

## R analysis

How do developmental and parental exposures to predation affect personality and immediate behavioural plasticity in the snail *Physa acuta*?

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Proceedings of the Royal Society B  
doi:10.1098/rspb.2020.1761

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29/10/2020

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## Load packages and data

### Load packages

```
# data manipulation
library(dplyr)
library(tidyr)
# graphics
library(ggplot2)
library(cowplot)
theme_set(theme_classic())
```

```

# statistics
library(lme4)
library(lmerTest)
library(emmeans)
library(MCMCglmm)
se <- function(x) sd(x, na.rm = TRUE)/sqrt(sum(!is.na(x)))
# table output in word format
library(flextable)
library(officer)
library(measurements) # for the function 'conv_unit'

```

## Load data

```

dat <- read.table("data.csv", header = T, sep=";", dec=".", stringsAsFactors = T)
str(dat)
nrow(dat) # total number of trials
dat %>% group_by(Developmental, Parental) %>% summarise(n = n_distinct(ID)) # number of individuals

# log10 transformation of time values to achieve normality
# and time values multiplied by -1
dat$logTime <- -log10(dat$Time)

# Mass standardization
dat$sMass <- scale(dat$Mass)

# Labels of graphics
xlab = "Immediate environment"

# Recode immediate, developmental and parental environments as numeric to have the intercept
# in a theoretical mean environment, i.e. a center environmental gradient
# see Dingemanse, N. J., A. J. N. Kazem, D. Réale, and J. Wright. 2010.
# Behavioural reaction norms: animal personality meets individual plasticity.
# Trends Ecol. Evol. 25:81-89. https://doi.org/10.1016/j.tree.2009.07.013.
dat$Immediate2 <- dat$Immediate
dat$Developmental2 <- dat$Developmental
dat$Parental2 <- dat$Parental
dat$Immediate <- as.numeric(dat$Immediate) - 1.5
dat$Developmental <- as.numeric(dat$Developmental) - 1.5
dat$Parental <- as.numeric(dat$Parental) - 1.5

```

## Group diversity in personality and immediate plasticity

### Model equations

In all LMMs,  $Y_{jkl}$  is a single measurement of escape behaviour (time to crawl-out the water in seconds) of:

- the individual  $j$  ( $j$  spreads from 1 to 80),
- in the immediate environment  $k$  ( $k = 1$  for immediate environment control C and  $k = 2$  for immediate environment predator-cue P),
- at the trial number  $l$  ( $l = 1$  for the first trial,  $l = 2$  for the second trial in the immediate environment  $k$ ).

$E_{jkl}$  is the residual value of the measurement  $Y_{jkl}$ .  $\sigma_{res}^2$  is the residual variance.

In our paper, fixed effects parameters were estimated with the LMM3. They are then only detailed in this model.

### Linear model 0 (LMM0, null model)

$$-\log_{10}(Y_{jkl}) = \beta_0 + \text{fixed effects} + E_{jkl}$$

$$[E_{jkl}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_{res}^2)$$

$\beta_0$  is the parameter for average intercept.

### Linear mixed model 1 (LMM1, random intercept model)

$$-\log_{10}(Y_{jkl}) = \beta_0 + \text{fixed effects} + U_{0j} + E_{jkl}$$

$$[E_{jkl}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_{res}^2)$$

$$[U_{0j}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_i^2)$$

$U_{0j}$  is the random intercept value of the individual j.  $\sigma_i^2$  is the variance in intercept, representing group diversity in personality.

