Additional file 4: R script for producing the simulations in this paper

```r
### SECTION 1 ###
# R script to produce the simulated reaction norms for Figure 2 in the main text. This script displays one realization.
# Written by JEB. Script is for illustrative purposes only
rm(list=ls())
# plotting of reaction norms variances and correlations
require(mvtnorm)
#
#function to plot the RNs
plotRN<-function(dat2plot, leftright) {
  if (leftright==1) {
    panel=c("(a)","(b)","(c)"
  } else {
    panel=c("(d)","(e)","(f)"
  }
  yminmax=c(round(min(dat2plot))-1,round(max(dat2plot))+1)
  plot(dat2plot[1,]~x,type="l",ylim=yminmax, ylab=list("Behavior",cex=1.2), xlab=list("Age", cex=1.2),main=panel[1])
  for (i in 2:n) {
    par(new=T)
    plot(dat2plot[i,]~x,type="l",ylim=yminmax, ylab=NA, xlab=NA, axes=F)
  }
  #plot vertical dotted lines at ages 2 and 4
  lines(c(2,2),yminmax,lty="dashed")
  lines(c(4,4),yminmax,lty="dashed")
  # variance over ages
  #par(new=F)
  plot(apply(dat2plot,2,var)~x,type="b",ylab=list("Variance",cex=1.2), xlab=list("Age", cex=1.2),main=panel[2])
  # correlation between young and old
  plot(dat2plot[,4]~dat2plot[,2],pch=19,ylab=list("Behavior at age 4", cex=1.2), xlab=list("Behavior at age 2", cex=1.2),main=panel[3],axes=T)
}

# generate some values; correlated elevation and slope
n=30
sigma <- matrix(c(4,1.3,1.3,1), ncol=2)
es <- rmvnorm(n=n, mean=c(0,0), sigma=sigma)
# plotting
layout(matrix(seq(6),3,2))
x<-seq(5)
dat2plot1<-matrix(es[,1],n,length(x))+matrix(es[,2],n,length(x))*matrix((x-3),n,length(x),byrow=T)
pplotRN(dat2plot1)
# generate some values; uncorrelated elevation and slope
sigma <- matrix(c(1,0,0,4), ncol=2)
es <- rmvnorm(n=n, mean=c(0,0), sigma=sigma)
# plotting
x<-seq(5)
dat2plot2<-matrix(es[,1],n,length(x))+
```

$$\text{matrix}({\text{es}[2], n, \text{length}(x)}) * \text{matrix}((x-3), n, \text{length}(x), \text{byrow}=T)$$

plotRN(dat2plot2)

### SECTION 2 ###
# script for simulation of expected correlation in
# two correlated behaviors as a function of age (Fig 4)
# script written by Barbara Class
# the script is for illustration purposes only
### construct a handy function for what we will do

library(mvtnorm)
getBiCop <- function(n, rho, X1) {
  C <- matrix(rho, nrow = 2, ncol = 2)
  diag(C) <- 1
  C <- chol(C)
  X2 <- rnorm(n, mean=mean(X1), sd=sd(X1))
  X <- cbind(X1, X2)
  # induce correlation (does not change X1)
  df <- X %% C
  return(df[,2])
}

# SIMULATION 1 ##############
# Simulation: rank order correlation of both traits vary from 0 to 0.9 across ontogeny
BS.onto<-array(0, dim= c(1000,4,10))
cross<-seq(from=0,to=0.9, by= 0.1)
rho=0.7
for (y in 1:10){
  for (i in 1:1000){
    #Generate data for trait 1 at age 1 and 2
    T1age1<-data.frame("Age"= "Age1", "Trait" =rnorm(1000),
      "ID"=seq(1:1000))
    T1age1$rank<-rank(T1age1$Trait)
    T1age1<-T1age1[order(T1age1$Trait),]
    rankt1<-getBiCop(1000,cross[y],T1age1$rank)
    rankt1int<-rank(rankt1)
    T1age2<-data.frame("Age"= "Age2", "Trait"=getBiCop(1000, rho, T1age1$Trait),
      "ID"=NA,"rank"=NA)
    T1age2$rank=rank(T1age2$Trait)
    T1age2<-T1age2[(order(T1age2$rank)[rankt1int]),]
    BS1<-data.frame("T1A1"= T1age1$Trait ,"T1A2"= T1age2$Trait, 
      "ID"=T1age1$ID )
    #Generate data for T2 at age 1 and 2, T1 and T2 are correlated
    # at age 1 (rho=0.7)
    T2age1<-data.frame("Age"= "Age1", "Trait" = getBiCop(1000, rho, 
      T1age1$Trait), "ID"=NA)
    BS2<-data.frame("T1A1"= T1age1$Trait ,"T2A1"= T2age1$Trait, 
      "ID"=T1age1$ID )
BS2$rankT2A1 <- rank(BS2$T2A1)
BS2 <- BS2[order(BS2$T2A1),]

