#Distance = square dissimilarity matrix expressing biological or cultural differences between groups #History = square distance matrix describing the hypothetical phylogenetic relationships between groups

#Geography = square matrix with geographic distances between groups.

#Results comprise partitioned variance due to History, Geography, History\*Geography interaction and associated p-values

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HierarchicalMantelTest<-function(Distance,History,Geography){

require(phytools)

require(vegan)

Distance<-as.matrix(Distance)

History<-as.matrix(History)

Geography<-as.matrix(Geography)

results<-data.frame(matrix(0,1,7))

colnames(results)<-c("Var Hist","Var Geo","Var Hist\*Geo"," Var Residual","p Hist","p Geo","p Hist\*Geo")

row.names(results)<-c("Results")

DxH<-mantel(Distance,History,permutations=9999)

DxG<-mantel(Distance,Geography,permutations=9999)

DxGxH<-multi.mantel(Distance,list(History,Geography),9999)

VarHG<-(DxG$statistic)^2+(DxH$statistic)^2-DxGxH$r.squared

VarH<-(DxH$statistic)^2-VarHG

VarG<-(DxG$statistic)^2-VarHG

Res<-1-VarHG-VarH-VarG

results[1,1:7]<-c(VarH,VarG,VarHG,Res,DxH$signif,DxG$signif,DxGxH$probF)

return(results)

}