### Linear mixed model 2 (LMM2, random slope model)

$$-\log_{10}(Y_{jkl}) = \beta_0 + \text{fixed effects} + U_{0j} + U_{1j} \times x_{jkl}^{(I)} + E_{jk}$$

$$[E_{jkl}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_{res}^2)$$

$$\begin{bmatrix} U_{0j} \\ U_{1j} \end{bmatrix} \stackrel{i.i.d.}{\sim} \mathcal{N}\left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_i^2 & cov_{is} \\ cov_{is} & \sigma_s^2 \end{bmatrix} \right)$$

$x_{jk}^{(I)}$  is the immediate environment for the individual j with:

- $x_{jk}^{(I)} = -0.5$  for  $k = 1$  (immediate environment control C)
- $x_{jk}^{(I)} = 0.5$  for  $k = 2$  (immediate environment predator-cue P)

$U_{1j}$  is the random slope value of the individual j.  $\sigma_s^2$  is the variance in slope, representing group diversity in immediate plasticity.

$cov_{is}$  is the covariance between intercept and slope and it uses for the calculation of the correlation between intercept and slope:  $cor_{is} = \frac{cov_{is}}{\sqrt{\sigma_i^2 \times \sigma_s^2}}$ .

## R code

### Load models and extract variance components

```
## LMM0 (null model)
LMM0 <- lm(logTime ~ sMass + Developmental*Parental*Immediate, data = dat)

## LMM1 (random intercept model)
LMM1 <- lmer(logTime ~ sMass + Developmental*Parental*Immediate + (1|ID), data = dat)
### Verification
```

```

plot(LMM1)
qqnorm(residuals(LMM1))
qqline(residuals(LMM1))
qqnorm(ranef(LMM1)$ID[,1])
qqline(ranef(LMM1)$ID[,1])
### Extract variance
(Var.LMM1 <- data.frame(VarCorr(LMM1)))
### Extract confidence intervals
#(confint.LMM1 <- confint(LMM1, method="boot", nsim =2000,oldNames = FALSE))
#save(confint.LMM1, file="confint.LMM1")
load("confint.LMM1")

## LMM2 (random slope model)
LMM2 <- lmer(logTime ~ sMass + Developmental*Parental*Immediate + (1+ Immediate|ID), data = dat)
### Verification
plot(LMM2)
qqnorm(residuals(LMM2))
qqline(residuals(LMM2))
qqnorm(ranef(LMM2)$ID[,1])
qqline(ranef(LMM2)$ID[,1])
qqnorm(ranef(LMM2)$ID[,2])
qqline(ranef(LMM2)$ID[,2])
### Extract variance
(Var.LMM2 <- data.frame(VarCorr(LMM2)))
### Extract confidence intervals
#(confint.LMM2 <- confint(LMM2, method="boot", nsim =2000,oldNames = FALSE))
#save(confint.LMM2, file="confint.LMM2")
load("confint.LMM2")

```

## Repeatability calculation

```

round(Var.LMM1[1,4]/(Var.LMM1[1,4]+Var.LMM1[2,4]),2)
round(confint.LMM1[1,1]^2/(confint.LMM1[1,1]^2+confint.LMM1[2,1]^2),2) ### lower CI
round(confint.LMM1[1,2]^2/(confint.LMM1[1,1]^2+confint.LMM1[2,2]^2),2) ### upper CI

```

## Likelihood ratio tests

```

(anova1 <- anova(LMM1,LMM0))
(anova2 <- anova(LMM2,LMM1,refit=FALSE))

```

## Table and Figure

### Table 2 - group diversity in personality and immediate plasticity

This code create a beautiful final table in word format with all variances and their confidence intervals, in addition to the results of the likelihood ratio tests

```

# function to calculate confidence interval of the residual variance of the LMM0 (null model)
V0 <- function(sigma, n, k, alpha = 0.05){
  # lm(y ~ x1 + x2)

