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>
> #consecutive seven minute sampling
>
> #repeatabilities for axyl 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 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
> 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.:2014-05-18	Min.:0.00	Min.:5.000	Length:4570	Min.:0.0000	Min.:0.0000
1st Qu.:	:12733	1st Qu.:2014-09-14	1st Qu.:0.00	1st Qu.:6.000	Class :character	1st Qu.:0.0000	1st Qu.:0.0000
Median :	:20488	Median :2017-08-27	Median :3.00	Median :7.000	Mode :character	Median :0.0000	Median :0.0000
Mean :	:18891	Mean :2017-08-08	Mean :3.05	Mean :7.185	Mean :0.1665	Mean :0.04333	Mean :0.1392
3rd Qu.:	:22290	3rd Qu.:2019-07-03	3rd Qu.:5.00	3rd Qu.:9.000	3rd Qu.:0.0000	3rd Qu.:0.00000	3rd Qu.:0.0000
Max.	:25225	Max.:2022-09-24	Max.:8.00	Max.:9.000	Max.:1.0000	Max.:1.00000	Max.:1.0000

nestnotmove	notmoving	travel	axy_id	sex	byear	dyear	litter_id
Min.	:0.0000	Min.:0.000	Min.:0.0000	Length:4570	Min.:2006	Min.:2010	Min.:37
1st Qu.:	:0.0000	1st Qu.:0.000	1st Qu.:0.0000	Class :character	1st Qu.:0.0000	1st Qu.:2016	1st Qu.:4891
Median :	:0.0000	Median :0.000	Median :0.0000	Mode :character	Median :2014	Median :2018	Median :5258
Mean :	:0.3492	Mean :0.086	Mean :0.2158	Mean :0.1371	Mean :2014	Mean :2018	Mean :5199
3rd Qu.:	:1.0000	3rd Qu.:0.000	3rd Qu.:0.0000	3rd Qu.:0.1429	3rd Qu.:2016	3rd Qu.:2019	3rd Qu.:5894
Max.	:1.0000	Max.:1.000	Max.:1.0000	Max.:1.0000	Max.:2020	Max.:2022	Max.:9751

axy_age	axy_ageclass	prop_feeding	prop_foraging	prop_nestmoving	prop_nestnotmoving	prop_notmoving	prop_travel
Min.	:2.00	Min.:0.0000	Min.:0.00000	Min.:0.0000	Min.:0.0000	Min.:0.00000	Min.:0.0000
1st Qu.:	:2.00	1st Qu.:0.0000	1st Qu.:0.00000	1st Qu.:0.0000	1st Qu.:0.0000	1st Qu.:0.00000	1st Qu.:0.0000
Median :	:3.00	Median :0.0000	Median :0.00000	Median :0.0000	Median :0.0000	Median :0.00000	Median :0.0000
Mean :	:3.43	Mean :0.1631	Mean :0.04072	Mean :0.1371	Mean :0.3431	Mean :0.08482	Mean :0.2183
3rd Qu.:	:4.00	3rd Qu.:0.2857	3rd Qu.:0.07143	3rd Qu.:0.1429	3rd Qu.:0.8571	3rd Qu.:0.00000	3rd Qu.:0.4286
Max.	:8.00	Max.:1.0000	Max.:0.64286	Max.:1.0000	Max.:1.0000	Max.:1.00000	Max.:1.0000

PC1	PC2	axy.local.density	axy_avg_fam	grid	grid_yr	b.axy.local.density
Min.	:-1.77306	Min.:0.000	Min.:0.0	Length:4570	Length:4570	Min.:0.000
1st Qu.:	:-1.65089	1st Qu.:0.000	1st Qu.:0.0	Class :character	Class :character	1st Qu.:0.000
Median :	:-0.52641	Median :0.439256	Median :0.565	Mode :character	Mode :character	Median :0.565
Mean :	:-0.09329	Mean :0.003167	Mean :1.142	Mean :189.6	Mean :1.142	Mean :1.142
3rd Qu.:	:1.43400	3rd Qu.:0.485015	3rd Qu.:1.883	3rd Qu.:307.9	3rd Qu.:1.883	3rd Qu.:1.883
Max.	:3.81539	Max.:2.168383	Max.:5.839	Max.:1140.8	Max.:5.839	Max.:5.839

b.axy_avg_fam
Min.:0.0
1st Qu.:0.0
Median :0.0
Mean :189.6
3rd Qu.:324.9
Max.:1140.8

