0.1722735 0.4162779
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
0.7672408
> coda::HPDinterval(bvar)
          lower     upper
var1 0.6240389 0.9422706
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
     var1
1.223962
> coda::HPDinterval(rvar)
        lower     upper
var1 1.068781 1.497985
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
     var1
0.3724105
> coda::HPDinterval(rID)
         lower    upper
var1 0.3368735 0.423964
attr(,"Probability")
[1] 0.95
>
>
> ###########################
> #adjusted repeatability
> ###########################
>
> m3b<-lmer(OFT1 ~ trialnumber +  sex + b.assay.local.density + b.assay_avg_fam + (1|squirrel_id) + (1| grid_yr), data= yearling_assay_all)
> summary(m3b)
Linear mixed model fit by REML ['lmerMod']
Formula: OFT1 ~ trialnumber + sex + b.assay.local.density + b.assay_avg_fam +      (1 | squirrel_id) + (1 | grid_yr)
   Data: yearling_assay_all

REML criterion at convergence: 918.9

Scaled residuals:
     Min      1Q   Median      3Q     Max
-1.89478 -0.58045 -0.07024  0.51535  1.80846

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.9058   0.9517
 grid_yr     (Intercept) 0.2988   0.5466
 Residual                1.0145   1.0072
Number of obs: 257, groups:  squirrel_id, 209; grid_yr, 27

Fixed effects:
                       Estimate Std. Error t value
(Intercept)            1.033901   0.300232   3.444
trialnumber           -0.530193   0.119538  -4.435
sexM                  -0.219874   0.202088  -1.088
b.assay.local.density  0.030099   0.113838   0.264
b.assay_avg_fam       -0.001502   0.001107  -1.357

Correlation of Fixed Effects:
            (Intr) trlnmb sexM   b.ss..
trialnumber -0.554
sexM        -0.343  0.070
b.ssy.lcl.d -0.503 -0.037 -0.036
b.ssy_vg_fm -0.135 -0.056  0.199 -0.171
>
> plot(m3b)
> hist(resid(m3b))
>
> #for OFT PC1 (i.e. OFT1)
```

```
> sm1<-arm::sim(m3b,1000)
> smfixef=sm1@fixef
> smranef=sm1@ranef
> smfixef=coda::as.mcmc(smfixef)
> MCMCglmm::posterior.mode(smfixef)
            (Intercept)            trialnumber                  sexM b.assay.local.density       b.assay_avg_fam
             0.85978982            -0.55043794            -0.22985059            0.02266417            -0.00138636
> coda::HPDinterval(smfixef) #potential issue w/grid RR, SU, SUX
                             lower        upper
(Intercept)             0.469641773  1.6813037166
trialnumber            -0.749236986 -0.3110988272
sexM                   -0.605412167  0.1800362336
b.assay.local.density  -0.204929807  0.2640256517
b.assay_avg_fam        -0.003662934  0.0005742376
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
0.8957067
> coda::HPDinterval(bvar)
         lower     upper
var1 0.7282004 1.082032
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
     var1
1.018672
> coda::HPDinterval(rvar)
         lower     upper
var1 0.8684369 1.206704
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
     var1
0.4764881
> coda::HPDinterval(rID)
         lower     upper
var1 0.4244891 0.5169974
attr(,"Probability")
[1] 0.95
>
>
> ###########################
> ####### OFT2 models #######
> ###########################
>
> ###########################
> #non-adjusted repeatability
> ###########################
>
> m4a<-lmer(OFT2 ~ (1|squirrel_id) + (1| year), data= yearling_assay_all) #note that fit is singular when I use grid_yr, so using year for this model
only
> summary(m4a)
Linear mixed model fit by REML ['lmerMod']
Formula: OFT2 ~ (1 | squirrel_id) + (1 | year)
   Data: yearling_assay_all

REML criterion at convergence: 724.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.4945 -0.4815  0.0420  0.5630  3.0254

Random effects:
 Groups      Name        Variance    Std.Dev.
 squirrel_id (Intercept) 0.000001069 0.001034
 year        (Intercept) 0.242500512 0.492443
 Residual                0.907125176 0.952431
Number of obs: 257, groups:  squirrel_id, 209; year, 13

