**SUPPLEMENTARY INFORMATION**

**Varona and González-Recio (2023).** **Invited review: Recursive models in animal breeding: Interpretation, limitations, and extensions Journal of Dairy Science. https://doi.org/10.3168/jds.2022-22578**

**R script for the calculation of the effects of the recursive parameter in the heritability of the dependent trait and in the genetic correlation between the independent and dependent trait in a bivariate recursive model.**

library(RColorBrewer)

library(ggplot2)

pal<-brewer.pal(9, "Blues")

################

# Parameters #

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var\_u1<-1 #additive variance trait 1

var\_u2<-1 #additive variance trait 2

var\_e2<-1 #residual variance trait 1

cov\_u1\_u2<-seq(-1,1,0.01) #additive covariance

cov\_e1\_e2<-0 #residual covariance

cov\_u1\_u2<-.5

h1<-seq(0,1,0.01)

ratio\_varu1\_vare1<-1

lambda<-seq(-3,3,0.01) #parameter space of the recursive parameter lambda

var\_e1<-var\_u1/ratio\_varu1\_vare1 #residual variance trait 2

##########################################################################

#Figure X. Parameter space of the heritability of the dependent trait,

#for different levels of recursiveness strength and additive genetic

#covariance between both traits.

############################################################################

cov\_u1\_u2<- -0.8 #starting value for additive genetic covariance

cov\_e1\_e2<-0 #assume residual covariance = 0

h2<-(var\_u2+2\*lambda\*cov\_u1\_u2+lambda\*lambda\*var\_u1)/(var\_u2+var\_e2+2\*lambda\*(cov\_u1\_u2+cov\_e1\_e2)+lambda\*lambda\*(var\_u1+var\_e1))

df<-data.frame(lambda=lambda,h2=h2,genetic\_covariance=rep(cov\_u1\_u2,length(h2)))

##This loop iterates along the genetic covariance parameter space

for (cov\_u1\_u2 in seq(-.6,0.8,0.2)){

 h2<-(var\_u2+2\*lambda\*cov\_u1\_u2+lambda\*lambda\*var\_u1)/(var\_u2+var\_e2+2\*lambda\*(cov\_u1\_u2+cov\_e1\_e2)+lambda\*lambda\*(var\_u1+var\_e1))

 #lines(lambda,h2,col="gray",col=2)

 df2<-data.frame(lambda=lambda,h2=h2,genetic\_covariance=rep(cov\_u1\_u2,length(h2)))

 df<-rbind(df,df2)

 }

##Plot the results

ggplot(data = df, aes(x=lambda, y=h2)) + geom\_line(aes(colour=genetic\_covariance)) +ylab("trait2 heritability")+ylim(c(0,1)) +scale\_color\_gradientn(colors=rev(pal))

###############################################################################

#Figure X. Parameter space of the genetic correlation between the independent

# and the dependent traits, for different levels of recursiveness strength and

#additive genetic covariance between both traits.

###############################################################################

cov\_u1\_u2<- -0.8 #starting value for additive genetic covariance

cov\_e1\_e2<-0 #assume residual covariance = 0

cg<-(cov\_u1\_u2+lambda\*var\_u1)/sqrt(var\_u1\*(var\_u2+2\*lambda\*cov\_u1\_u2+lambda\*lambda\*var\_u1))

df<-data.frame(lambda=lambda,corr.gen=cg,genetic\_covariance=rep(cov\_u1\_u2,length(cg)))

##This loop iterates along the genetic covariance parameter space

for (cov\_u1\_u2 in seq(-.6,0.8,0.2)){

 cg<-(cov\_u1\_u2+lambda\*var\_u1)/sqrt(var\_u1\*(var\_u2+2\*lambda\*cov\_u1\_u2+lambda\*lambda\*var\_u1))

 df2<-data.frame(lambda=lambda,corr.gen=cg,genetic\_covariance=rep(cov\_u1\_u2,length(cg)))

 df<-rbind(df,df2)

}

##Plot the results

ggplot(data = df, aes(x=lambda, y=corr.gen)) + geom\_line(aes(colour=genetic\_covariance)) +ylab("genetic correlation")+scale\_color\_gradientn(colors=rev(pal))