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> (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) #4570 records
[1] 4570
>
> #####
> #####      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: 16287.8

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.0974 -0.8387 -0.1809  0.9262  2.6077

Random effects:
 Groups      Name                Variance Std.Dev.
squirrel_id (Intercept)  0.07273   0.2697
grid_yr      (Intercept)  0.24956   0.4996
Residual                        1.99145   1.4112
Number of obs: 4570, groups:  squirrel_id, 177; grid_yr, 28

Fixed effects:
              Estimate Std. Error t value
(Intercept) -0.07318    0.10308   -0.71
>
> 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)
-0.08834315
> coda::HPDinterval(smfixef)
              lower      upper
(Intercept) -0.2640667  0.1260219
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
0.06737243
> coda::HPDinterval(bvar)
              lower      upper
var1 0.0570283 0.08303111
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
var1
1.982043
> coda::HPDinterval(rvar)
              lower      upper
var1 1.899567 2.061116
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
var1
0.03530732
> coda::HPDinterval(rID)
              lower      upper

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var1 0.02759367 0.03978716
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: 16308.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.0930 -0.8410 -0.1771  0.9199  2.6121

Random effects:
Groups      Name      Variance Std.Dev.
squirrel_id (Intercept) 0.07667  0.2769
grid_yr      (Intercept) 0.23131  0.4810
Residual                        1.99086  1.4110
Number of obs: 4570, groups:  squirrel_id, 177; grid_yr, 28

Fixed effects:
              Estimate Std. Error t value
(Intercept)  -0.1546515  0.1152372  -1.342
sexM          0.0558693  0.0877608   0.637
b.axy.local.density 0.0311955  0.0409403   0.762
b.axy_avg_fam  0.0001595  0.0001625   0.982

Correlation of Fixed Effects:
              (Intr) sexM   b.xy..
sexM          -0.174
b.xy.lcl.dn   -0.383  -0.070
b.axy_vg_fm   -0.150  -0.043  -0.202
>
> 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
-0.1007501246      0.0902002442      0.0387915486      0.0001692402
> coda::HPDinterval(smfixef)
              lower      upper
(Intercept)  -0.3515534211  0.0946321932
sexM          -0.1142900300  0.2133143073
b.axy.local.density -0.0556511870  0.1144919537
b.axy_avg_fam  -0.0001544184  0.0004690986
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
0.06893334
> coda::HPDinterval(bvar)
              lower      upper
var1 0.05916598 0.08806742
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
var1
1.979092
> coda::HPDinterval(rvar)
              lower      upper
var1 1.910227 2.070405
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
var1
0.03420929
> coda::HPDinterval(rID)
              lower      upper

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var1 0.02949983 0.04300589
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: 13430.7

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.0907 -0.1213  0.2834  0.4856  2.0510

Random effects:
Groups             Name                Variance Std.Dev.
squirrel_id (Intercept) 0.06861      0.2619
grid_yr      (Intercept) 0.06790      0.2606
Residual                    1.05842      1.0288
Number of obs: 4570, groups:  squirrel_id, 177; grid_yr, 28

Fixed effects:
              Estimate Std. Error t value
(Intercept) -0.002828   0.059215  -0.048
>
> 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)
-0.04064539
> coda::HPDinterval(smfixef2)
              lower      upper
(Intercept) -0.1144515 0.1076468
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
0.06936834
> coda::HPDinterval(bvar2)
              lower      upper
var1 0.05606657 0.08118197
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
var1
1.061382
> coda::HPDinterval(rvar2)
              lower      upper
var1 1.02002 1.101554
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
var1
0.05862777
> coda::HPDinterval(rID2)
              lower      upper
var1 0.05079762 0.07194259
attr(,"Probability")
[1] 0.95
>
> #####
> #adjusted repeatability