```

```

# n <- length(y)
# k = number of parameters
lower <- (n-(k+1))*sigma^2/qchisq(alpha/2, df = n-(k+1), lower.tail = FALSE)
upper <- (n-(k+1))*sigma^2/qchisq(1-alpha/2, df = n-(k+1), lower.tail = FALSE)
(temp <- format(round(c(sigma^2, lower,upper), digits = 3)))
(temp <- paste0(temp[1], " [",temp[2],", ", ",temp[3],"]"))
}

# function to concatenate variance with confidence interval in brackets
V1 <- function(variance, confint){
  (temp <- c(variance, confint[1],confint[2]))
  (temp <- format(round(temp, digits = 3)))
  (temp <- paste0(temp[1], " [",temp[2],", ", ",temp[3],"]"))
  return(temp)
}

(Vresidual = c(V0(sigma(LMM0), length(dat$logTime),8),
  V1(Var.LMM1[2,4], confint.LMM1[2,]^2),
  V1(Var.LMM2[4,4], confint.LMM2[4,]^2)))

(Vintercept = c("",
  V1(Var.LMM1[1,4], confint.LMM1[1,]^2),
  V1(Var.LMM2[1,4], confint.LMM2[1,]^2)))

(Vslope = c("", "", V1(Var.LMM2[2,4], confint.LMM2[3,]^2)))

(Coris = c("", "", V1(Var.LMM2[3,5], confint.LMM2[2,])))

(`Chisqdf` = c("", format(round(c(anova1$Chisq[2],
  anova2$Chisq[2]), digits = 2))))

(P = c("", "<0.0001",format(round( anova2$`Pr(>Chisq)`[2], digits = 3))))

table <- data.frame(Model = c("LMO", "LMM1", "LMM2"),
  Vresidual = Vresidual,
  Vintercept = Vintercept,
  Vslope = Vslope,
  Coris = Coris,
  `Tested models` = c("", "0 vs 1", "1 vs 2"),
  `Chisqdf` = `Chisqdf`,
  P = P) %>%
  flextable(.)%>%
  flextable::align(.,align = "left", part = "all") %>%
  hline(i =3,border = fp_border())%>%
  bg(i=2, bg = grey(0.9))%>%
  font(fontname = "Times", part = "all")%>%
  fontsize(size = 12, part = "all")%>%
  width(j = 1, width = conv_unit(1.6, "cm", "inch"))%>%
  width(j = 2:4, width = conv_unit(3.9, "cm", "inch"))%>%
  width(j = 5, width = conv_unit(4.3, "cm", "inch"))%>%
  width(j = 6:7, width = conv_unit(1.6, "cm", "inch"))%>%
  width(j = 8, width = conv_unit(1.8, "cm", "inch"))%>%

```

```

bold( ~ P == "<0.0001", ~ P)
table

# run if you want to create the output in word format
#doc <- read_docx() %>%
# body_end_section_continuous() %>%
# body_add_flextable(value = table) %>%
# body_end_section_landscape()
# print(doc, target = "Table 2.docx")

rm(Vresidual,Vintercept,Vslope,Coris,Chisqdf,P,table)

```

Figure 3 - group diversity in immediate plasticity

```

fig3 <- dat %>%
  group_by(ID, Immediate2, Parental2, Developmental2) %>%
  dplyr::summarise(Value = mean(logTime)) %>%
  ggplot(., aes(x = Immediate2, y = Value, group = ID)) +
  geom_line(alpha = 0.7) +
  xlab(xlab)+
  ylab("Espace behaviour (sec) \nSlow Fast")+
  scale_y_continuous(breaks = c(- 2.39794, -2.198657, -2, -1.799341),
                    labels = c(250, 158, 100, 63),
                    limits = c(-2.48, -1.62))

fig3

# run if you want to create the output
#ggsave(fig3, filename = "Figure 3.pdf", height = 9, width = 9, units="cm")