rankT2 <- getBiCop(1000, cross[y], BS2$rankT2A1)
rankT2int <- rank(rankT2)

T2age2 <- data.frame("Age" = "Age2", "Trait" = rnorm(1000),
"ID" = NA, "rank" = NA)
T2age2$rank <- rank(T2age2$Trait)
T2age2 <- T2age2[(order(T2age2$rank)[rankT2int]),]

BS2$T2A2 <- T2age2$Trait
BS2 <- BS2[order(BS2$ID),]
BS1 <- BS1[order(BS1$ID),]

BS <- data.frame("T1A1" = BS1$T1A1, "T1A2" = BS1$T1A2
,"T2A1" = BS2$T2A1, "T2A2" = BS2$T2A2, "ID" = BS2$ID )

BS.onto[i, 1,y] <-
cor.test(BS$T1A1, BS$T2A1, method = "spearman")$estimate
BS.onto[i, 2,y] <-
cor.test(BS$T1A2, BS$T2A2, method = "spearman")$estimate
BS.onto[i, 3,y] <-
cor.test(BS$T1A1, BS$T1A2, method = "spearman")$estimate
BS.onto[i, 4,y] <-
cor.test(BS$T2A1, BS$T2A2, method = "spearman")$estimate

require(MCMCglmm)

results.sim <- data.frame("Spearman corr" = NA,
"BS1" = NA, "BS1inf" = NA, "BS1sup" = NA, "BS2" = NA, "BS2inf" = NA, "BS2sup" = NA,
"BS3" = NA, "BS3inf" = NA, "BS3sup" = NA, "BS4" = NA, "BS4inf" = NA, "BS4sup" = NA)

for (i in 1:10){
  results.sim[i,1] <- cross[i]
  results.sim[i,2] <-
  as.numeric(posterior.mode(as.mcmc((BS.onto[,1,i]))))
  results.sim[i,3] <-
  as.numeric(HPDinterval(as.mcmc((BS.onto[,1,i])), 0.95))[1]
  results.sim[i,4] <-
  as.numeric(HPDinterval(as.mcmc((BS.onto[,1,i])), 0.95))[2]
  results.sim[i,5] <-
  as.numeric(posterior.mode(as.mcmc((BS.onto[,2,i]))))
  results.sim[i,6] <-
  as.numeric(HPDinterval(as.mcmc((BS.onto[,2,i])), 0.95))[1]
  results.sim[i,7] <-
  as.numeric(HPDinterval(as.mcmc((BS.onto[,2,i])), 0.95))[2]
  results.sim[i,8] <-
  as.numeric(posterior.mode(as.mcmc((BS.onto[,3,i]))))
  results.sim[i,9] <-
  as.numeric(HPDinterval(as.mcmc((BS.onto[,3,i])), 0.95))[1]
# SIMULATION 2

Generate random values for 1000 individuals for each scenario

# First scenario: rank orders do not change for both traits, T1 and T2 are correlated ($\rho=0.7$) at age 1

# Trait 1:

T1age1 <- data.frame("Age" = "Age1", "Trait" = rnorm(1000),
"ID" = seq(1:1000))

slope1 <- getBiCop(1000, 0.9, T1age1$Trait)