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> #####
>
> 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: 13454.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.0874 -0.1222  0.2815  0.4874  2.0252

Random effects:
Groups             Name                Variance Std.Dev.
squirrel_id (Intercept) 0.07129   0.2670
grid_yr      (Intercept) 0.06820   0.2612
Residual                        1.05810   1.0286
Number of obs: 4570, groups:  squirrel_id, 177; grid_yr, 28

Fixed effects:
              Estimate Std. Error t value
(Intercept)   -0.00772820  0.07434364  -0.104
sexM           0.05918698  0.07039308   0.841
b.axy.local.density -0.01262662  0.03098055  -0.408
b.axy_avg_fam    0.00001641  0.00013540   0.121

Correlation of Fixed Effects:
              (Intr) sexM   b.xy..
sexM          -0.226
b.xy.lcl.dn   -0.432  -0.095
b.axy_vg_fm   -0.182  -0.041  -0.249
>
> 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
1.00620915322      0.05333989554      -0.00488881328      -0.00003660851
> coda::HPDinterval(smfixef2)
              lower      upper
(Intercept) -0.1616810543  0.1268766053
sexM         -0.0731905953  0.1967046213
b.axy.local.density -0.0706545748  0.0484363332
b.axy_avg_fam  -0.0002519571  0.0002719529
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
0.07249207
> coda::HPDinterval(bvar2)
              lower      upper
var1 0.05839203  0.08432272
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
var1
1.054513
> coda::HPDinterval(rvar2)
              lower      upper
var1 1.014074  1.103754
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
var1
0.05965134
> coda::HPDinterval(rID2)
              lower      upper
var1 0.05237633  0.0739809
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   tod   feed   forage   nestmove
Min.   :19537   Min.   :2014-08-26   Min.   :0.000   Min.   :5.00   Length:1792   Min.   :0.0000   Min.   :0.00000   Min.   :0.00000
1st Qu.:21473   1st Qu.:2015-09-19   1st Qu.:1.000   1st Qu.:7.00   Class :character   1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:0.00000
Median :23263   Median :2017-09-22   Median :3.000   Median :8.00   Mode  :character   Median :0.0000   Median :0.00000   Median :0.00000
Mean   :22792   Mean   :2017-11-21   Mean   :3.278   Mean   :7.84   Mean :0.1886   Mean :0.05246   Mean :0.09542
3rd Qu.:23869   3rd Qu.:2019-06-15   3rd Qu.:5.000   3rd Qu.:9.00   3rd Qu.:0.0000   3rd Qu.:0.00000   3rd Qu.:0.00000
Max.   :25314   Max.   :2022-09-15   Max.   :8.000   Max.   :9.00   Max. :1.0000   Max. :1.00000   Max. :1.00000

  nestnotmove   notmoving   travel   axy_id   sex   byear   dyear   litter_id   axy_age
Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   Length:1792   Length:1792   Min.   :2013   Min.   :2014   Min.   : 77   Min.   :1
1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000   Class :character   Class :character   1st Qu.:2014   1st Qu.:2018   1st Qu.:5801   1st Qu.:1
Median :0.0000   Median :0.0000   Median :0.0000   Mode  :character   Mode  :character   Median :2016   Median :2019   Median :5982   Median :1
Mean   :0.2913   Mean   :0.0904   Mean   :0.2818   Mean :0.07143   Mean :0.07143   Mean :2016   Mean :2018   Mean :6316   Mean :1
3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:0.07143   3rd Qu.:0.07143   3rd Qu.:2018   3rd Qu.:2019   3rd Qu.:7779   3rd Qu.:1
Max.   :1.0000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000   Max.   :2021   Max.   :2022   Max.   :9878   Max.   :1
                                     NA's :1186
  axy_ageclass   prop_feeding   prop_foraging   prop_nestmoving   prop_nestnotmoving   prop_notmoving   prop_travel   PC1
Length:1792   Min.   :0.00000   Min.   :0.00000   Min.   :0.00000   Min.   :0.0000   Min.   :0.00000   Min.   :0.0000   Min.   : -2.1621
Class :character   1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.: -1.6295
Mode  :character   Median :0.07143   Median :0.00000   Median :0.00000   Median :0.0000   Median :0.00000   Median :0.1429   Median : 0.8014
Mean   :0.20197   Mean :0.04915   Mean :0.09522   Mean :0.2869   Mean :0.08163   Mean :0.2750   Mean : 0.2379
3rd Qu.:0.35714   3rd Qu.:0.07143   3rd Qu.:0.07143   3rd Qu.:0.7857   3rd Qu.:0.00000   3rd Qu.:0.5000   3rd Qu.: 1.6094
Max.   :1.00000   Max.   :0.78571   Max.   :1.00000   Max.   :1.0000   Max.   :1.00000   Max.   :1.0714   Max.   : 4.2022

