

# Supplemental file to “Testing for heterogeneous rates of discrete character evolution on phylogenies” – analysis of *Anolis* caudal vertebrae number

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This code reiterates the analysis of *Anolis* caudal vertebrae evolution for the *phytools* method `fitmultiMk` as described in the study titled “Testing for heterogeneous rates of discrete character evolution on phylogenies” by Revell et al.

```
## load packages
library(phytools)

## Loading required package: ape
## Loading required package: maps
library(geiger)
library(foreach)
library(doParallel)

## Loading required package: iterators
## Loading required package: parallel
## check package version
packageVersion("phytools")

## [1] '2.3.13'
## set seed
set.seed(99)

## read tree from file
anolis_tree<-read.tree("Gamble_MCC.phy")
anolis_tree

##
## Phylogenetic tree with 219 tips and 218 internal nodes.
##
## Tip labels:
##   grahami, conspersus, garmani, opalinus, valencienni, lineatopus, ...
##
## Rooted; includes branch lengths.
## scale edge lengths to match dewlap analysis
anolis_tree$edge.length<-anolis_tree$edge.length*(7.36138587/11.94994231)

## read data
anolis_dat<-read.csv("anolis_caudal_vertebrae_data.csv",
```

```

row.names=1)
## data columns are species labels, average caudal vertebrae,
## average caudal vertebrae rounded to nearest
head(anolis_dat)

##      Species AvgNumber Vert
## 1      ahli  40.40000  40
## 2     allogus 42.66667  43
## 3 rubribarbus 44.00000  44
## 4       imias 41.50000  42
## 5      sagrei 46.20000  46
## 6     bremeri 45.50000  46

## convert numeric vector to factor
anolis_vert<-factor(setNames(anolis_dat[,3],anolis_dat[,1]),
  levels=min(anolis_dat[,3]):max(anolis_dat[,3]))
head(anolis_vert)

##      ahli      allogus rubribarbus      imias      sagrei      bremeri
##      40      43      44      42      46      46
## 22 Levels: 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 ... 55

## prune tree to match data
pruned.anolis_tree<-drop.tip(anolis_tree,
  setdiff(anolis_tree$tip.label,anolis_dat[,1]))
## check names match
name.check(pruned.anolis_tree,anolis_vert,
  data.names=names(anolis_vert))

## [1] "OK"

## create design matrix for ordered evolution
k<-length(levels(anolis_vert))
ordered<-matrix(0,k,k,dimnames=list(levels(anolis_vert),
  levels(anolis_vert)))
for(i in 1:(k-1)){
  ordered[i,i+1]<-1
  ordered[i,i-1]<-2
}
ordered[k,k-1]<-2

## check first 5 rows & columns of matrix
ordered[1:5,1:5]

##      34 35 36 37 38
## 34  0  1  0  0  0
## 35  2  0  1  0  0
## 36  0  2  0  1  0
## 37  0  0  2  0  1
## 38  0  0  0  2  0

## check bottom 5 rows & columns of matrix
ordered[(nrow(ordered)-5):nrow(ordered),
  (ncol(ordered)-5):ncol(ordered)]

##      50 51 52 53 54 55
## 50  0  1  0  0  0  0
## 51  2  0  1  0  0  0