T1age2 <- data.frame("Age" = "Age2", "Trait" = T1age1$Trait + (slope1/9),
"ID" = seq(1:1000))

T1age3 <- data.frame("Age" = "Age3", "Trait" = T1age1$Trait + (slope1*2/9),
"ID" = seq(1:1000))

T1age4 <- data.frame("Age" = "Age4", "Trait" = T1age1$Trait + (slope1*3/9),
"ID" = seq(1:1000))

T1age5 <- data.frame("Age" = "Age5", "Trait" = T1age1$Trait + (slope1*4/9),
"ID" = seq(1:1000))

T1age6 <- data.frame("Age" = "Age6", "Trait" = T1age1$Trait + (slope1*5/9),
"ID" = seq(1:1000))

T1age7 <- data.frame("Age" = "Age7", "Trait" = T1age1$Trait + (slope1*6/9),
"ID" = seq(1:1000))

T1age8 <- data.frame("Age" = "Age8", "Trait" = T1age1$Trait + (slope1*7/9),
"ID" = seq(1:1000))

T1age9 <- data.frame("Age" = "Age9", "Trait" = T1age1$Trait + (slope1*8/9),
"ID" = seq(1:1000))

T1age10 <- data.frame("Age" = "Age10", "Trait" = T1age1$Trait + (slope1),
"ID" = seq(1:1000))

# Trait 2:

T2age1 <- data.frame("Age" = "Age1", "Trait" = getBiCop(1000, 0.7, T1age1$Trait),
"ID" = seq(1:1000))

slope2 <- getBiCop(1000, 0.9, T2age1$Trait)

T2age2 <- data.frame("Age" = "Age2", "Trait" = T2age1$Trait + (slope2/9),
"ID" = seq(1:1000))

T2age3 <- data.frame("Age" = "Age3", "Trait" = T2age1$Trait + (slope2*2/9),
"ID" = seq(1:1000))

T2age4 <- data.frame("Age" = "Age4", "Trait" = T2age1$Trait + (slope2*3/9),
"ID" = seq(1:1000))
T2age5<-data.frame("Age"= "Age5", "Trait" =T2age1$Trait+(slope2*(4/9)), "ID"=seq(1:1000))
T2age6<-data.frame("Age"= "Age6", "Trait" =T2age1$Trait+(slope2* (5/9)), "ID"=seq(1:1000))
T2age7<-data.frame("Age"= "Age7", "Trait" =T2age1$Trait+(slope2* (6/9)), "ID"=seq(1:1000))
T2age8<-data.frame("Age"= "Age8", "Trait" =T2age1$Trait+(slope2* (7/9)), "ID"=seq(1:1000))
T2age9<-data.frame("Age"= "Age9", "Trait" =T2age1$Trait+(slope2* (8/9)), "ID"=seq(1:1000))
T2age10<-data.frame("Age"= "Age10", "Trait" =T2age1$Trait+(slope2), "ID"=seq(1:1000))

#Calculate the correlations between Trait 1 and 2 at different ages
BSage1<-cbind("age1"=cor.test(T1age1$Trait,T2age1$Trait,method="spearman")$estimate,
"age2"=cor.test(T1age2$Trait,T2age2$Trait,method="spearman")$estimate,
"age3"=cor.test(T1age3$Trait,T2age3$Trait,method="spearman")$estimate,
"age4"=cor.test(T1age4$Trait,T2age4$Trait,method="spearman")$estimate,
"age5"=cor.test(T1age5$Trait,T2age5$Trait,method="spearman")$estimate,
"age6"=cor.test(T1age6$Trait,T2age6$Trait,method="spearman")$estimate,
"age7"=cor.test(T1age7$Trait,T2age7$Trait,method="spearman")$estimate,
"age8"=cor.test(T1age8$Trait,T2age8$Trait,method="spearman")$estimate,
"age9"=cor.test(T1age9$Trait,T2age9$Trait,method="spearman")$estimate,
"age10"=cor.test(T1age10$Trait,T2age10$Trait,method="spearman")$estimate)