  PC2   axy.local.density   axy_avg_fam   grid   grid_yr   b.axy.local.density   b.axy_avg_fam
Min.   : -4.012720   Min.   :0.0000   Min.   : 0.00   Length:1792   Length:1792   Min.   :0.0000   Min.   : 0.00
1st Qu.: -0.132548   1st Qu.:0.0000   1st Qu.: 0.00   Class :character   Class :character   1st Qu.:0.0000   1st Qu.: 0.00
Median : 0.439256   Median :0.1883   Median : 0.00   Mode  :character   Mode  :character   Median :0.1883   Median : 0.00
Mean   : -0.008076   Mean :1.2501   Mean :24.15   Mean :1.2501   Mean :24.15
3rd Qu.: 0.475400   3rd Qu.:2.2602   3rd Qu.:30.67   3rd Qu.:2.2602   3rd Qu.:30.67
Max.   : 2.553459   Max.   :5.8388   Max.   :241.94   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] 1792
>
> #####
> ##### Yearlings #####
> ##### n = 86 #####
> #####
>
> #####
> ##### PC1 models #####
> #####
>
> #####
> #non-adjusted repeatability
> #####
>
> mla<-lmer(PC1 ~ (1|squirrel_id) + (1|grid_yr), data=yearling_axy_all)
> summary(mla)
Linear mixed model fit by REML ['lmerMod']
Formula: PC1 ~ (1 | squirrel_id) + (1 | grid_yr)
Data: yearling_axy_all

REML criterion at convergence: 6443.2

```

```

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.1829 -0.9212  0.2490  0.8538  2.2799

Random effects:
    Groups       Name             Variance Std.Dev.
squirrel_id (Intercept) 0.1404      0.3746
grid_yr      (Intercept) 0.2644      0.5142
Residual                2.0158      1.4198
Number of obs: 1792, groups:  squirrel_id, 86; grid_yr, 21

Fixed effects:
              Estimate Std. Error t value
(Intercept)   0.2241     0.1347   1.664
>
> 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)
0.2150938
> coda::HPDinterval(smfixef)
              lower      upper
(Intercept) -0.06074411 0.4497811
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
0.13514
> coda::HPDinterval(bvar)
              lower      upper
var1 0.09391408 0.170029
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
var1
2.000525
> coda::HPDinterval(rvar)
              lower      upper
var1 1.883502 2.14268
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
var1
0.06410457
> coda::HPDinterval(rID)
              lower      upper
var1 0.04577277 0.0783096
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: 6453.8

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.1818 -0.9086  0.2687  0.8440  2.2866

Random effects:
    Groups       Name             Variance Std.Dev.
squirrel_id (Intercept) 0.1304      0.3611
grid_yr      (Intercept) 0.2247      0.4741
Residual                2.0173      1.4203
Number of obs: 1792, groups:  squirrel_id, 86; grid_yr, 21

```

```

Fixed effects:
              Estimate Std. Error t value
(Intercept)    0.128145   0.166768    0.768
sexM            0.362006   0.147155    2.460
b.axy.local.density 0.009194  0.061831    0.149
b.axy_avg_fam  -0.001415   0.001364   -1.037