```

```

## 52 0 2 0 1 0 0
## 53 0 0 2 0 1 0
## 54 0 0 0 2 0 1
## 55 0 0 0 0 2 0

## convert factor to matrix
anolis_vert<-to.matrix(anolis_vert,levels(anolis_vert))

## set number of optimization iterations per model
niter<-10
## open cluster for parallelized optimization
ncores<-min(niter,parallel::detectCores()-2)
mc<-makeCluster(ncores,type="PSOCK")
registerDoParallel(cl=mc)

## run niter parallelized optimizations of single
## regime model
fits<-foreach(i=1:niter)%dopar%{
  phytools::fitMk(pruned.anolis_tree,anolis_vert,
    model=ordered,rand_start=TRUE)
}
logL<-sapply(fits,logLik)
print(logL)

## [1] -305.0839 -305.0839 -305.0839 -305.0839 -305.0839 -305.0839 -305.0839
## [8] -305.0839 -305.0839 -305.0839

## select best-fitting of niter iterations
fit.single<-fits[[which(logL==max(logL))[1]]]
print(fit.single,digits=3)

## Object of class "fitMk".
##
## Fitted (or set) value of Q:
##      34      35      36      37      38      39      40      41      42      43      44
## 34 -0.318  0.318  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 35  0.494 -0.812  0.318  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 36  0.000  0.494 -0.812  0.318  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 37  0.000  0.000  0.494 -0.812  0.318  0.000  0.000  0.000  0.000  0.000  0.000
## 38  0.000  0.000  0.000  0.494 -0.812  0.318  0.000  0.000  0.000  0.000  0.000
## 39  0.000  0.000  0.000  0.000  0.494 -0.812  0.318  0.000  0.000  0.000  0.000
## 40  0.000  0.000  0.000  0.000  0.000  0.494 -0.812  0.318  0.000  0.000  0.000
## 41  0.000  0.000  0.000  0.000  0.000  0.000  0.494 -0.812  0.318  0.000  0.000
## 42  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.494 -0.812  0.318  0.000
## 43  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.494 -0.812  0.318
## 44  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.494 -0.812
## 45  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.494
## 46  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 47  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 48  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 49  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 50  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 51  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 52  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 53  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## 54  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000

```

```

## 55 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
##      45      46      47      48      49      50      51      52      53      54      55
## 34 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 35 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 36 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 37 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 38 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 39 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 40 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 41 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 42 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 43 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 44 0.318 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 45 -0.812 0.318 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 46 0.494 -0.812 0.318 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 47 0.000 0.494 -0.812 0.318 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 48 0.000 0.000 0.494 -0.812 0.318 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## 49 0.000 0.000 0.000 0.494 -0.812 0.318 0.000 0.000 0.000 0.000 0.000 0.000
## 50 0.000 0.000 0.000 0.000 0.494 -0.812 0.318 0.000 0.000 0.000 0.000 0.000
## 51 0.000 0.000 0.000 0.000 0.000 0.494 -0.812 0.318 0.000 0.000 0.000 0.000
## 52 0.000 0.000 0.000 0.000 0.000 0.000 0.494 -0.812 0.318 0.000 0.000 0.000
## 53 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.494 -0.812 0.318 0.000 0.000
## 54 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.494 -0.812 0.318 0.000
## 55 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.494 -0.494
##
## Fitted (or set) value of pi:
##      34      35      36      37      38      39      40      41      42      43      44      45      46
## 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045
##      47      48      49      50      51      52      53      54      55
## 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045
## due to treating the root prior as (a) flat.
##
## Log-likelihood: -305.084
##
## Optimization method used was "nlminb"
##
## R thinks it has found the ML solution.

```

```

## graph regimes on pruned tree
## note this is not for publication as taxon sampling different
## from other analysis (though the tree is the same)
nodes<-c(218,119,123)
pruned.anolis_tree<-paintSubTree(pruned.anolis_tree,
  nodes[1],"M","I",stem=0.5)
pruned.anolis_tree<-paintSubTree(pruned.anolis_tree,
  nodes[2],"M","I",stem=0.5)
pruned.anolis_tree<-paintSubTree(pruned.anolis_tree,
  nodes[3],"I","M",stem=0.5)
cols<-setNames(c("brown","blue"),c("M","I"))
plot(pruned.anolis_tree,cols,type="arc",arc_height=0.1,
  part=1,fs=0.7,ftype="i")

