

```
##reading libraries required
```

```
library(phytools)
```

```
library(ape)
```

```
library(maps)
```

```
library(tidyverse)
```

```
library(geiger)
```

```
##reading original phylogenetic tree
```

```
rodent.tree<-read.nexus( "pone.0183070.s015.tre")
```

```
rodent.tree
```

```
##checking muridae data file and tree node name
```

```
chk2<-name.check(rodent.tree,muridae_adapt)
```

```
##dropping unmatched tips
```

```
muridae.tree<-drop.tip(rodent.tree,chk2$tree_not_data)
```

```
muridae.tree
```

```
##checking new tree
```

```
murid<-muridae_adapt[muridae.tree$tip.label,]
```

```
head(murid)
```

```
##specifying clade 1 to 6
```

```
clade1.species<-c("Deomys_ferrugineus", "Meriones_shawi")
```

```
nodes1<-supply(clade1.species,grep,x=muridae.tree$tip.label)
```

nodes1

```
clade2.species<-c("Phloeomys_pallidus", "Batomys_granti")
```

```
nodes2<-sapply(clade2.species,grep,x=muridae.tree$tip.label)
```

nodes2

```
clade3.species<-c("Maxomys_bartelsii", "Rattus_rattus")
```

```
nodes3<-sapply(clade3.species,grep,x=muridae.tree$tip.label)
```

nodes3

```
clade4.species<-c("Apomys_aurorae", "Melomys_burtoni")
```

```
nodes4<-sapply(clade4.species,grep,x=muridae.tree$tip.label)
```

nodes4

```
clade5.species<-c("Millardia_kathleenae", "Arvicanthis_niloticus")
```

```
nodes5<-sapply(clade5.species,grep,x=muridae.tree$tip.label)
```

nodes5

```
clade6.species<-c("Malacomys_longipes", "Praomys_daltoni")
```

```
nodes6<-sapply(clade6.species,grep,x=muridae.tree$tip.label)
```

nodes6

```
##getting MRCA node1<-getMRCA(muridae.tree,clade1.species)
```

node1

```
node2<-getMRCA(muridae.tree,clade2.species)
```

node2

```
node3<-getMRCA(muridae.tree,clade3.species)
```

node3

```
node4<-getMRCA(muridae.tree,clade4.species)
```

node4

```
node5<-getMRCA(muridae.tree,clade5.species)
```

node5

```
node6<-getMRCA(muridae.tree,clade6.species)
```

```
node6
```

```
##Specifying colors for plot
```

```
muridae.tree<-paintSubTree(muridae.tree,node1,state="1",anc="0")
```

```
muridae.tree<-paintSubTree(muridae.tree,node2,state="2")
```

```
muridae.tree<-paintSubTree(muridae.tree,node3,state="3")
```

```
muridae.tree<-paintSubTree(muridae.tree,node4,state="4")
```

```
muridae.tree<-paintSubTree(muridae.tree,node5,state="5")
```

```
muridae.tree<-paintSubTree(muridae.tree,node6,state="6")
```

```
##plotting tree with clades
```

```
plotSimmap(muridae.tree,pts=FALSE)
```

```
##linear regression
```

```
clade1Fit = linear_reg() %>%
```

```
  set_engine("lm") %>%
```

```
  fit(HFL~WT, data = clade1)
```

```
clade1Fit
```

```
##seeing r-squared
```

```
glance(clade1Fit)$r-squared
```

```
##pgls analysis
```

```
spp<-rownames(murid)
```

```
corBM<-corBrownian(phy=muridae.tree,form=~spp)
```

```
corBM
```

```
pgls.muridae<-gls(log(HFL)~log(Mean_Temp),  
                  data=murid,correlation=corBM)
```

```
##Plotting graphs central code
```

```
muridae_adapted%>%
```

```
ggplot(mapping=aes(x= `Lat.mid`, y= HFL))+
```

```
geom_point()+ geom_smooth(se=FALSE)+
```

```
labs(title= "Latitude and Hindfoot Correlation", x= "Latitude midpoint", y="Hindfoot Length")+
```

```
theme_bw()
```