Correlation of Fixed Effects:
              (Intr) sexM  b.xy..
sexM          -0.334
b.xy.lcl.dn  -0.530  0.079
b.axy_vg_fm  -0.026 -0.086 -0.351
>
> 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
1.188330556      0.398444804      -0.003585765      -0.001151508
> coda::HPDinterval(smfixef)
              lower      upper
(Intercept) -0.238850082  0.4372092345
sexM         0.048338229  0.6244585878
b.axy.local.density -0.102149182  0.1386973772
b.axy_avg_fam  -0.004168032  0.0009402981
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
0.115479
> coda::HPDinterval(bvar)
              lower      upper
var1 0.093859 0.1687674
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar<-sm1@sigma^2
> rvar<-coda::as.mcmc(rvar)
> MCMCglmm::posterior.mode(rvar)
var1
1.99954
> coda::HPDinterval(rvar)
              lower      upper
var1 1.883806 2.144821
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID<-bvar/(bvar+rvar)
> MCMCglmm::posterior.mode(rID)
var1
0.05773994
> coda::HPDinterval(rID)
              lower      upper
var1 0.0420239 0.07428722
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: 5261.7

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.1045 -0.1587  0.2961  0.5244  2.4964

Random effects:
Groups      Name      Variance Std.Dev.

```



```

squirrel_id (Intercept) 0.02839 0.1685
grid_yr      (Intercept) 0.04243 0.2060
Residual      1.06830 1.0336
Number of obs: 1792, groups:  squirrel_id, 86; grid_yr, 21

Fixed effects:
              Estimate Std. Error t value
(Intercept) 0.0007746 0.0608612 0.013
>
> 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)
0.03499913
> coda::HPDinterval(smfixef2)
              lower      upper
(Intercept) -0.1153889 0.1150815
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
0.02641274
> coda::HPDinterval(bvar2)
              lower      upper
var1 0.01940201 0.03569145
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
var1
1.076971
> coda::HPDinterval(rvar2)
              lower      upper
var1 1.004215 1.137176
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
var1
0.02367676
> coda::HPDinterval(rID2)
              lower      upper
var1 0.01716651 0.03112793
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: 5277.9

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.1398 -0.1582  0.2954  0.5374  2.5286

Random effects:
Groups      Name              Variance Std.Dev.
squirrel_id (Intercept) 0.02857 0.1690
grid_yr      (Intercept) 0.03040 0.1744
Residual      1.06934 1.0341
Number of obs: 1792, groups:  squirrel_id, 86; grid_yr, 21

Fixed effects:
              Estimate Std. Error t value
(Intercept)   -0.0463213  0.0755897  -0.613
sexM           0.1709241  0.0842056   2.030
b.axy.local.density -0.0167978  0.0318230  -0.528
b.axy.avg_fam   0.0005133  0.0008408   0.610

```

```

Correlation of Fixed Effects:
              (Intr) sexM   b.xy..
sexM          -0.331
b.xy.lcl.dn   -0.506 -0.011
b.axy_vg_fm   0.002 -0.107 -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
-0.0484820366          0.1361766268      -0.0150447317      0.0003608882
> coda::HPDinterval(smfixef2)
              lower      upper
(Intercept)  -0.192617034  0.101724544
sexM          0.008083034  0.317739138
b.axy.local.density -0.081379629  0.043140549
b.axy_avg_fam   -0.001087085  0.002084497
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
0.02796609
> coda::HPDinterval(bvar2)
              lower      upper
var1 0.02053227  0.03727399
attr(,"Probability")
[1] 0.95
>
> ##residual variance
> rvar2<-sm2@sigma^2
> rvar2<-coda::as.mcmc(rvar2)
> MCMCglmm::posterior.mode(rvar2)
var1
1.066791
> coda::HPDinterval(rvar2)
              lower      upper
var1 0.9994742  1.137085
attr(,"Probability")
[1] 0.95
>
> ##repeatability
> rID2<-bvar2/(bvar2+rvar2)
> MCMCglmm::posterior.mode(rID2)
var1
0.02493073
> coda::HPDinterval(rID2)
              lower      upper
var1 0.01870662  0.03304014
attr(,"Probability")
[1] 0.95
2024-04-24 09:54:15.832 R[72471:4848088] allowedContentsTypes : UTType pdf does not have a valid preferredFilenameExtension and will be ignored when
validating the file name
>

```