Fixed effects:
            Estimate Std. Error t value
(Intercept)  -0.1401     0.1622  -0.864
>
> plot(m4a)
> hist(resid(m4a))
>
> #for OFT PC2 (i.e. OFT2)
> sm2<-arm::sim(m4a,1000)
> smfixef2=sm2@fixef
```

```
> smranef2=sm2@ranef
> smfixef2=coda::as.mcmc(smfixef2)
> MCMCglmm::posterior.mode(smfixef2)
(Intercept)
 -0.2048684
> coda::HPDinterval(smfixef2) #potential issues w/ grid RR
                lower     upper
(Intercept) -0.4479458 0.1652241
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
0.000001034817
> coda::HPDinterval(bvar2)
              lower           upper
var1 0.0000007829851 0.000001311455
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
      var1
0.8783637
> coda::HPDinterval(rvar2)
        lower     upper
var1 0.7658971 1.063581
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
         var1
0.000001100936
> coda::HPDinterval(rID2)
              lower           upper
var1 0.0000009202025 0.000001360874
attr(,"Probability")
[1] 0.95
>
>
> ############################
> #adjusted repeatability
> ############################
>
> m4b<-lmer(OFT2 ~ trialnumber +  sex + b.assay.local.density + b.assay_avg_fam + (1|squirrel_id) + (1| grid_yr), data= yearling_assay_all)
> summary(m4b)
Linear mixed model fit by REML ['lmerMod']
Formula: OFT2 ~ trialnumber + sex + b.assay.local.density + b.assay_avg_fam +      (1 | squirrel_id) + (1 | grid_yr)
   Data: yearling_assay_all

REML criterion at convergence: 738.4

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.3111 -0.4629  0.0169  0.4765  2.9282

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.1633   0.4041
 grid_yr     (Intercept) 0.3856   0.6210
 Residual                0.6839   0.8270
Number of obs: 257, groups:  squirrel_id, 209; grid_yr, 27

Fixed effects:
                       Estimate Std. Error t value
(Intercept)           -0.5705710  0.2390575  -2.387
trialnumber            0.2206911  0.0917352   2.406
sexM                  -0.0044102  0.1337012  -0.033
b.assay.local.density  0.0656764  0.0828217   0.793
b.assay_avg_fam        0.0002142  0.0007238   0.296

Correlation of Fixed Effects:
           (Intr) trlnmb sexM   b.ss..
trialnumber -0.538
sexM        -0.275  0.058
b.ssy.lcl.d -0.479 -0.004 -0.046
b.ssy_vg_fm -0.106 -0.078  0.219 -0.137
>
> plot(m4b)
> hist(resid(m4b))
>
> #for OFT PC2 (i.e. OFT2)
> sm2<-arm::sim(m4b,1000)
> smfixef2=sm2@fixef
```

