

# Supplementary Materials: Venomous Landmines: Clinical Implications of Extreme Coagulotoxic Diversification and Differential Neutralization by Antivenom of Venoms within the Viperid Snake Genus *Bitis*

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## Phytools script

```
>library(ape)
>library(maps)
>library(phytools)
># senci.contMap is a slight modification of errorbar.contMap that trims 95% CIs of
ancestral state reconstructions to a sensible range, e.g., for traits bound between 0 and 1
  # Example of code for implementing it would be as follows (lines separated by
  semicolons): pasr<-contMap(tree,mapdat,plot=F,lims=c(0,1)) ;
  plot(setMap(pasr,invert=T)); senci.contMap(setMap(pasr,invert=T),mini=0,maxi=1)
  senci.contMap<-function(obj,...){
  if (hasArg(x))
  x <- list(...)$x
  else x <- setNames(sapply(1:Ntip(obj$tree), function(x, obj) {
  ii <- which(obj$tree$edge[, 2] == x)
  ss <- names(obj$tree$maps[[ii]][length(obj$tree$maps[[ii]])])
  obj$lims[1 ] + as.numeric(ss)/(length(obj$cols) - 1) *
  diff(obj$lims)
  }, obj = obj), obj$tree$tip.label)
  if (hasArg(scale.by.ci))
  scale.by.ci <- list(...)$scale.by.ci
  else scale.by.ci <- TRUE
  if (hasArg(lwd))
  lwd <- list(...)$lwd
  else lwd <- 14
  tree <- obj$tree
  aa <- fastAnc(tree, x, CI = TRUE)
  if (hasArg(min))#added lines here
  for (i in 1:length(aa$CI95[,1])){ #added lines here
  aa$CI95[i,1]<-ifelse(aa$CI95[i,1]<list(...)$min,list(...)$min,aa$CI95[i,1]) #added lines
  here
  } #added lines here
```

```

else aa$CI95[,1]<-aa$CI95[,1] #added lines here
if (hasArg(max)) #added lines here
for (i in 1:length(aa$CI95[,2])){ #added lines here
aa$CI95[i,2]<-ifelse(aa$CI95[i,2]>list(...)$max,list(...)$max,aa$CI95[i,2]) # added
lines here
} #added lines here
else aa$CI95[,2]<-aa$CI95[,2] #added lines here
xlim <- range(aa$CI95)
if (xlim[2] > obj$lims[2] || xlim[1] < obj$lims[1]) {
cat(paste(" ----\n The range of the contMap object, presently (" ,
round(obj$lims[1], 4), ", ", round(obj$lims[2], 4),
"), should be equal to\n or greater than the range of the CIs on ancestral states: (" ,
round(xlim[1], 4), ", ", round(xlim[2], 4), ").\n",
sep = ""))
cat(paste(" To ensure that your error bars are correctly plotted, please recompute
your\n",
" contMap object and increase lims.\n ----\n",
sep = ""))
}
d <- diff(obj$lims)
if (scale.by.ci) {
v <- aa$CI95[, 2] - aa$CI95[, 1]
v <- v/max(v)
}
else v <- rep(0.5, tree$Nnode)
n <- length(obj$cols) - 1
lastPP <- get("last_plot.phylo", envir = .PlotPhyloEnv)
h <- max(nodeHeights(tree))
for (i in 1:tree$Nnode) {
ii <- round((aa$CI95[i, 1] - obj$lims[1])/d * n)
jj <- round((aa$CI95[i, 2] - obj$lims[1])/d * (n + 1))
cols <- obj$cols[ii:jj]
add.color.bar(leg = 0.1 * h * v[i], cols = cols, prompt = FALSE,
x = lastPP$xx[i + Ntip(tree)] - 0.05 * h * v[i],
y = lastPP$yy[i + Ntip(tree)], title = "", subtitle = "",
lims = NULL, lwd = lwd)
}
}
>data<-read.csv(file.choose())
>dat<-data
>mapvar<-dat$var

```

```
>names(mapvar)<-dat$species  
>tree<-read.tree(file.choose())  
>tree<-chronos(tree)  
>asr<-contMap(tree,mapvar,plot=F)  
>plot(setMap(asr,col=c(2,7,3,5,4)),lwd=3)  
>senci.contMap(setMap(asr,col=c(2,7,3,5,4)),lwd=6,min=[minimum value from the  
dataset],max=[minimum value from the dataset])
```