```

## Effects of developmental and parental environments

### Model equation

**Linear mixed model 3 (LMM3, model with random intercepts for each combination of developmental and parental environments)**

$$-\log_{10}(Y_{jkl}) = \beta_0 + \beta_1 \times x_j^{(W)} + \beta_2 \times x_{jk}^{(I)} + \beta_3 \times x_j^{(D)} + \beta_4 \times x_j^{(P)} + \gamma_1 \times x_{jk}^{(I)} \times x_j^{(D)} + \gamma_2 \times x_{jk}^{(I)} \times x_j^{(P)} + \gamma_3 \times x_j^{(D)} \times x_j^{(P)} + \delta_1 \times x_{jk}^{(I)} \times x_j^{(D)} \times x_j^{(P)} + U_{0j}^{CC} \times I^{CC} + U_{0j}^{CP} \times I^{CP} + U_{0j}^{PC} \times I^{PC} + U_{0j}^{PP} \times I^{PP} + E_{jkl}$$

$$[E_{jkl}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_{res}^2)$$

$$[U_{0j}^{CC}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_i^{2,CC})$$

$$[U_{0j}^{CP}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_i^{2,CP})$$

$$[U_{0j}^{PC}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_i^{2,PC})$$

$$[U_{0j}^{PP}] \stackrel{i.i.d.}{\sim} \mathcal{N}(0, \sigma_i^{2,PP})$$

### Fixed effects:

$\beta$  are parameters for main fixed effects,  $\gamma$  are parameters for double-interaction terms and  $\delta$  is the parameter for the triple-interaction term.

$x_j^{(W)}$  is the snail total weight for the individual j.

$x_j^{(D)}$  is the developmental environment for the individual j with:

- $x_j^{(D)} = -0.5$  for unexposed snails
- $x_j^{(D)} = 0.5$  for predator-exposed snails

$x_j^{(P)}$  is the parental environment for the individual j with:

- $x_j^{(P)} = -0.5$  for snails from unexposed parents
- $x_j^{(P)} = 0.5$  for snails from predator-exposed parents

### Random effects:

For unexposed snails from predator-exposed parents,  $U_{0_i}^{PC}$  is the random intercept value of the individual j.  $\sigma_i^{2,PC}$  is the variance in intercept, representing group diversity in personality when snails were not exposed to predator cues and from predator-exposed parents. The same logic applied for CC, CP and PP snails.

$I^{CC}$ ,  $I^{CP}$ ,  $I^{PC}$ ,  $I^{PP}$  are dummy variables:

- $I^{CC} = 1$  if individual j was unexposed from unexposed parents, 0 otherwise
- $I^{CP} = 1$  if individual j was predator-exposed from unexposed parents, 0 otherwise
- $I^{PC} = 1$  if individual j was unexposed from predator-exposed parents, 0 otherwise
- $I^{PP} = 1$  if individual j was predator-exposed from predator-exposed parents, 0 otherwise

## R code and Bayesian procedure

### Priors

We used a non-informative prior with an inverse-Wishart distribution (expected variance  $V = 1$ ; degree of belief  $\nu = 0.002$ ; corresponding to a Gamma distribution with shape = 1 and scale = 1).

```
prior.normal <-list(R=list(V=1, nu=0.002), G=list(G1=list(V=1, nu=0.002),G2=list(V=1, nu=0.002),
                                                G3=list(V=1, nu=0.002),G4=list(V=1, nu=0.002)))
```

### Models

We used a chain of 700 000 iterations with a thin of 100 iterations (1 out of 100 iterations kept) and a burnin of 200 000 iterations (the first 200 000 iterations were discarded). Posterior distribution of each fixed effects parameters and random variances were then made on the 5 000 remaining iterations after thinning and burning.

```
# Create dummy variables
dat$CC=as.numeric(dat$Parental===-0.5&dat$Developmental===-0.5)
dat$CP=as.numeric(dat$Parental===-0.5&dat$Developmental==0.5)
dat$PC=as.numeric(dat$Parental==0.5&dat$Developmental===-0.5)
dat$PP=as.numeric(dat$Parental==0.5&dat$Developmental==0.5)

# Run model

#LMM3 <-MCMCglmm(logTime ~ sMass + Immediate*Developmental*Parental,
```

```

#           random=~us(CC):ID + (CP):ID + us(PC):ID + us(PP):ID,
#           rcov=~units, data=dat, prior=prior.normal,
#           pr=F, nitt=700000, thin=100, burnin=200000)
# save(file = "LMM3",LMM3)
load("LMM3")
summary(LMM3)$solutions
summary(LMM3)$Gcovariances