```
> smranef2=sm2@ranef
> smfixef2=coda::as.mcmc(smfixef2)
> MCMCglmm::posterior.mode(smfixef2)
        (Intercept)         trialnumber              sexM b.assay.local.density      b.assay_avg_fam
       -0.4942736031         0.2463325448        0.0451402741        0.0598992451        0.0004340012
> coda::HPDinterval(smfixef2) #potential issues w/ grid RR
                            lower        upper
(Intercept)           -1.083259093 -0.106370196
trialnumber            0.047548774  0.391454365
sexM                  -0.245893211  0.263830407
b.assay.local.density -0.109182765  0.229254681
b.assay_avg_fam       -0.001208158  0.001668337
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
0.156799
> coda::HPDinterval(bvar2)
         lower     upper
var1 0.1193463 0.1939192
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
    var1
0.697069
> coda::HPDinterval(rvar2)
         lower     upper
var1 0.5775173 0.8079934
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
     var1
0.1843247
> coda::HPDinterval(rID2)
         lower     upper
var1 0.1579022 0.2143956
attr(,"Probability")
[1] 0.95
> #repeatabilities for axy1 file, adults only
> ##KEEP IN MIND: Some squirrels had axy conducted when they were in different ageclasses (e.g., A and Y)
> ###these squirrels cause imbalances when looking at ageclass summaries
> #original code by A. R. Martinig
> #last edited April 23, 2024 by A. R. Martinig
>
> #run the following prior to running script:
> #start-up code.R
> #axy data subsets.R
> #PCA generation code - axy.R
> #local density (global datasets).R
> #familiarity axy (global datasets).R
>
>
> #create working dataframe
> adult_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=="A") %>%
+   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(adult_axy_all)
  squirrel_id      axy_date            axy_yr        axy_month          tod                feed             forage             nestmove
 Min.   :10418   Min.   :2014-02-09   Min.   :0.000   Min.   : 1.000   Length:29144       Min.   :    0   Min.   :    0.0   Min.   :    0
 1st Qu.:12825   1st Qu.:2015-04-26   1st Qu.:1.000   1st Qu.: 4.000   Class :character   1st Qu.:    0   1st Qu.:    0.0   1st Qu.:  237
 Median :20198   Median :2016-12-15   Median :2.000   Median : 7.000   Mode  :character   Median :  143   Median :    5.0   Median :  861
 Mean   :18395   Mean   :2017-02-17   Mean   :2.628   Mean   : 6.577                      Mean   : 2509   Mean   :  459.5   Mean   : 2623
 3rd Qu.:21393   3rd Qu.:2018-09-28   3rd Qu.:4.000   3rd Qu.: 9.000                      3rd Qu.: 2133   3rd Qu.:  248.0   3rd Qu.: 3538
 Max.   :25225   Max.   :2022-09-23   Max.   :8.000   Max.   :12.000                      Max.   :27433   Max.   :12675.0   Max.   :38618


  nestnotmove       notmoving          travel           axy_id              sex                byear           dyear          litter_id
 Min.   :    0   Min.   :    0   Min.   :    0   Length:29144       Length:29144       Min.   :2006   Min.   :2010   Min.   :  17
 1st Qu.: 2344   1st Qu.:    0   1st Qu.:    0   Class :character   Class :character   1st Qu.:2011   1st Qu.:2016   1st Qu.:4907
 Median : 4974   Median :   95   Median :  111   Mode  :character   Mode  :character   Median :2013   Median :2018   Median :5546
 Mean   :11926   Mean   : 1618   Mean   : 2607                                         Mean   :2013   Mean   :2018   Mean   :5110
```

```
      3rd Qu.:18650    3rd Qu.: 1308    3rd Qu.: 1457                          3rd Qu.:2014    3rd Qu.:2019    3rd Qu.:5898
      Max.   :56852    Max.   :58198    Max.   :32518                          Max.   :2020    Max.   :2022    Max.   :9751
                                                                                                               NA's   :15240
       axy_age          axy_ageclass        prop_feeding       prop_foraging        prop_nestmoving    prop_nestnotmoving prop_notmoving
 Min.   :2.000    Length:29144       Min.   :0.00000     Min.   :0.0000000    Min.   :0.00000     Min.   :0.0000     Min.   :0.000000
 1st Qu.:2.000    Class :character   1st Qu.:0.00000     1st Qu.:0.0000000    1st Qu.:0.04645     1st Qu.:0.3561     1st Qu.:0.000000
 Median :3.000    Mode  :character   Median :0.01347     Median :0.0002048    Median :0.08347     Median :0.7304     Median :0.008104
 Mean   :3.443                       Mean   :0.07747     Mean   :0.0148672    Mean   :0.12118     Mean   :0.6258     Mean   :0.078869
 3rd Qu.:4.000                       3rd Qu.:0.13823     3rd Qu.:0.0162313    3rd Qu.:0.15669     3rd Qu.:0.9208     3rd Qu.:0.054953
 Max.   :8.000                       Max.   :0.93931     Max.   :0.3418058    Max.   :0.99964     Max.   :1.0000     Max.   :1.000000

