

# An empirical example: *Rhynoclemmys* data.

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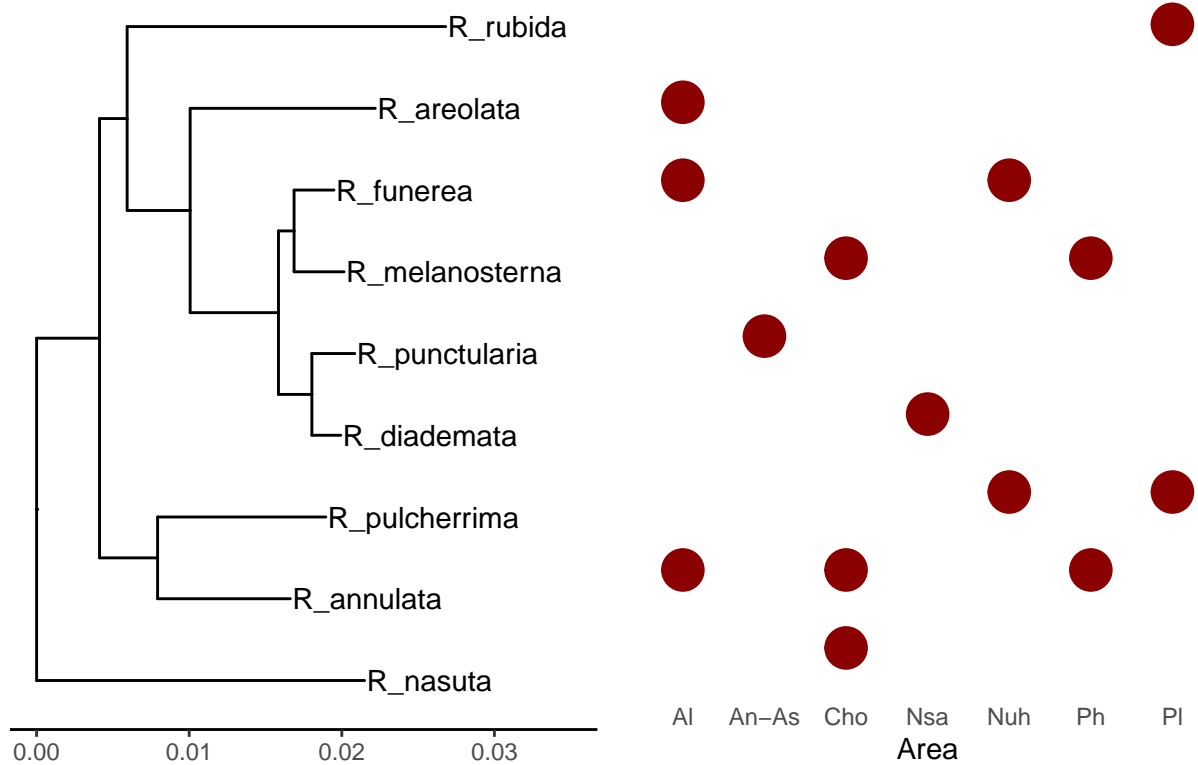
2020 - 10 - 18

We read the data, distribution and tree.