#Calculate variances for each trait across ontogeny
ontoT1S1<-cbind(T1age1$Trait,T1age2$Trait,T1age3$Trait,T1age4$Trait,T1age5$Trait,T1age6$Trait,T1age7$Trait,T1age8$Trait,T1age9$Trait,T1age10$Trait)
ontoT1S1<-as.data.frame(ontoT1S1)
varianceT1S1<-apply(ontoT1S1,2,var)
ontoT2S1 <-
cbind(T2age1$Trait, T2age2$Trait, T2age3$Trait, T2age4$Trait, T2age5$Trait, T2age6$Trait, T2age7$Trait, T2age8$Trait, T2age9$Trait, T2age10$Trait)
ontoT2S1 <- as.data.frame(ontoT2S1)
varianceT2S1 <- apply(ontoT2S1, 2, var)

# Second scenario: rank orders crossed for Trait 2, not for Trait 1

Tlagel <- data.frame("Age" = "Age1", "Trait" = rnorm(1000), "ID" = seq(1:1000))
slope1 <- getBiCop(1000, 0.9, Tlagel$Trait)
Tlage2 <- data.frame("Age" = "Age2", "Trait" = Tlagel$Trait + (slope1/9), "ID" = seq(1:1000))
Tlage3 <- data.frame("Age" = "Age3", "Trait" = Tlagel$Trait + (slope1*(2/9)), "ID" = seq(1:1000))
Tlage4 <- data.frame("Age" = "Age4", "Trait" = Tlagel$Trait + (slope1*(3/9)), "ID" = seq(1:1000))
Tlage5 <- data.frame("Age" = "Age5", "Trait" = Tlagel$Trait + (slope1*(4/9)), "ID" = seq(1:1000))
Tlage6 <- data.frame("Age" = "Age6", "Trait" = Tlagel$Trait + (slope1*(5/9)), "ID" = seq(1:1000))
Tlage7 <- data.frame("Age" = "Age7", "Trait" = Tlagel$Trait + (slope1*(6/9)), "ID" = seq(1:1000))
Tlage8 <- data.frame("Age" = "Age8", "Trait" = Tlagel$Trait + (slope1*(7/9)), "ID" = seq(1:1000))
Tlage9 <- data.frame("Age" = "Age9", "Trait" = Tlagel$Trait + (slope1*(8/9)), "ID" = seq(1:1000))
Tlage10 <- data.frame("Age" = "Age10", "Trait" = Tlagel$Trait + (slope1), "ID" = seq(1:1000))

# Generate values for Trait 2

T2age1 <- data.frame("Age" = "Age1", "Trait" = getBiCop(1000, 0.7, Tlage1$Trait), "ID" = NA)
BS2 <- data.frame("T1A1" = Tlage1$Trait, "T2A1" = T2age1$Trait, "ID" = Tlage1$ID)

BS2$rankT2A1 <- rank(BS2$T2A1)
BS2 <- BS2[order(BS2$T2A1),]
r ank12 <- getBiCop (1000,-0.9,BS2$rankT2A1)
rankt2int <- rank(rank12)
T2age10 <- data.frame("Age" = "Age2", "Trait" = rnorm(1000), "ID" = NA, "rank" = NA)
T2age10$rank <- rank(T2age10$Trait)
T2age10 <- T2age10[order(T2age10$rank)[rankt2int]],]
BS2$T2A2<-T2age10$Trait
BS2<-BS2[order(BS2$ID),]

Trait2<-BS2[,c(2,5,3)]
Trait2$Slope<- Trait2[,2]-Trait2[,1]