   prop_travel           PC1                 PC2           axy.local.density  axy_avg_fam          grid             grid_yr
 Min.   :0.000000   Min.   :-1.65883   Min.   :-5.221415   Min.   :0.000     Min.   :   0.0    Length:29144       Length:29144
 1st Qu.:0.000000   1st Qu.:-1.44508   1st Qu.:-0.019986   1st Qu.:0.000     1st Qu.:   0.0    Class :character   Class :character
 Median :0.007353   Median :-0.85393   Median : 0.174625   Median :1.695     Median : 174.0    Mode  :character   Mode  :character
 Mean   :0.081806   Mean   :-0.04844   Mean   :-0.008494   Mean   :1.739     Mean   : 241.3
 3rd Qu.:0.122161   3rd Qu.: 1.02609   3rd Qu.: 0.415635   3rd Qu.:3.014     3rd Qu.: 439.5
 Max.   :0.862271   Max.   : 7.67479   Max.   : 3.593773   Max.   :6.027     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 :1.695     Median : 189.9
 Mean   :1.739     Mean   : 241.3
 3rd Qu.:3.137     3rd Qu.: 412.2
 Max.   :6.027     Max.   :1140.8

>
> (adult_axy_all) %>% as_tibble() %>% dplyr::count(squirrel_id) %>% nrow() #259 adults
[1] 259
> (adult_axy_all) %>% as_tibble() %>% dplyr::count(squirrel_id, axy_yr, axy_date) %>% nrow() #7334 deployment days
[1] 7334
> nrow(adult_axy_all) #29144 records
[1] 29144
>
> #########################################
> ############       Adults       #############
> ############      n = 259       #############
> #########################################
>
> ###########################
> ####### PC1 models #######
> ###########################
>
> ###########################
> #non-adjusted repeatability
> ###########################
>
> m1a<-lmer(PC1 ~ (1|squirrel_id) + (1|grid_yr) + (1|tod), data=adult_axy_all, control = lmerControl(optimizer ="Nelder_Mead"))
> summary(m1a)
Linear mixed model fit by REML ['lmerMod']
Formula: PC1 ~ (1 | squirrel_id) + (1 | grid_yr) + (1 | tod)
   Data: adult_axy_all
Control: lmerControl(optimizer = "Nelder_Mead")

REML criterion at convergence: 97309.1

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.3373 -0.6269 -0.1468  0.4369  5.3011

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.2563   0.5063
 grid_yr     (Intercept) 0.2921   0.5405
 tod         (Intercept) 1.2880   1.1349
 Residual                1.6053   1.2670
Number of obs: 29144, groups:  squirrel_id, 259; grid_yr, 32; tod, 4

Fixed effects:
            Estimate Std. Error t value
(Intercept) -0.07657    0.57709  -0.133
>
> 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)
 -0.3176903
> coda::HPDinterval(smfixef)
               lower    upper
(Intercept) -1.225392 1.053889
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
0.2582881
> coda::HPDinterval(bvar)
          lower     upper
var1 0.2345529 0.2795553
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
    var1
1.611172
> coda::HPDinterval(rvar)
         lower    upper
var1 1.57902 1.630987
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
    var1
0.136828
> coda::HPDinterval(rID)
          lower     upper
var1 0.1264498 0.1478799
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) + (1|tod), 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) + (1 | tod)
   Data: adult_axy_all

REML criterion at convergence: 97281

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.3122 -0.6267 -0.1465  0.4358  5.3214

Random effects:
 Groups      Name         Variance Std.Dev.
 squirrel_id (Intercept) 0.2028   0.4504
 grid_yr     (Intercept) 0.3111   0.5578
 tod         (Intercept) 1.2880   1.1349
 Residual                1.6053   1.2670
Number of obs: 29144, groups:  squirrel_id, 259; grid_yr, 32; tod, 4

Fixed effects:
                      Estimate Std. Error t value
(Intercept)         -0.0131824  0.5796013  -0.023
sexM                -0.4114651  0.0765996  -5.372
b.axy.local.density  0.1302487  0.0285816   4.557
b.axy_avg_fam       -0.0004033  0.0001553  -2.596

