# BIOS6643 HW5 Due Friday, October 25, 2019, 11:59pm

We can use SAS or R to fit linear mixed models directly with relatively short code. This semester we have talked a lot about matrix quantities and in HW2 you derived the form of . For this exercise, I would like you to carry out t tests for the test of linear trend (considering age as class) or for the slope of age (considering age as continuous) for the Ramus data using a matrix quantity approach, in order to better learn what is going on ‘behind the scenes’. Make sure data are sorted consistently for each part of the quantity you are calculating (e.g., sort all elements by boy and then age). Use the AR(1) structure for R, and no random effects. You can use R or SAS PROC IML, although I have included some R code below that you might find helpful; use the given estimated covariance parameters via REML as a starting point. The form of the test statistic you will need is . You can work with subject-level or complete data forms for estimates and variance quantities of interest, or both (see p. 141 in course notes, HW2, #3 and note that  when subjects have the same structure and repeated measures). Once you have obtained the test statistics, determine the p-values using a relevant function (need the degrees of freedom for the test). You can always check your work (and get the correct DF) by fitting an LMM in SAS or R using standard methods.

1. Perform the t-test for the slope of age in predicting Ramus bone height in two ways (stated below). Turn in your brief code and output, and write a sentence to interpret the results, meaningful to the application.
   1. Use age as a class variable and then perform the t-test for linear age trend. (Starting point: residual variance=6.8793; correlation=0.9527)
   2. Use age as continuous and perform the t-test for the slope of age. (Starting point: residual variance=6.8783; correlation=0.9542)
2. If you were to publish the results in a journal article, would you go with Approach a or b? Or does it matter? Briefly justify your response.

Helpful R code (this is relevant for 1a; you will need to tweak for 1b):

# The package below allows you to use ginv function (Moore-Penrose inverse of a

# less-than-full-rank matrix

library(MASS)

# Create X\_i, the subject-level X matrix

X\_i=matrix(c(1,1,1,1,1,0,0,0,0,1,0,0,0,0,1,0,0,0,0,1),nrow=4,ncol=5)

# Create X, the complete data X matrix

X=NULL

for(i in 1:20){X=rbind(X,X\_i)}

# Create V\_i, the subject-level Var(Y) matrix.

# Note that covariance parameter estimates are given for part a.

sigma\_e\_sq=6.8793; phi=0.9527

V\_i=sigma\_e\_sq\*matrix(c(1,phi,phi^2,phi^3,phi,1,phi,phi^2,phi^2,phi,1,phi,

phi^3,phi^2,phi,1),nrow=4,ncol=4)

#Create V, the complete data V matrix

V=kronecker(diag(20),V\_i)