T2age1<-data.frame("Age"= "Age1", "Trait" =Trait2[,1], "ID"=Trait2[,3])
T2age2<-data.frame("Age"= "Age2", "Trait" =Trait2[,1]+(Trait2$Slope/9), "ID"=BS2[,3])
T2age3<-data.frame("Age"= "Age3", "Trait" =Trait2[,1]+(Trait2$Slope*(2/9)), "ID"=BS2[,3])
T2age4<-data.frame("Age"= "Age4", "Trait" =Trait2[,1]+(Trait2$Slope*(3/9)), "ID"=BS2[,3])
T2age5<-data.frame("Age"= "Age5", "Trait" =Trait2[,1]+(Trait2$Slope*(4/9)), "ID"=BS2[,3])
T2age6<-data.frame("Age"= "Age6", "Trait" =Trait2[,1]+(Trait2$Slope*(5/9)), "ID"=BS2[,3])
T2age7<-data.frame("Age"= "Age7", "Trait" =Trait2[,1]+(Trait2$Slope*(6/9)), "ID"=BS2[,3])
T2age8<-data.frame("Age"= "Age8", "Trait" =Trait2[,1]+(Trait2$Slope*(7/9)), "ID"=BS2[,3])
T2age9<-data.frame("Age"= "Age9", "Trait" =Trait2[,1]+(Trait2$Slope*(8/9)), "ID"=BS2[,3])
T2age10<-data.frame("Age"= "Age10", "Trait" =Trait2[,2], "ID"=Trait2[,3])

#Calculate the correlations between Trait 1 and 2 at different ages
BSage2<-cbind("age1"=cor.test(T1age1$Trait,T2age1$Trait,method="spearman")$estimate,
    "age2"=cor.test(T1age2$Trait,T2age2$Trait,method="spearman")$estimate,
    "age3"=cor.test(T1age3$Trait,T2age3$Trait,method="spearman")$estimate,
    "age4"=cor.test(T1age4$Trait,T2age4$Trait,method="spearman")$estimate,
    "age5"=cor.test(T1age5$Trait,T2age5$Trait,method="spearman")$estimate,
    "age6"=cor.test(T1age6$Trait,T2age6$Trait,method="spearman")$estimate,
    "age7"=cor.test(T1age7$Trait,T2age7$Trait,method="spearman")$estimate,
    "age8"=cor.test(T1age8$Trait,T2age8$Trait,method="spearman")$estimate,
"age9"=cor.test(T1age9$Trait,T2age9$Trait,method="spearman")$estimate,
"age10"=cor.test(T1age10$Trait,T2age10$Trait,method="spearman")$estimate)

#Calculate variances for each trait across ontogeny
ontoT1S2<-cbind(T1age1$Trait,T1age2$Trait,T1age3$Trait,T1age4$Trait,T1age5$Trait,
                 T1age6$Trait,T1age7$Trait,T1age8$Trait,T1age9$Trait,T1age10$Trait)
ontoT1S2<-as.data.frame(ontoT1S2)
varianceT1S2<-apply(ontoT1S2,2,var)
ontoT2S2<-cbind(T2age1$Trait,T2age2$Trait,T2age3$Trait,T2age4$Trait,T2age5$Trait,
                 T2age6$Trait,T2age7$Trait,T2age8$Trait,T2age9$Trait,T2age10$Trait)
ontoT2S2<-as.data.frame(ontoT2S2)
varianceT2S2<-apply(ontoT2S2,2,var)

#Scenario 3: Rank orders changed for both traits
#Trait 1
T1age1<-data.frame("Age"= "Age1", "Trait" =rnorm(1000),
                   "ID"=seq(1:1000))
T1age1$rank<-rank(T1age1$Trait)
T1age1<-T1age1[order(T1age1$Trait),]
rankt1<- getBiCop(1000,-0.9,T1age1$rank)
rankt1int<-rank(rankt1)
T1age10<-data.frame("Age"= "Age10", "Trait"=rnorm(1000),
                    "ID"=NA,"rank"=NA)
T1age10$rank=rank(T1age10$Trait)
T1age10<-T1age10[(order(T1age10$rank)[rankt1int]),]
BS1<-data.frame("T1A1"= T1age1$Trait ,"T1A10"= T1age10$Trait,
                 "ID"=T1age1$ID )

#Trait 2
T2age1<-data.frame("Age"= "Age1", "Trait" = getBiCop(1000, 0.7, T1age1$Trait), "ID"=NA)
BS2<-data.frame("T1A1"= T1age1$Trait ,"T2A1"= T2age1$Trait,
                 "ID"=T1age1$ID )
BS2$rankT2A1 <- rank(BS2$T2A1)
BS2 <- BS2[order(BS2$T2A1),]

rankt2 <- getBiCop(1000, -0.9, BS2$rankT2A1)
rankt2int <- rank(rankt2)