Correlation of Fixed Effects:
           (Intr) sexM   b.xy..
sexM       -0.049
b.xy.lcl.dn -0.056  0.061
b.axy_vg_fm -0.025 -0.167 -0.286
>
> 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
      -0.0867911406       -0.4189364416         0.1351172128        -0.0003722356
> coda::HPDinterval(smfixef)
                           lower        upper
(Intercept)         -1.1844781159  1.0804758371
sexM                -0.5550444160 -0.2709688892
b.axy.local.density  0.0660478857  0.1767910520
b.axy_avg_fam       -0.0006721254 -0.0000969517
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
0.2059033
> coda::HPDinterval(bvar)
          lower     upper
var1 0.1799065 0.2219159
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
     var1
1.607526
> coda::HPDinterval(rvar)
         lower   upper
var1 1.578974 1.63201
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
     var1
0.113767
> coda::HPDinterval(rID)
          lower    upper
var1 0.1007414 0.121589
attr(,"Probability")
[1] 0.95
>
>
>
> ###########################
> ####### PC2 models #######
> ###########################
>
> ###########################
> #non-adjusted repeatability
> ###########################
>
> m2a<-lmer(PC2 ~ (1|squirrel_id) + (1|grid_yr) + (1|tod), data=adult_axy_all)
> summary(m2a)
Linear mixed model fit by REML ['lmerMod']
Formula: PC2 ~ (1 | squirrel_id) + (1 | grid_yr) + (1 | tod)
   Data: adult_axy_all

REML criterion at convergence: 84792.2

Scaled residuals:
    Min      1Q  Median      3Q     Max
-5.8196 -0.1900  0.1185  0.4539  4.9795

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.25262  0.5026
 grid_yr     (Intercept) 0.31339  0.5598
 tod         (Intercept) 0.01773  0.1332
 Residual                1.04135  1.0205
Number of obs: 29144, groups:  squirrel_id, 259; grid_yr, 32; tod, 4

Fixed effects:
            Estimate Std. Error t value
(Intercept) -0.09831    0.12666  -0.776
>
> 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)
-0.09302741
> coda::HPDinterval(smfixef2)
                 lower     upper
(Intercept) -0.3457825 0.1674541
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
```

```
0.2529814
> coda::HPDinterval(bvar2)
         lower     upper
var1 0.2275618 0.2837089
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
   var1
1.03959
> coda::HPDinterval(rvar2)
        lower    upper
var1 1.023973 1.057747
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
     var1
0.1904241
> coda::HPDinterval(rID2)
        lower     upper
var1 0.1777404 0.2130731
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) + (1|tod), 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) + (1 | tod)
   Data: adult_axy_all

REML criterion at convergence: 84805.4

Scaled residuals:
    Min      1Q  Median      3Q     Max
-5.8283 -0.1903  0.1186  0.4536  4.9764

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.24619  0.4962
 grid_yr     (Intercept) 0.33592  0.5796
 tod         (Intercept) 0.01773  0.1332
 Residual                1.04121  1.0204
Number of obs: 29144, groups:  squirrel_id, 259; grid_yr, 32; tod, 4

Fixed effects:
                      Estimate Std. Error t value
(Intercept)         -0.1201862  0.1403046  -0.857
sexM                 0.0904383  0.0813441   1.112
b.axy.local.density -0.0680630  0.0300535  -2.265
b.axy_avg_fam        0.0003932  0.0001651   2.382

