

The script that performs the PGLS analyses in R

```
library(ape)
library(caper)
#load in trees
Tre=read.nexus("birdtree.nex")
#load in the data which are presented in the supplements of the paper
data <- read.csv("Table_S1.csv", header=T)
dat<-comparative.data(Tre, data, "Species")
#PGLS model
mod1<- pglS(1/Mismatch~log(Body_mass),dat, lambda="ML")
mod2<- pglS(1/Mismatch~log(Body_mass)+asin(sqrt(GC_content)),dat,
lambda="ML")
#summary of the models
summary(mod1,mod2)
```