T2age10 <- data.frame("Age" = "Age10", "Trait" = rnorm(1000),
"ID" = NA, "rank" = NA)
T2age10$rank <- rank(T2age10$Trait)
T2age10$rank <- T2age10[(order(T2age10$rank)[rankt2int]),]

BS2$T2A10 <- T2age10$Trait

BS2 <- BS2[order(BS2$ID),]
BS1 <- BS1[order(BS1$ID),]

BS <- data.frame("T1A1" = BS1$T1A1, "T1A10" = BS1$T1A10,
"T2A1" = BS2$T2A1, "T2A10" = BS2$T2A10, "ID" = BS2$ID)

# Calculate values for ages between 1 and 10 for Trait 1
Trait1 <- BS[, c(1:2, 5)]
Trait1$Slope <- Trait1[, 2] - Trait1[, 1]
T1age1 <- data.frame("Age" = "Age1", "Trait" = Trait1[, 1],
"ID" = Trait1[, 3])
T1age2 <- data.frame("Age" = "Age2", "Trait" = Trait1[, 1] + (Trait1$Slope / 9),
"ID" = Trait1[, 3])
T1age3 <- data.frame("Age" = "Age3", "Trait" = Trait1[, 1] + (Trait1$Slope * (2 / 9)),
"ID" = Trait1[, 3])
T1age4 <- data.frame("Age" = "Age4", "Trait" = Trait1[, 1] + (Trait1$Slope * (3 / 9)),
"ID" = Trait1[, 3])
T1age5 <- data.frame("Age" = "Age5", "Trait" = Trait1[, 1] + (Trait1$Slope * (4 / 9)),
"ID" = Trait1[, 3])
T1age6 <- data.frame("Age" = "Age6", "Trait" = Trait1[, 1] + (Trait1$Slope * (5 / 9)),
"ID" = Trait1[, 3])
T1age7 <- data.frame("Age" = "Age7", "Trait" = Trait1[, 1] + (Trait1$Slope * (6 / 9)),
"ID" = Trait1[, 3])
T1age8 <- data.frame("Age" = "Age8", "Trait" = Trait1[, 1] + (Trait1$Slope * (7 / 9)),
"ID" = Trait1[, 3])
T1age9 <- data.frame("Age" = "Age9", "Trait" = Trait1[, 1] + (Trait1$Slope * (8 / 9)),
"ID" = Trait1[, 3])
T1age10 <- data.frame("Age" = "Age10", "Trait" = Trait1[, 2],
"ID" = Trait1[, 3])

# The same for Trait 2
Trait2 <- BS[, c(3:5)]
Trait2$Slope <- Trait2[, 2] - Trait2[, 1]
T2age1 <- data.frame("Age" = "Age1", "Trait" = Trait2[, 1],
"ID" = Trait2[, 3])
T2age2 <- data.frame("Age" = "Age2", "Trait" = Trait2[, 1] + (Trait2$Slope / 9),
"ID" = Trait2[, 3])
T2age3<-data.frame("Age" = "Age3", "Trait" = Trait2[,1]+(Trait2$Slope*(2/9)), "ID" = Trait2[,3])
T2age4<-data.frame("Age" = "Age4", "Trait" = Trait2[,1]+(Trait2$Slope*(3/9)), "ID" = Trait2[,3])
T2age5<-data.frame("Age" = "Age5", "Trait" = Trait2[,1]+(Trait2$Slope*(4/9)), "ID" = Trait2[,3])
T2age6<-data.frame("Age" = "Age6", "Trait" = Trait2[,1]+(Trait2$Slope*(5/9)), "ID" = Trait2[,3])
T2age7<-data.frame("Age" = "Age7", "Trait" = Trait2[,1]+(Trait2$Slope*(6/9)), "ID" = Trait2[,3])
T2age8<-data.frame("Age" = "Age8", "Trait" = Trait2[,1]+(Trait2$Slope*(7/9)), "ID" = Trait2[,3])
T2age9<-data.frame("Age" = "Age9", "Trait" = Trait2[,1]+(Trait2$Slope*(8/9)), "ID" = Trait2[,3])
T2age10<-data.frame("Age" = "Age10", "Trait" = Trait2[,2], "ID" = Trait2[,3])