Correlation of Fixed Effects:
           (Intr) sexM   b.xy..
sexM       -0.219
b.xy.lcl.dn -0.246  0.067
b.axy_vg_fm -0.110 -0.171 -0.281
>
> 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
      -0.2156761710        0.0901457436       -0.0533932107         0.0004446016
> coda::HPDinterval(smfixef2)
                          lower        upper
(Intercept)         -0.38362629621  0.1490750183
sexM                -0.07216900716  0.2463614140
b.axy.local.density -0.12909366359 -0.0146179347
b.axy_avg_fam        0.00007395387  0.0007385089
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
0.2421112
> coda::HPDinterval(bvar2)
         lower     upper
var1 0.2183953 0.2734419
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
     var1
1.040643
> coda::HPDinterval(rvar2)
        lower   upper
var1 1.023359 1.05757
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
      var1
0.1897516
> coda::HPDinterval(rID2)
         lower     upper
var1 0.1747961 0.2094601
attr(,"Probability")
[1] 0.95
> #repeatabilities for axy1 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 23, 2024 by A. R. Martinig
>
>
> #run the following prior to running script:
> #start-up code.R
> #axy data subsets.R
> #PCA generation code - axy.R
> #local density (global datasets).R
> #familiarity axy (global datasets).R
>
> #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           tod               feed            forage          nestmove
 Min.   :19537   Min.   :2014-02-10   Min.   :0.000   Min.   : 2.000   Length:9136        Min.   :    0   Min.   :    0.0   Min.   :    0
 1st Qu.:21004   1st Qu.:2015-12-05   1st Qu.:1.000   1st Qu.: 7.000   Class :character   1st Qu.:    0   1st Qu.:    0.0   1st Qu.:  230
 Median :23215   Median :2017-09-10   Median :3.000   Median : 9.000   Mode  :character   Median :  137   Median :   10.0   Median :  871
 Mean   :22507   Mean   :2017-08-06   Mean   :2.974   Mean   : 7.986                      Mean   : 2832   Mean   :  610.4   Mean   : 2196
 3rd Qu.:23867   3rd Qu.:2019-06-08   3rd Qu.:5.000   3rd Qu.: 9.000                      3rd Qu.: 2170   3rd Qu.:  269.0   3rd Qu.: 3097
 Max.   :25314   Max.   :2022-09-14   Max.   :8.000   Max.   :12.000                      Max.   :27959   Max.   :10870.0   Max.   :36005

   nestnotmove       notmoving          travel           axy_id              sex               byear          dyear         litter_id       axy_age
 Min.   :    0    Min.   :    0    Min.   :    0    Length:9136        Length:9136        Min.   :2013    Min.   :2014    Min.   :  77    Min.   :1
 1st Qu.: 2145    1st Qu.:    0    1st Qu.:    0    Class :character   Class :character   1st Qu.:2014    1st Qu.:2017    1st Qu.:5740    1st Qu.:1
 Median : 4446    Median :   66    Median :  142    Mode  :character   Mode  :character   Median :2016    Median :2019    Median :5982    Median :1
 Mean   :11120    Mean   : 1505    Mean   : 3421                                          Mean   :2016    Mean   :2018    Mean   :6109    Mean   :1
 3rd Qu.:17648    3rd Qu.: 1112    3rd Qu.: 1598                                          3rd Qu.:2018    3rd Qu.:2019    3rd Qu.:7779    3rd Qu.:1
 Max.   :56722    Max.   :63983    Max.   :32920                                          Max.   :2021    Max.   :2022    Max.   :9878    Max.   :1
                                                                                                                          NA's   :5382
 axy_ageclass       prop_feeding      prop_foraging      prop_nestmoving   prop_nestnotmoving prop_notmoving      prop_travel
 Length:9136        Min.   :0.00000   Min.   :0.0000000   Min.   :0.00000   Min.   :0.0000     Min.   :0.000000   Min.   :0.000000
 Class :character   1st Qu.:0.00000   1st Qu.:0.0000000   1st Qu.:0.04516   1st Qu.:0.3016     1st Qu.:0.000000   1st Qu.:0.000000
 Mode  :character   Median :0.01405   Median :0.0005291   Median :0.07868   Median :0.7124     Median :0.005788   Median :0.008996
                    Mean   :0.08747   Mean   :0.0188390   Mean   :0.11422   Mean   :0.6073     Mean   :0.068456   Mean   :0.103708
                    3rd Qu.:0.16301   3rd Qu.:0.0241952   3rd Qu.:0.14156   3rd Qu.:0.9178     3rd Qu.:0.042751   3rd Qu.:0.164374
                    Max.   :0.77350   Max.   :0.2735921   Max.   :0.99606   Max.   :1.0000     Max.   :1.000000   Max.   :0.903063

