```
R version 4.3.2 (2023-10-31 ucrt) -- "Eye Holes"
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Platform: x86_64-w64-mingw32/x64 (64-bit)

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  Natural language support but running in an English locale

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Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> #working directory here
> #Last edited on Jan 4, 2024 by A. R. Martinig
>
> #Delete previous information stored
> rm(list=ls(all=T))
>
> ##set wd to the folder with all your csv's in it
> setwd("C:/Users/SpenserBurk/Desktop/axy assay stuff")
>
> library(MCMCglmm)
Loading required package: Matrix
Loading required package: coda
Loading required package: ape
Warning messages:
1: package 'MCMCglmm' was built under R version 4.3.3
2: package 'coda' was built under R version 4.3.3
3: package 'ape' was built under R version 4.3.3
> library(data.table)
data.table 1.15.2 using 8 threads (see ?getDTthreads).  Latest news: r-datatable.com
Warning message:
package 'data.table' was built under R version 4.3.3
> library(dplyr)

Attaching package: 'dplyr'

The following objects are masked from 'package:data.table':

    between, first, last

The following object is masked from 'package:ape':

    where

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union

Warning message:
package 'dplyr' was built under R version 4.3.3
>
>
> final_MCMC<-read.csv("final_dataset.csv", header=T)
>
> final_MCMC %>% filter(is.na(age))
 [1] X                     squirrel_id         grid                    sex                     ageclass
        age                   cohort              year                    trialnumber             trialdate
           assay.local.density
```

```
[12] assay_avg_fam          OFT1                  OFT2                  PC1                    PC2
        date                  age2          local.density         avg_fam
<0 rows> (or 0-length row.names)
> #make sure to always check for new NAs after standardization because it doesnt work when a squi
rrel is the only individual in their grid and year; give mean values (0) to these records
>
> summary(final_MCMC)
       X            squirrel_id         grid                sex               ageclass                ag
e             cohort            year          trialnumber          trialdate          assay.local.de
nsity assay_avg_fam          OFT1
 Min.   :    1    Min.   : 6244    Length:39467         Length:39467         Length:39467         Min.
:-17.464342    Min.   :1998    Min.   : 0.00    Length:39467         Length:39467         Min.   :0.000
        Min.   :   0.00    Min.   :-3.15
 1st Qu.: 9868    1st Qu.:13305    Class :character    Class :character    Class :character    1st Qu.
: -0.679227    1st Qu.:2012    1st Qu.:10.00    Class :character    Class :character    1st Qu.:0.000
        1st Qu.:   0.00    1st Qu.:-1.21
 Median :19734    Median :20739    Mode  :character    Mode  :character    Mode  :character    Median
:  0.057073    Median :2014    Median :11.00    Mode  :character    Mode  :character    Median :1.507
        Median :  76.67    Median :-0.04
 Mean   :19734    Mean   :19234                                                                Mean
:  0.000045    Mean   :2014    Mean   :11.56                                          Mean   :1.717
        Mean   : 189.32    Mean   : 0.00
 3rd Qu.:29601    3rd Qu.:22450                                                                3rd Qu.
:  0.783870    3rd Qu.:2016    3rd Qu.:14.00                                          3rd Qu.:3.014
        3rd Qu.: 339.00    3rd Qu.: 1.24
 Max.   :39467    Max.   :26017                                                                Max.
:  3.528898    Max.   :2022    Max.   :18.00                                          Max.   :6.027
        Max.   :1140.75    Max.   : 4.57


                     NA's   :38288
      OFT2                  PC1                   PC2                   date                  age2          loc
al.density          avg_fam
 Min.   :-3.87    Min.   :-1.6589    Min.   :-5.2216    Min.   :-2.968169    Min.   :-17.464342    Min
.   :-1.943931    Min.   :-1.20217
 1st Qu.:-0.72    1st Qu.:-1.4426    1st Qu.:-0.0130    1st Qu.:-0.917171    1st Qu.: -0.772041    1st
Qu.:-0.665259    1st Qu.:-0.83558
 Median :-0.08    Median :-0.8387    Median : 0.1755    Median : 0.230918    Median : -0.191138    Med
ian :-0.031472    Median :-0.13011
 Mean   : 0.00    Mean   : 0.0000    Mean   : 0.0000    Mean   : 0.000009    Mean   :  0.000023    Mea
n   : 0.000049    Mean   : 0.00003
 3rd Qu.: 0.66    3rd Qu.: 1.1047    3rd Qu.: 0.4095    3rd Qu.: 0.750158    3rd Qu.:  0.542515    3rd
Qu.: 0.533884    3rd Qu.: 0.52261
 Max.   : 3.26    Max.   : 7.6746    Max.   : 3.5941    Max.   : 3.812292    Max.   :  5.721127    Max
.   :17.464342    Max.   : 8.44751
 NA's   :38288    NA's   :1183       NA's   :1183

> head(final_MCMC)
  X squirrel_id grid sex ageclass        age cohort year trialnumber  trialdate assay.local.dens
ity assay_avg_fam         OFT1        OFT2 PC1 PC2        date        age2 local.density     avg_fam
1 1        6244  AG   F        A  1.58402905   2000    0           1 2005-05-24          0.0000
