# Supplementary code supporting the statistical analyses from Dupoué et al. Climate and foraging mode explain interspecific variation in snake metabolic rates

library(nlme)

library(ape)

library(coxme)

library(AICcmodavg)

'loading nexus file from Pyron et al (2013)'

Tree <- read.tree("C:/Users/andreaz/Documents/squamate phylogeny.txt")

'loading dataset'

snake\_MR <-read.table("C:/Users/andreaz/Documents/snake\_MR.txt", h=T, sep="\t", dec=",", na.strings="NA")

str(snake\_MR)

'Phylogenetic Variance-covariance for different estimates of lambda'

speciescors0 <- vcv(corPagel(0,phy=Tree),corr=T)

speciescors0.1 <- vcv(corPagel(0.1,phy=Tree),corr=T)

speciescors0.2 <- vcv(corPagel(0.2,phy=Tree),corr=T)

speciescors0.3 <- vcv(corPagel(0.3,phy=Tree),corr=T)

speciescors0.4 <- vcv(corPagel(0.4,phy=Tree),corr=T)

speciescors0.5 <- vcv(corPagel(0.5,phy=Tree),corr=T)

speciescors0.6 <- vcv(corPagel(0.6,phy=Tree),corr=T)

speciescors0.7 <- vcv(corPagel(0.7,phy=Tree),corr=T)

speciescors0.8 <- vcv(corPagel(0.8,phy=Tree),corr=T)

speciescors0.9 <- vcv(corPagel(0.9,phy=Tree),corr=T)

speciescors1 <- vcv(corPagel(1,phy=Tree),corr=T)

'AICc based model selection to compare different lambda'

METABO.mod <- list()

METABO.mod[[1]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0)

METABO.mod[[2]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.1)

METABO.mod[[3]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.2)

METABO.mod[[4]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.3)

METABO.mod[[5]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.4)

METABO.mod[[6]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.5)

METABO.mod[[7]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.6)

METABO.mod[[8]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.7)

METABO.mod[[9]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.8)

METABO.mod[[10]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors0.9)

METABO.mod[[11]] <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,method='REML',varlist=speciescors1)

Modnames <- c("lambda0", "lambda0.1", "lambda0.2", "lambda0.3", "lambda0.4", "lambda0.5", "lambda0.6", "lambda0.7", "lambda0.8", "lambda0.9", "lambda1")

aictab(cand.set = METABO.mod, modnames=Modnames)

'Statistical results in the selected model'

'logVO2=> log transformed snake oxygen consumption'

'logBM => log transformed snake body mass'

'T\_trial => trial temperature'

'method => open or closed system respirometry method'

'metabolic\_state => resting or standard metabolic rate'

'foraging\_mode => active or ambush predation mode'

'T\_clim => average habitat temperature'

'P\_total => total precipitation'

model\_final <-lmekin( logVO2 ~ logBM + T\_trial + method + metabolic\_state + foraging\_mode + T\_clim + P\_total + (1|Species), data=snake\_MR,varlist=speciescors0.2)

print(model\_final)