      PC1               PC2           axy.local.density  axy_avg_fam          grid              grid_yr         b.axy.local.density
 Min.   :-1.6588   Min.   :-5.221415   Min.   :0.0000   Min.   :  0.00   Length:9136        Length:9136        Min.   :0.0000
 1st Qu.:-1.4340   1st Qu.: 0.003319   1st Qu.:0.0000   1st Qu.:  0.00   Class :character   Class :character   1st Qu.:0.0000
 Median :-0.7862   Median : 0.178173   Median :0.7534   Median :  0.00   Mode  :character   Mode  :character   Median :0.7534
 Mean   : 0.1545   Mean   : 0.027095   Mean   :1.6553   Mean   : 36.37                                         Mean   :1.6553
 3rd Qu.: 1.4471   3rd Qu.: 0.390145   3rd Qu.:3.2019   3rd Qu.: 69.00                                         3rd Qu.:3.2019
 Max.   : 6.8627   Max.   : 3.580799   Max.   :5.8388   Max.   :241.94                                         Max.   :5.8388

 b.axy_avg_fam
 Min.   :  0.00
```

```
 1st Qu.:  0.00
 Median :  0.00
 Mean   : 36.37
 3rd Qu.: 69.00
 Max.   :241.94


>
> (yearling_axy_all) %>% as_tibble() %>% dplyr::count(squirrel_id) %>% nrow() #119 individuals
[1] 119
> (yearling_axy_all) %>% as_tibble() %>% dplyr::count(squirrel_id, axy_yr, axy_date) %>% nrow() #2293 deployment days
[1] 2293
> nrow(yearling_axy_all) #9136 records
[1] 9136
>
> #########################################
> ############     Yearlings        ############
> ############        n = 119         ############
> #########################################
>
> ###########################
> ######## PC1 models ########
> ###########################
>
> ###########################
> #non-adjusted repeatability
> ###########################
>
> m1a<-lmer(PC1 ~ (1|squirrel_id) + (1|grid_yr) + (1|tod), data=yearling_axy_all)
> summary(m1a)
Linear mixed model fit by REML ['lmerMod']
Formula: PC1 ~ (1 | squirrel_id) + (1 | grid_yr) + (1 | tod)
   Data: yearling_axy_all

REML criterion at convergence: 31455.7

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.7506 -0.6369 -0.1487  0.4773  4.7392

Random effects:
 Groups      Name         Variance Std.Dev.
 squirrel_id (Intercept) 0.2311   0.4807
 grid_yr     (Intercept) 0.2126   0.4611
 tod         (Intercept) 2.0699   1.4387
 Residual                1.7691   1.3301
Number of obs: 9136, groups:  squirrel_id, 119; grid_yr, 24; tod, 4

Fixed effects:
            Estimate Std. Error t value
(Intercept)  0.07276    0.72845     0.1
>
> 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)
-0.07130175
> coda::HPDinterval(smfixef)
                lower    upper
(Intercept) -1.533258 1.222786
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
0.2365983
> coda::HPDinterval(bvar)
        lower     upper
var1 0.192453 0.2756952
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
    var1
1.757274
> coda::HPDinterval(rvar)
        lower     upper
var1 1.718427 1.818979
attr(,"Probability")
[1] 0.95
```

```
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
      var1
0.1178584
> coda::HPDinterval(rID)
          lower    upper
var1 0.09845723 0.135646
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) + (1|tod), 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) + (1 | tod)
   Data: yearling_axy_all

REML criterion at convergence: 31473.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.7508 -0.6364 -0.1482  0.4773  4.7461

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.2330   0.4827
 grid_yr     (Intercept) 0.2286   0.4782
 tod         (Intercept) 2.0698   1.4387
 Residual                1.7691   1.3301
Number of obs: 9136, groups:  squirrel_id, 119; grid_yr, 24; tod, 4

Fixed effects:
                      Estimate Std. Error t value
(Intercept)          0.0112674  0.7361032   0.015
sexM                -0.0355854  0.1239600  -0.287
b.axy.local.density  0.0499845  0.0512907   0.975
b.axy_avg_fam       -0.0001858  0.0009078  -0.205

Correlation of Fixed Effects:
            (Intr) sexM   b.xy..
sexM        -0.082
b.xy.lcl.dn -0.111  0.121
b.axy_vg_fm -0.006 -0.102 -0.310
>
> 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
       0.2410696970        0.0155473846        0.0720062688         0.0001329062
> coda::HPDinterval(smfixef)
                            lower       upper
(Intercept)         -1.582129293 1.298731480
sexM                -0.266228065 0.209713950
b.axy.local.density -0.045337321 0.151431315
b.axy_avg_fam       -0.001982264 0.001606442
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
0.2306923
> coda::HPDinterval(bvar)
          lower     upper
var1 0.1936139 0.2802281
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
     var1
1.769736
> coda::HPDinterval(rvar)
        lower   upper
var1 1.719807 1.81841
```