000       0.0000  2.32091671  0.3317803  NA  NA -0.67567031  1.64875749   -1.21468180 -0.9863304
2 2        6312  KL   M        A  0.15867378   2002    0           1 2005-06-26          0.9417
452     396.0000 -0.02796909  1.5539460  NA  NA -0.02950984 -0.08867096   -1.30459522  0.6903829
3 3        6313  KL   M        Y -1.13305804   2004    0           1 2005-06-07          0.9417
452     109.2000 -1.07484455 -0.1802682  NA  NA -0.18861899 -0.81002688   -1.30459522 -0.6802864
4 4        6317  AG   F        J -1.82043073   2005    0           1 2005-06-27          0.0000
000       0.0000 -1.75684669 -0.5710115  NA  NA -0.41736056 -0.97743734   -1.21468180 -0.9863304
5 5        6338  SU   F        A  0.06091802   2002    0           1 2005-05-23          1.1300
943     331.3333  0.69241398  1.0074066  NA  NA -1.13186640 -0.19113760   -0.41418559  0.8248840
6 6        6340  AG   F        A -0.45864682   2003    0           1 2005-07-02          2.0718
395       0.0000 -0.50934812 -0.3390378  NA  NA -0.37937383 -0.55724617   -0.03108223 -0.9863304
> names(final_MCMC)
 [1] "X"                  "squirrel_id"        "grid"               "sex"                "age
class"           "age"                "cohort"             "year"               "trialnumber"
        "trialdate"
[11] "assay.local.density" "assay_avg_fam"      "OFT1"               "OFT2"               "PC1
"                "PC2"                "date"               "age2"               "local.densit
y"        "avg_fam"
>
```

```
> (final_MCMC) %>% as_tibble() %>% count(squirrel_id) %>% nrow() #1094 individuals
[1] 1094
>
> #make sure variables aren't standardized before running this
> attach(final_MCMC);tt=cbind(year, age, age2, local.density, avg_fam, date)
> cor(tt)
                    year          age         age2 local.density      avg_fam         date
year           1.00000000 -0.01772367 -0.01115771    -0.1947808 -0.017916816  0.066428432
age           -0.01772367  1.00000000  0.96459376    -0.1392789  0.291175610 -0.282784736
age2          -0.01115771  0.96459376  1.00000000    -0.1226591  0.238826533 -0.248950747
local.density -0.19478076 -0.13927887 -0.12265912     1.0000000  0.249792504  0.205311224
avg_fam       -0.01791682  0.29117561  0.23882653     0.2497925  1.000000000 -0.009677467
date           0.06642843 -0.28278474 -0.24895075     0.2053112 -0.009677467  1.000000000
>
> #age & age2 = 0.96454021
> #next highest correlation was 0.29079603
>
>
> #bayesian multivariate generalized linear model analysis
>
> ###you will have to model priors. Good to test for different prior settings to ensure results a
re not sensitive to prior.
> #R is residual structure, G is random effects structure, B is fixed effects
> #numbers inside diag() indicate the number of response variables in my model
> #number of zeros in alpha.mu=c() need to match the number of response variables in model
>
> #this is a parameter expanded prior
> prior.iw<-list(
+ R=list(V=diag(4), nu=1),
+ G=list(
+ G1=list(V=diag(4), nu= 1,
+ alpha.mu=c(0,0,0,0),
+ alpha.V=diag(4)*1000), #when alpha.V is non-zero, parameter expanded algorithms are used #for t
his the last number should be something large (e.g. 1000, depending on the scale of the data)
+
+ #need to repeat to deal with second random effect
+ G2=list(V=diag(4), nu= 1,
+ alpha.mu=c(0,0,0,0),
+ alpha.V=diag(4)*1000)))
> #the use of parameter expansion means the priors are no longer inverse-Wishart but scaled-F
> #parameter expanded models can be used, which enable prior specifications from the scaled non-c
entral F-distribution
>
> final_MCMC<-as.data.frame(final_MCMC)
>
>
>
> #to get the gelman-rubin stat:
> chains <- as.mcmc.list(lapply(1:2, function(i)
+ MCMCglmm(cbind(OFT1, OFT2, PC1, PC2) ~ trait-1 + trait:sex + trait:age+ trait:date + trait:loca
l.density + trait:avg_fam, random = ~us(trait):squirrel_id + us(trait):year, rcov = ~us(trait):un
its, family = c("gaussian", "gaussian", "gaussian", "gaussian"), data= final_MCMC, prior = prior.
iw, verbose=FALSE, nitt= 303000, thin=300, burnin=3000)$Sol ))
>
> gelman.diag(chains) #if it has converged, the scale reduction should be 1 (i.e., none)
Potential scale reduction factors:
```

	Point est.	Upper C.I.
traitOFT1	1.070	1.28
traitOFT2	1.006	1.03
traitPC1	1.001	1.00
traitPC2	1.011	1.05
traitOFT1:sexM	1.009	1.04
traitOFT2:sexM	1.000	1.00
traitPC1:sexM	1.002	1.01
traitPC2:sexM	1.002	1.01
traitOFT1:age	1.000	1.00
traitOFT2:age	1.012	1.05
traitPC1:age	1.001	1.00
traitPC2:age	1.004	1.00

```
traitOFT1:date                 1.432        2.29
traitOFT2:date                 1.012        1.02
traitPC1:date                  1.009        1.04
traitPC2:date                  0.999        1.00
traitOFT1:local.density        1.002        1.01
traitOFT2:local.density        1.006        1.03
traitPC1:local.density         1.002        1.01
traitPC2:local.density         1.001        1.01
traitOFT1:avg_fam              1.055        1.23
traitOFT2:avg_fam              1.033        1.15
traitPC1:avg_fam               1.000        1.00
traitPC2:avg_fam               1.003        1.01

Multivariate psrf

1.33
> gelman.plot(chains)
>
```