```



[illegible]



```

## Log-likelihood: -304.358
##
## Optimization method used was "nlminb"
stopCluster(cl=mc)

## compare models
anova(fit.single,fit.multi)

##          log(L) d.f.      AIC    weight
## fit.single -305.0839    2 614.1679 0.7814869
## fit.multi  -304.3583    4 616.7166 0.2185131

## print rates for each model
fit.single$rates

## [1] 0.3180502 0.4938762
fit.multi$rates

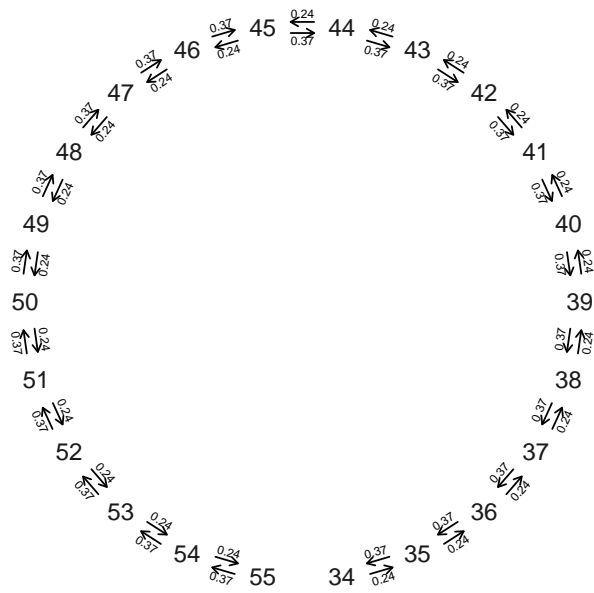
## [1] 0.3329482 0.5230044 0.2374578 0.3730183

## graph fitted models
par(mfrow=c(2,1),mar=c(1.1,1.1,1.1,1.1))
obj<-fit.multi
obj$rates<-round(obj$rates[3:4],2)
obj$regimes<-NULL
class(obj)<-"fitMk"
plot(obj,show.zeros=F,mar=rep(2.1,4),show.zeros=F,
      tol=1e-3,cex.traits=0.8,cex.rates=0.4)
mtext(text="a) Mainland caudal vertebra number",
      adj=0,line=-1,cex=0.9)
obj<-fit.multi
obj$rates<-round(obj$rates[1:2],2)
obj$regimes<-NULL
class(obj)<-"fitMk"
plot(obj,show.zeros=F,mar=rep(2.1,4),show.zeros=F,
      tol=1e-3,cex.traits=0.8,cex.rates=0.4)
mtext(text="b) Caribbean caudal vertebra number",
      adj=0,line=-1,cex=0.9)

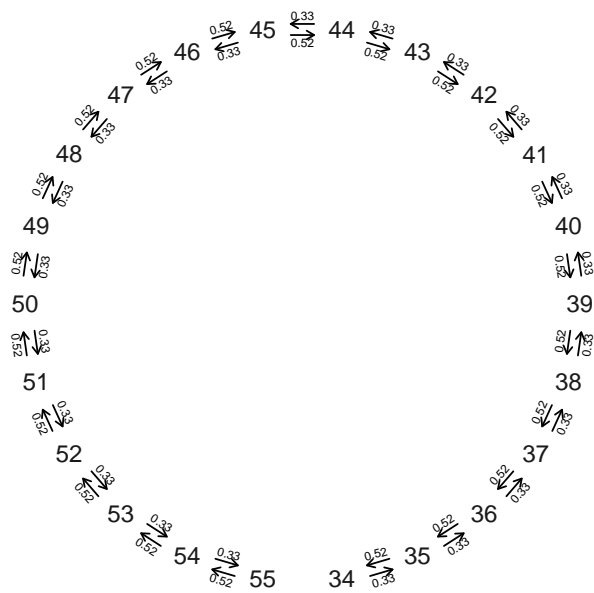
```



a) Mainland caudal vertebra number



b) Caribbean caudal vertebra number



```

## repeat graph, but to export as PDF
pdf(file="Figure_S2.pdf",width=6,height=10)
par(mfrow=c(2,1),mar=c(1.1,1.1,1.1,1.1))
obj<-fit.multi
obj$rates<-round(obj$rates[3:4],2)
obj$regimes<-NULL
class(obj)<-"fitMk"
plot(obj,show.zeros=F,mar=rep(2.1,4),show.zeros=F,
      tol=1e-3,cex.traits=0.8,cex.rates=0.4)
mtext(text="a) Mainland caudal vertebra number",
      adj=0,line=-1,cex=0.9)
obj<-fit.multi
obj$rates<-round(obj$rates[1:2],2)
obj$regimes<-NULL
class(obj)<-"fitMk"
plot(obj,show.zeros=F,mar=rep(2.1,4),show.zeros=F,
      tol=1e-3,cex.traits=0.8,cex.rates=0.4)
mtext(text="b) Caribbean caudal vertebra number",
      adj=0,line=-1,cex=0.9)
dev.off()

## pdf
## 2

save.image(file="morph-analysis.Rdata")

```