```

## Check of MCMC algorithms

Convergence of MCMC algorithms was checked by:

- (1) running separately three other chains and analysing between-chain variance with Gelman & Rubin diagnostic implemented in the package coda (Plummer et al. 2006);

```

#LMM3.chain2 <- MCMCglmm(logTime ~ sMass + Immediate*Developmental*Parental,
#           random=~us(CC):ID + us(CP):ID + us(PC):ID + us(PP):ID,
#           rcov=~units, data=dat, prior=prior.normal,
#           pr=F, nitt=700000, thin=100, burnin=200000)
#save(LMM3.chain2 ,file = "LMM3.chain2")
load("LMM3.chain2")
#LMM3.chain3 <- MCMCglmm(logTime ~ sMass + Immediate*Developmental*Parental,
#           random=~us(CC):ID + us(CP):ID + us(PC):ID + us(PP):ID,
#           rcov=~units, data=dat, prior=prior.normal,
#           pr=F, nitt=700000, thin=100, burnin=200000)
#save(LMM3.chain3 ,file = "LMM3.chain3")
load("LMM3.chain3")
#LMM3.chain4 <- MCMCglmm(logTime ~ sMass + Immediate*Developmental*Parental,
#           random=~us(CC):ID + us(CP):ID + us(PC):ID + us(PP):ID,
#           rcov=~units, data=dat, prior=prior.normal,
#           pr=F, nitt=700000, thin=100, burnin=200000)
#save(LMM3.chain4 ,file = "LMM3.chain4")
load("LMM3.chain4")

# Convergence of fixed effects parameters
gelman.diag(list(LMM3$Sol,LMM3.chain2$Sol,LMM3.chain3$Sol,LMM3.chain4$Sol))
gelman.plot(list(LMM3$Sol,LMM3.chain2$Sol,LMM3.chain3$Sol,LMM3.chain4$Sol))

# Convergence of random effects parameters
gelman.diag(list(LMM3$VCV,LMM3.chain2$VCV,LMM3.chain3$VCV,LMM3.chain4$VCV))
gelman.plot(list(LMM3$VCV,LMM3.chain2$VCV,LMM3.chain3$VCV,LMM3.chain4$VCV))

```

- (2) looking at the trace and shape of posterior distributions;

```

plot(LMM3$Sol)
plot(LMM3$VCV)

```

- (3) looking at 95 % CI of cumulative values of iterations for each parameter and at each iteration;

```

cumuplot(LMM3$Sol)
cumuplot(LMM3$VCV)

```

- (4) calculating effective size of our parameters (5 000 independent iterations for variances and at least 4 500 independent iterations for fixed effects parameters).

```
effectiveSize(LMM3$Sol)
effectiveSize(LMM3$VCV)
```

