

# An empirical example: *Rhynoclemmys* data.

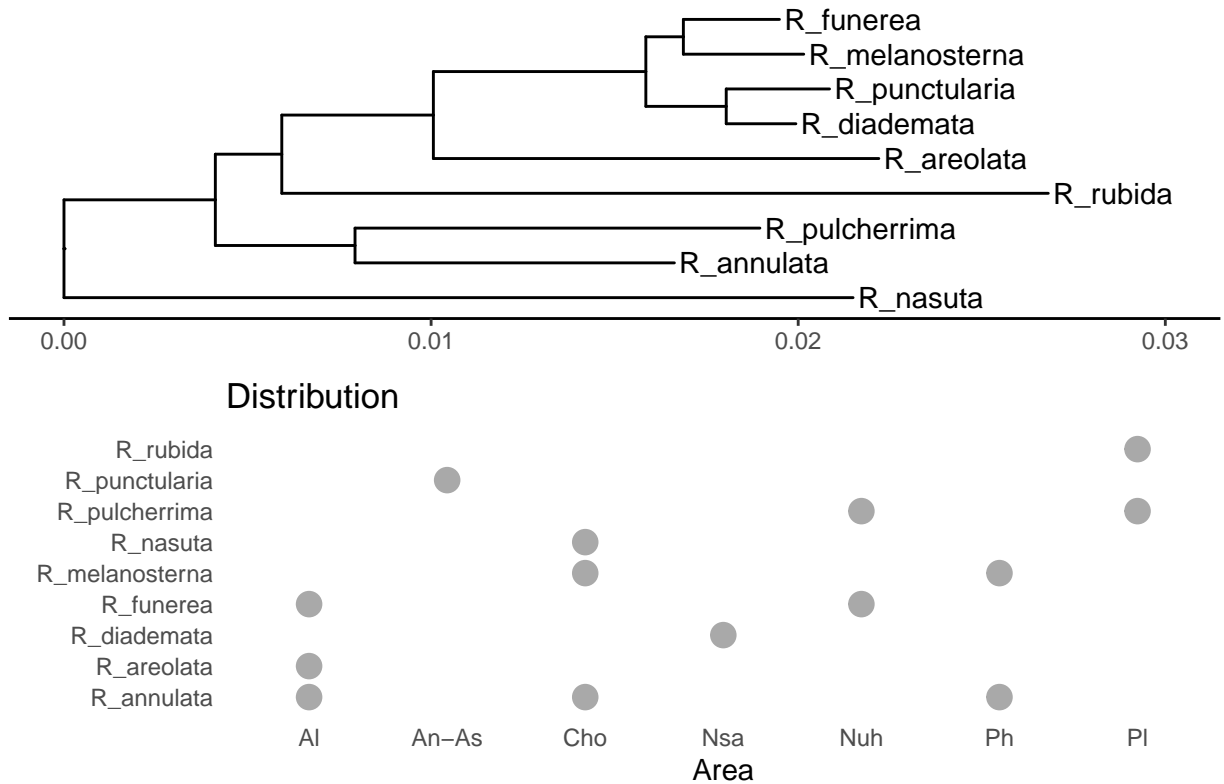
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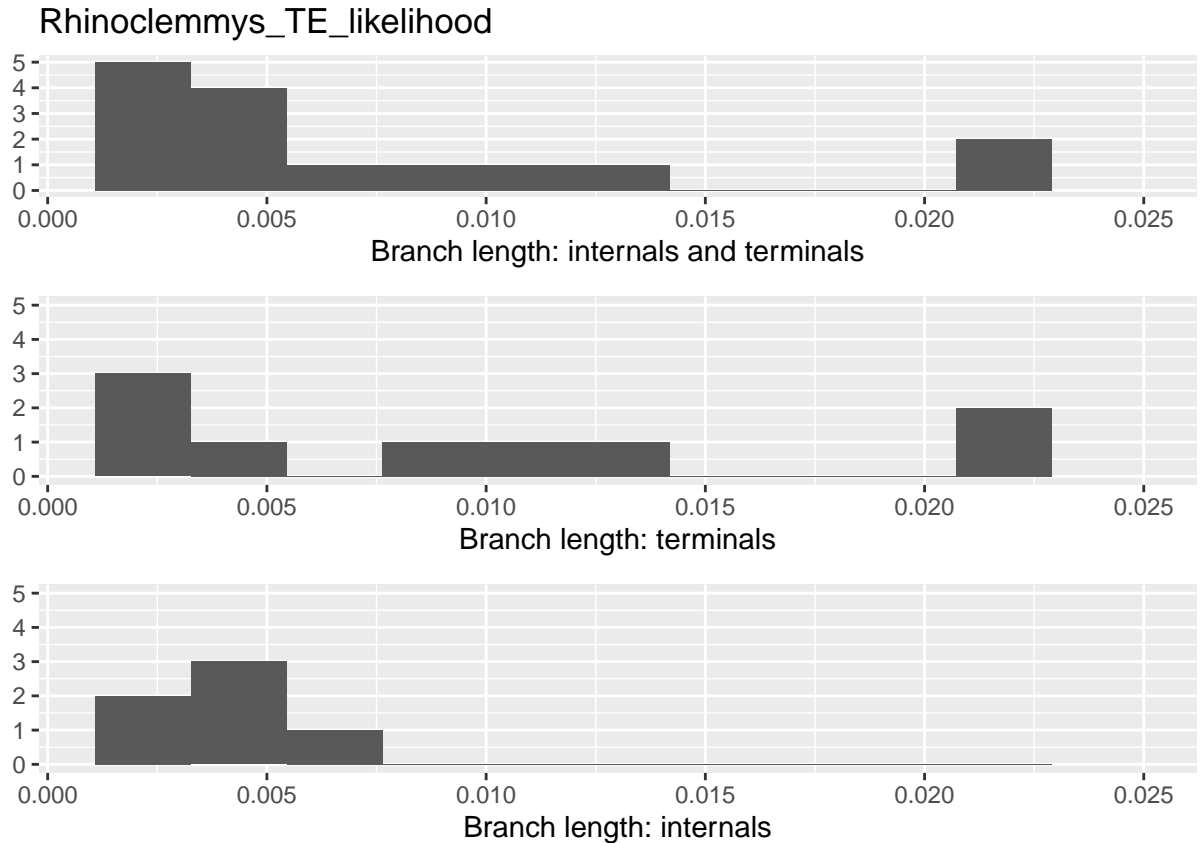
We read the distribution and the tree.

```
## Analyses made with blepd version: 0 1 8 2020 11 17
```