#Calculate the correlations between Trait 1 and 2 at different ages
BSage3<-cbind("age1" = cor.test(T1age1$Trait, T2age1$Trait, method="spearman")$estimate,
             "age2" = cor.test(T1age2$Trait, T2age2$Trait, method="spearman")$estimate,
             "age3" = cor.test(T1age3$Trait, T2age3$Trait, method="spearman")$estimate,
             "age4" = cor.test(T1age4$Trait, T2age4$Trait, method="spearman")$estimate,
             "age5" = cor.test(T1age5$Trait, T2age5$Trait, method="spearman")$estimate,
             "age6" = cor.test(T1age6$Trait, T2age6$Trait, method="spearman")$estimate,
             "age7" = cor.test(T1age7$Trait, T2age7$Trait, method="spearman")$estimate,
             "age8" = cor.test(T1age8$Trait, T2age8$Trait, method="spearman")$estimate,
             "age9" = cor.test(T1age9$Trait, T2age9$Trait, method="spearman")$estimate,
             "age10" = cor.test(T1age10$Trait, T2age10$Trait, method="spearman")$estimate)

#Calculate variances for each trait across ontogeny
ontoT1S3<-cbind(T1age1$Trait, T1age2$Trait, T1age3$Trait, T1age4$Trait, T1age5$Trait,
T1age6$Trait, T1age7$Trait, T1age8$Trait, T1age9$Trait, T1age10$Trait)
ontoT1S3 <- as.data.frame(ontoT1S3)
varianceT1S3 <- apply(ontoT1S3, 2, var)
ontoT2S3 <- cbind(T2age1$Trait, T2age2$Trait, T2age3$Trait, T2age4$Trait, T2age5$Trait,
                  T2age6$Trait, T2age7$Trait, T2age8$Trait, T2age9$Trait, T2age10$Trait)
ontoT2S3 <- as.data.frame(ontoT2S3)
varianceT2S3 <- apply(ontoT2S3, 2, var)

# Plot the results
### simulation 1 in panel a, 2 in panel b
layout(matrix(c(1, 2), 1, 2, byrow=TRUE))
# panel a
# we plot the results of the second behavioral syndrome
y <- results.sim$BS2
x <- seq(from=0, to=0.9, by=0.1)
sdinf <- results.sim$BS2inf
sdsup <- results.sim$BS2sup
plot(x, y, main="(a)", xlab="Correlation juvenile - adult",
     ylab="Correlation between traits", cex=1.3, ylim=c(-0.1, 0.7),
     pch=16, cex=2)
arrows(x, sdinf, x, sdsup, code=3, angle=90, length=0.1)
lines(c(-0.2, 0.95), c(0, 0), lty=2)

### panel b
x <- seq(1:10)
plot(as.vector(BSage1) ~ x, type="b", lwd=3, col="red", lty=1, main="(b)"
     , xlab="Age ", ylab="Correlation between traits ", cex=1.3, ylim=c(-0.6, 0.8), xlim=c(1, 10),
     cex.lab=1, cex.axis=1)
par(new=T)
plot(as.vector(BSage2) ~ x, type="b", col="blue", lwd=3, lty=1, xlab=NA, ylab="Correlation between traits ", cex=1.3, ylim=c(-0.6, 0.8), xlim=c(1, 10),
     cex.lab=1, cex.axis=1)
par(new=T)
plot(as.vector(BSage3) ~ x, type="b", col="black", lwd=3, lty=1, xlab=NA, ylab="Correlation between traits ", cex=1.3, ylim=c(-0.6, 0.8), xlim=c(1, 10),
     cex.lab=1, cex.axis=1)