## Sensitivity to prior

Sensitivity to prior was checked by ran two other chains with an improper prior (inverse-Wishart with  $V = 0$  and  $\nu = -2$ ) and a flat prior (inverse-Wishart with  $V = 1$  and  $\nu = 0$ ).

```
prior.flat <-list(R=list(V=1, nu=0), G=list(G1=list(V=1, nu=0),G2=list(V=1, nu=0),
                                           G3=list(V=1, nu=0),G4=list(V=1, nu=0)))
prior.improper <-list(R=list(V=1e-16, nu=-2), G=list(G1=list(V=1e-16, nu=-2),G2=list(V=1e-16, nu=-2),
                                                    G3=list(V=1e-16, nu=-2),G4=list(V=1e-16, nu=-2)))

#LMM3.flat <-MCMCglmm(logTime ~ sMass + Immediate*Developmental*Parental,
#                    random=~us(CC):ID + us(CP):ID + us(PC):ID + us(PP):ID,
#                    rcov=~units, data=dat,prior=prior.flat,
#                    pr=F,nitt=700000, thin=100, burnin=200000)
#save(LMM3.flat ,file = "LMM3.flat")
load("LMM3.flat")

#LMM3.improper <-MCMCglmm(logTime ~ sMass + Immediate*Developmental*Parental,
#                        random=~us(CC):ID + us(CP):ID + us(PC):ID + us(PP):ID,
#                        rcov=~units, data=dat,prior=prior.improper,
#                        pr=F,nitt=700000, thin=100, burnin=200000)
#save(LMM3.improper ,file = "LMM3.improper")
load("LMM3.improper")

summary(LMM3)$solutions
summary(LMM3.flat)$solutions
summary(LMM3.improper)$solutions

posterior.mode(LMM3$VCV)
posterior.mode(LMM3.flat$VCV)
posterior.mode(LMM3.improper$VCV)

gelman.diag(list(LMM3$Sol, LMM3.flat$Sol, LMM3.improper$Sol))
gelman.plot(list(LMM3$VCV, LMM3.flat$VCV, LMM3.improper$VCV))

plot(LMM3.flat$VCV)
plot(LMM3.improper$VCV)
cumuplot(LMM3.flat$VCV)
cumuplot(LMM3.improper$VCV)
effectiveSize(LMM3.flat$VCV)
effectiveSize(LMM3.improper$VCV)
```

## Post-hoc tests

Supplementary material - contrasts for significance of group mean in immediate plasticity for each treatment

```

contrasts <- as.data.frame(emmeans(LMM3, pairwise ~ Immediate | Developmental*Parental, data=dat,
                                at = list(Immediate=c(-0.5,0.5),Developmental=c(-0.5,0.5),Parental=c(
mutate(Developmental = ifelse(Developmental==-0.5,"C","P"),
      Parental = ifelse(Parental==-0.5,"C","P"),
      `Treatment` = paste0(Parental,Developmental),
      estimate = format(round(-estimate, digits = 3)),
      lower.HPD = format(round(-lower.HPD, digits = 3)),
      upper.HPD = format(round(-upper.HPD, digits = 3)))%>%
mutate(Estimate = paste0(estimate, " (",upper.HPD," ", "lower.HPD,")"))%>%
select(`Treatment`,Estimate) %>%
flextable() %>%
autofit() %>%
bg(i=c(2,4), bg = grey(0.9))
contrasts

```

Contrasts to test the effects of parental and developmental environments on group mean in personality in each immediate environments

```

# Immediate env = C
emmeans(LMM3, pairwise~ Parental, data=dat, at = list(Immediate = -0.5, sMass = 0))$contrasts
emmeans(LMM3, pairwise~ Developmental, data=dat, at = list(Immediate = -0.5, sMass = 0))$contrasts
# Immediate env = P
emmeans(LMM3, pairwise~ Parental, data=dat, at = list(Immediate = 0.5, sMass = 0))$contrasts
emmeans(LMM3, pairwise~ Developmental, data=dat, at = list(Immediate = 0.5, sMass = 0))$contrasts

```

Effects of developmental environment on group diversity in personality

```

# more group diversity in personality in the C developmental group than in the P developmental group?
round(table(LMM3$VCV[,1]+ LMM3$VCV[,3] >= LMM3$VCV[,2] + LMM3$VCV[,4])/dim(LMM3$VCV)[1],3)

# more group diversity in personality in the C parental group than in the P parental group?
round(table(LMM3$VCV[,1]+ LMM3$VCV[,2] >= LMM3$VCV[,3] + LMM3$VCV[,4])/dim(LMM3$VCV)[1],3)