## Rhynoclemmys\_TE\_likelihoood



We want to test whether the branch lengths will have any effect in the area(s) chosen for conservation, based on a a Phylogenetic Diversity (PD) analysis for the *Rhynoclemmys* genus. The topology corresponds to a Total Evidence analysis from R-Alarcon and Miranda-Esquivel (2020), and the distribution is taken and modified from Le and McCord (2008).



The branch length histograms and the tree plot, show the internal length branches are similar, and different to terminals'; there are two longer branches, *R. aerolata* (inhabiting Al) and *R. rubida* (Pl), while the areas Al and Cho are the richest.

Fist we calculate the PD value for the tree, we save the values as a table and later we convert the table to a matrix.

```
##      PD value
## Cho  0.054150
## Al   0.044127
## Pl   0.041646
## Nuh  0.034323
## Ph   0.032655
## An-As 0.020853
## Nsa  0.019937
```

The highest PD is for area Cho, followed by Al, the two richest areas, and the difference in PD value is not given by the richness but the species inhabiting each area.

Now, we test the effect of the branch length on the PD values, swapping terminal and internal branch lengths, using the three available models.

```
## model to test simpleswap reps 100
##
## Tree= Rhinoclemmys_TE_likelihoood
## Model= simpleswap
## Branchs swapped= terminals
##
## BestInitial:Cho
```

```

##   AreaSelected Freq Percent
## 1           Al   13      13
## 2           Cho  86      86
## 3           Pl   1       1
##
##
##
## model to test simpleswap reps 100
##
##   Tree= Rhinoclemmys_TE_likelihoood
##   Model= simpleswap
##   Branchs swapped= internals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Cho 100      100
##
##
##
## model to test allswap reps 100
##
##   Tree= Rhinoclemmys_TE_likelihoood
##   Model= allswap
##   Branchs swapped= terminals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al   34      34
## 2           Cho  54      54
## 3           Nuh  10      10
## 4           Pl   2       2
##
##
##
## model to test allswap reps 100
##
##   Tree= Rhinoclemmys_TE_likelihoood
##   Model= allswap
##   Branchs swapped= internals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Cho 100      100
##
##
##
## model to test uniform reps 100
##
##   Tree= Rhinoclemmys_TE_likelihoood
##   Model= uniform
##   Branchs swapped= terminals
##
## BestInitial:Cho
##   AreaSelected Freq Percent