```
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
    var1
0.1138557
> coda::HPDinterval(rID)
         lower    upper
var1 0.09952538 0.1381047
attr(,"Probability")
[1] 0.95
>
>
> ###########################
> ####### PC2 models #######
> ###########################
>
> ###########################
> #non-adjusted repeatability
> ###########################
>
> m2a<-lmer(PC2 ~ (1|squirrel_id) + (1|grid_yr) + (1|tod), data=yearling_axy_all)
> summary(m2a)
Linear mixed model fit by REML ['lmerMod']
Formula: PC2 ~ (1 | squirrel_id) + (1 | grid_yr) + (1 | tod)
   Data: yearling_axy_all

REML criterion at convergence: 26375.1

Scaled residuals:
    Min      1Q  Median      3Q     Max
-5.7160 -0.1625  0.1177  0.4581  3.6429

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.07192  0.2682
 grid_yr     (Intercept) 0.11554  0.3399
 tod         (Intercept) 0.02223  0.1491
 Residual                1.02151  1.0107
Number of obs: 9136, groups:  squirrel_id, 119; grid_yr, 24; tod, 4

Fixed effects:
            Estimate Std. Error t value
(Intercept) -0.01327    0.10927  -0.121
>
> 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)
 0.03520741
> coda::HPDinterval(smfixef2)
                 lower     upper
(Intercept) -0.2342815 0.1874495
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
0.07130624
> coda::HPDinterval(bvar2)
         lower    upper
var1 0.05803727 0.08501587
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
    var1
1.017983
> coda::HPDinterval(rvar2)
        lower   upper
var1 0.9924963 1.04855
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
```

```
        var1
0.06783115
> coda::HPDinterval(rID2)
         lower      upper
var1 0.05436773 0.07700434
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) + (1|tod), 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) + (1 | tod)
   Data: yearling_axy_all

REML criterion at convergence: 26394.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
-5.7159 -0.1652  0.1155  0.4585  3.6457

Random effects:
 Groups      Name        Variance Std.Dev.
 squirrel_id (Intercept) 0.07505  0.2740
 grid_yr     (Intercept) 0.09558  0.3092
 tod         (Intercept) 0.02223  0.1491
 Residual                1.02155  1.0107
Number of obs: 9136, groups:  squirrel_id, 119; grid_yr, 24; tod, 4

Fixed effects:
                      Estimate Std. Error t value
(Intercept)         -0.0732752  0.1225332  -0.598
sexM                 0.0513970  0.0751417   0.684
b.axy.local.density  0.0070083  0.0312313   0.224
b.axy_avg_fam        0.0007174  0.0005462   1.313

Correlation of Fixed Effects:
            (Intr) sexM   b.xy..
sexM        -0.304
b.xy.lcl.dn -0.408  0.128
b.axy_vg_fm -0.025 -0.097 -0.297

>
> 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
        -0.1490153681          0.0506624778          0.0181556801          0.0006859441
> coda::HPDinterval(smfixef2)
                          lower       upper
(Intercept)         -0.3133840936 0.166863099
sexM                -0.0838084025 0.204150641
b.axy.local.density -0.0501704853 0.071409965
b.axy_avg_fam       -0.0003511544 0.001767099
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
0.07315544
> coda::HPDinterval(bvar2)
         lower      upper
var1 0.06003657 0.08895683
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
    var1
1.022766
> coda::HPDinterval(rvar2)
        lower     upper
var1 0.9950551 1.054965
attr(,"Probability")
[1] 0.95
>
> ##repeatability
```

```
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
      var1
0.06695625
> coda::HPDinterval(rID2)
          lower      upper
var1 0.05567473 0.08018638
attr(,"Probability")
[1] 0.95
2024-04-23 09:50:47.712 R[30498:3977986] allowedContentsTypes : UTType pdf does not have a valid preferredFilenameExtension and will be ignored when
validating the file name
>
```