```

## Table and figures

Table 1 - effects on developmental and parental environments on group mean in personality and immediate plasticity

```

Fixed <- summary(LMM3)$solutions %>%
as.data.frame(.)%>% round(., digits =3) %>%
format(., digits =3) %>%
mutate(`beta [95% CI]` = paste0(post.mean," [",`l-95% CI`,`", "`,`u-95% CI`,`"]"),
      pMCMC =replace(pMCMC, pMCMC=="0.000","<0.001"),
      `Fixed effects` = c("Intercept","Mass","Immediate (Im.) ","Developmental (Dev.)",
        "Parental (Par.)","Im. x Dev.","Im. x Par.","Dev. x Par.",
        "Im. x Dev. x Par.") %>%
select(`Fixed effects`,`beta [95% CI]`,pMCMC)
Fixed

```

```

# Final
table1 <- flextable(Fixed) %>%
  flextable::align(align = "left", part = "all" )%>%
  bold( ~ pMCMC <= 0.05, ~ pMCMC) %>%
  bg(i=c(2,4,6,8), bg = grey(0.9))%>%
  font(fontname = "Times", part = "all")%>%
  fontsize(size = 12, part = "all")%>%
  width(j = 1, width = conv_unit(4.2, "cm", "inch"))%>%
  width(j = 2, width = conv_unit(4.3, "cm", "inch"))%>%
  width(j = 3, width = conv_unit(1.9, "cm", "inch"))
table1

# run if you want to create the output in word format
#doc <- read_docx()
#doc <- body_add_flextable(doc, value = table1)
#print(doc, target = "Table 1.docx")

```

Figure 2 - effects of developmental and parental environments on group mean in personality and immediate plasticity

```

dodgi =0.2 # setting dodge between dots

fig2 <- dat %>% group_by(Immediate2, Developmental2, Parental2) %>%
  dplyr::summarise(Temps = mean(logTime), SE = se(logTime)) %>%
  ggplot(., aes(x = Immediate2, y =Temps,
               group = interaction(Parental2,Developmental2),
               shape = interaction(Parental2,Developmental2),
               fill = Parental2))+
  geom_line(aes(linetype= Parental2, color = Developmental2),
            size = 0.5,
            position = position_dodge(width = dodgi))+
  geom_errorbar(aes(ymin=Temps-SE, ymax=Temps +SE),
                width= 0.1, size = 0.1,
                position = position_dodge(width = dodgi))+
  geom_point(aes(color = Developmental2), size = 4, position = position_dodge(width = dodgi))+
  xlab(xlab)+
  ylab("Espace behaviour (sec) \nSlow                                     Fast")+
  scale_shape_manual(values =c(21,16,22,15))+
  scale_linetype_manual(values =c(2,1))+
  scale_fill_manual(values =c("white","black"))+
  scale_color_manual(values = c("#3182bd","#de2d26"))+
  scale_y_continuous(breaks = c(-2.158362,-2.079181,-2,-1.920819,-1.841638),
                     labels =c(144,120,100,83,69),
                     limits = c(-2.175,-1.825)) +
  guides(linetype = "none",shape = "none",fill = "none", color = "none")
fig2

# run if you want to create the output
# ggsave(fig2, filename = "Figure 2 input.pdf", height = 9, width = 9, units="cm")

```

Figure 4 - effect of developmental environment on group diversity in personality

```
variance <- summary(LMM3)$Gcovariances %>%
  as.data.frame()%>%
  mutate(history = c("CC","CP","PC","PP"), min = `l-95% CI`, max = `u-95% CI`)
variance

fig4 <- ggplot(variance,aes(x = history, y = post.mean,
                             shape = history,
                             fill = history,
                             color = history))+
  geom_errorbar(aes(ymin = min, ymax = max), width = 0)+
  geom_point(size = 3)+
  scale_shape_manual(values =c(21,22,16,15))+
  scale_fill_manual(values =c("white","white","black","black"))+
  scale_color_manual(values = c("#3182bd","#de2d26","#3182bd","#de2d26"))+
  theme(legend.position = "none")+
  xlab("Combination of parental and\ndevelopmental environments")+
  ylab("Variance in escape behaviour")+
  ylim(0,0.05)
fig4

# run if you want to create the output
# ggsave(fig4, filename = "Figure 4.pdf", height = 9, width = 9, units="cm")
```