```

```

## 1      Al    59    59
## 2      Cho   38    38
## 3      Nuh    3     3
##
##
##
## model to test uniform reps 100
##
##   Tree= Rhinoclemmys_TE_likelihoood
##   Model= uniform
##   Branchs swapped= internals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1      Cho   100    100

```

The terminal branch length is critical in the decision taken, if we swap all terminal branch lengths (model=*allswap*), or if we replace them with a uniform distribution (model=*uniform*), the area selected might change from Cho to Al.

As the terminal branch lengths are distributed unequally, we might suspect that the results could depend on the longest branches that inhabit the areas Cho/Al.

But first, let us see if the number of replicates has any effect.

```

## model to test allswap reps 2
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1      Al     1     50
## 2      Cho     1     50
## model to test allswap reps 4
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1      Al     2     50
## 2      Cho     2     50
## model to test allswap reps 8
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1      Al     3    37.5
## 2      Cho     5    62.5
## model to test allswap reps 16
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1      Al     5    31.25
## 2      Cho     8    50.00
## 3      Nsa     1     6.25
## 4      Nuh     2    12.50

```

Roughly speaking from 1000 on the results are alike, and the largest difference is using 10 or 100 replicates. As a rule of thumb, we must use at least 100 replicates, but 1000 will be better.

now, let us see if the possible difference in results could be assigned to both of our longest branches.

```

##
## Terminal: R_annulata, has NO effect on branch length == 0 or Max
## Terminal: R_pulcherrima, has NO effect on branch length == 0 or Max
## Terminal: R_diademata, has NO effect on branch length == 0 or Max
## Terminal: R_punctularia, has NO effect on branch length == 0 or Max
## Terminal: R_melanosterna, has NO effect on branch length == 0 or Max
## Terminal: R_funerea, has NO effect on branch length == 0 or Max
## Terminal: R_areolata, has NO effect on branch length == 0 or Max
## Terminal: R_rubida, has NO effect on branch length == 0 or Max

##
## Delta (%)      Terminal      Initial Selected      Evaluating lower
## -47.1751      R_nasuta      Cho Al
## 0      R_annulata      Cho Cho
## 0      R_pulcherrima      Cho Cho
## 0      R_diademata      Cho Cho
## 0      R_punctularia      Cho Cho
## 0      R_melanosterna      Cho Cho
## 0      R_funerea      Cho Cho
## 0      R_areolata      Cho Cho
## 0      R_rubida      Cho Cho

##
## Terminal: R_nasuta, has NO effect on branch length == 0 or Max
## Terminal: R_annulata, has NO effect on branch length == 0 or Max
## Terminal: R_melanosterna, has NO effect on branch length == 0 or Max

##
## Delta (%)      Terminal      Initial Selected      Evaluating upper
## 0      R_nasuta      Cho Cho
## 0      R_annulata      Cho Cho
## 116.0762      R_pulcherrima      Cho Pl
## 1819.585      R_diademata      Cho Nsa
## 1202.582      R_punctularia      Cho An-As
## 0      R_melanosterna      Cho Cho
## 391.0176      R_funerea      Cho Al
## 84.9504      R_areolata      Cho Al
## 61.3248      R_rubida      Cho Pl

```

The area selected depends on the branch length. If the terminal branch length of *R. nasuta* is -47.18% shorter, or if the terminal branch length is 84.95% larger for *R. areolata*, the area selected will change from Cho to Al.

## Literature cited

- Le, Minh, and William P. McCord. 2008. "Phylogenetic relationships and biogeographical history of the genus *Rhinoclemmys* Fitzinger, 1835 and the monophyly of the turtle family Geoemydidae (Testudines: Testudinoidea)." *Zoological Journal of the Linnean Society* 153 (4): 751–67. <https://doi.org/10.1111/j.1096-3642.2008.00413.x>.
- R-Alarcon, L. Viviana, and Daniel Rafael Miranda-Esquivel. 2020. "A Total-Evidence Phylogeny of the Crown and Stem-Groups of Turtles (Pantestudines: Testudinata)." *Cladistics: Submitted*.