## Analyses made with blepd version: 0 1 7 2020 10 19

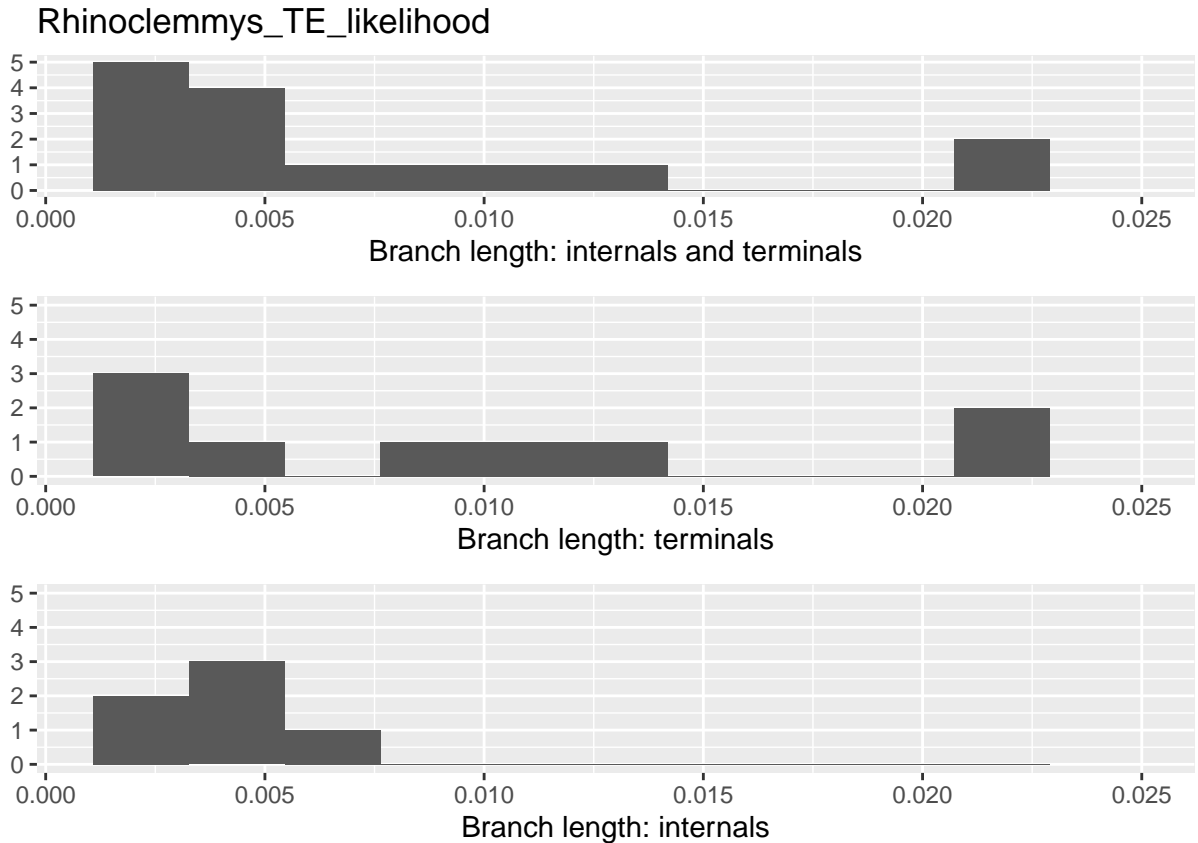
Rhynoclemmys\_TE\_likelihoood

Distributions



We want to test whether the branch lengths will have any effect in the area(s) chosen for conservation using a Phylogenetic Diversity (PD) analysis.

The topology corresponds to a Total Evidence analysis for the *Rhynoclemmys* genus, from R-Alarcon and Miranda-Esquivel (2020), and the distribution is taken and modified from Le and McCord (2008).



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

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.

```
##           [,1]
## Al      0.044127
## An-As   0.020853
## Cho     0.054150
## Nsa     0.019937
## Nuh     0.034323
## Ph      0.032655
## Pl      0.041646
```

Now, we test the efect of branch length swapping, terminal and internal branch lengths.

```
## 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_likelihood      Model= simpleswap   Branchs swapped= internals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Cho  100      100
##
##
##
## model to test allswap reps 100
##
## Tree= Rhinoclemmys_TE_likelihood      Model= allswap   Branchs swapped= terminals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           A1   34       34
## 2           Cho  54       54
## 3           Nuh  10       10
## 4           Pl   2        2
##
##
##
## model to test allswap reps 100
##
## Tree= Rhinoclemmys_TE_likelihood      Model= allswap   Branchs swapped= internals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Cho  100      100
##
##
##
## model to test uniform reps 100
##
## Tree= Rhinoclemmys_TE_likelihood      Model= uniform   Branchs swapped= terminals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           A1   59       59
## 2           Cho  38       38
## 3           Nuh   3        3
##
##
##
## model to test uniform reps 100
##
## Tree= Rhinoclemmys_TE_likelihood      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 depend heavily on the longest branches that inhabit the area.

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

```
## model to test allswap reps 10
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al    5      50
## 2           Cho    5      50
## model to test allswap reps 100
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al   41      41
## 2           Cho   43      43
## 3           Nsa    1       1
## 4           Nuh   11      11
## 5           Pl    4       4
## model to test allswap reps 1000
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al  379     37.9
## 2          An-As   13      1.3
## 3           Cho  429     42.9
## 4           Nsa    9       0.9
## 5           Nuh  148     14.8
## 6           Pl   22       2.2
```

Roughly speaking from 1000 – 10000 the results are alike, and the largest difference is in 10 –100. As a rule of thumb, we most use at least 100 replicates, but 1000 will be better.

now, let's 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
## 116.077  R_pulcherrima  Cho Pl
## 1819.587      R_diademata      Cho Nsa
## 1202.589      R_punctularia  Cho An-As
## 0      R_melanosterna      Cho Cho
## 391.0172      R_funerea      Cho Al
## 84.9473  R_areolata      Cho Al
## 61.3246  R_rubida       Cho Pl

```

The area selected depends heavily in the branch length of *R. aerolata* and *R. rubida*, if the branch length is just a little shorter, the area selected will change from area A to area B.

To test whether internal branches have more impact than terminal branches, we can use the function eval-TerminalvsInternal.

```

## model to test allswap reps 100
## model to test allswap reps 100
## model to test allswap reps 100

## model to test allswap reps 100
## model to test allswap reps 100
## model to test allswap reps 100

## Evaluated: All equal      Branch swapped: terminals
##
## BestInitial:AlCho
##   AreaSelected Freq Percent
## 1      AlCho  100      100
## Evaluated: All equal      Branch swapped: internals
##
## BestInitial:AlCho
##   AreaSelected Freq Percent
## 1      AlCho  100      100
## Evaluated: Terminals      Branch swapped: terminals
##
## BestInitial:AlCho
##   AreaSelected Freq Percent
## 1      AlCho  100      100
## Evaluated: Terminals      Branch swapped: internals
##
## BestInitial:AlCho
##   AreaSelected Freq Percent
## 1      Al      40      40
## 2      AlCho  52      52
## 3      Cho    8       8
## Evaluated: Internals      Branch swapped: terminals

```

```

##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al   43      43
## 2           Cho  40      40
## 3           Nuh  17      17
## Evaluated: Internals      Branch swapped: internals
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Cho  100     100

```

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*.