An empirical example: *Rhynoclemmys* data.
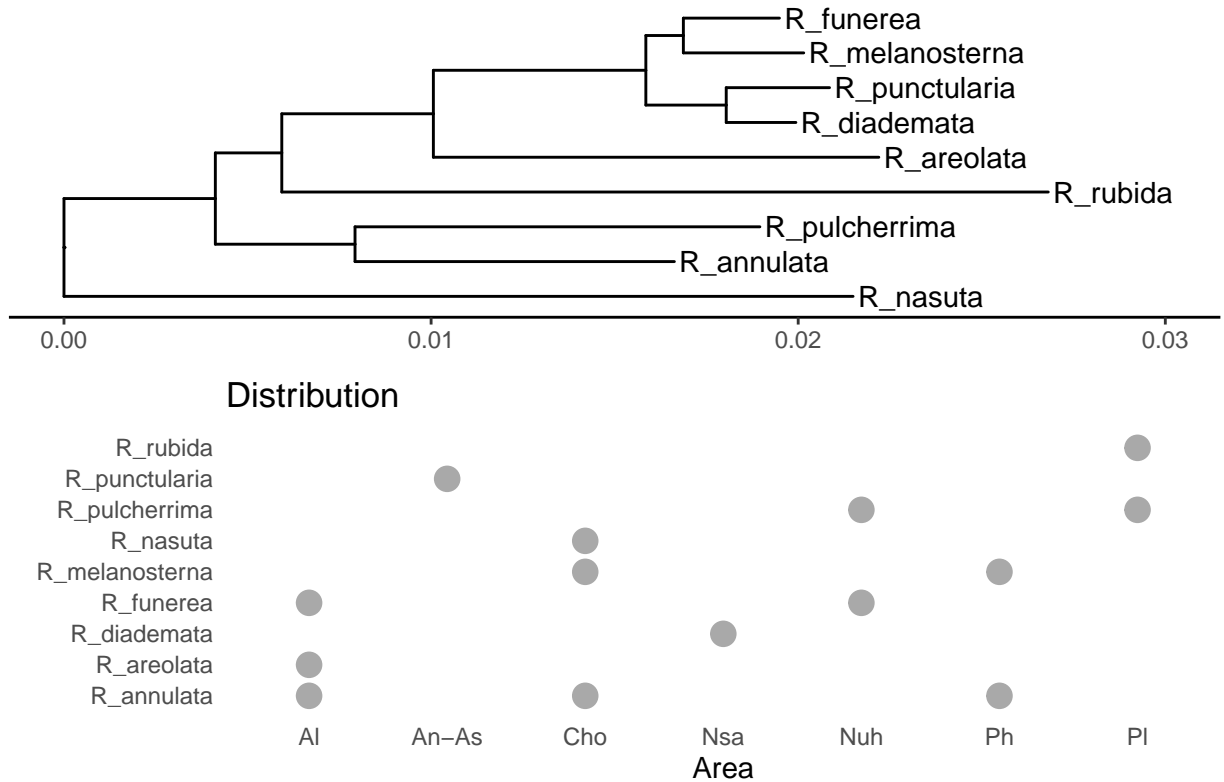
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2021 - 12 - 01

We read the distribution and the tree.

```
## Analyses made with blepd version: 0 1 8 2021 11 21
```

Rhinoclemmys_TE_likelihood

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).

Rhinoclemmys_TE_likelihood
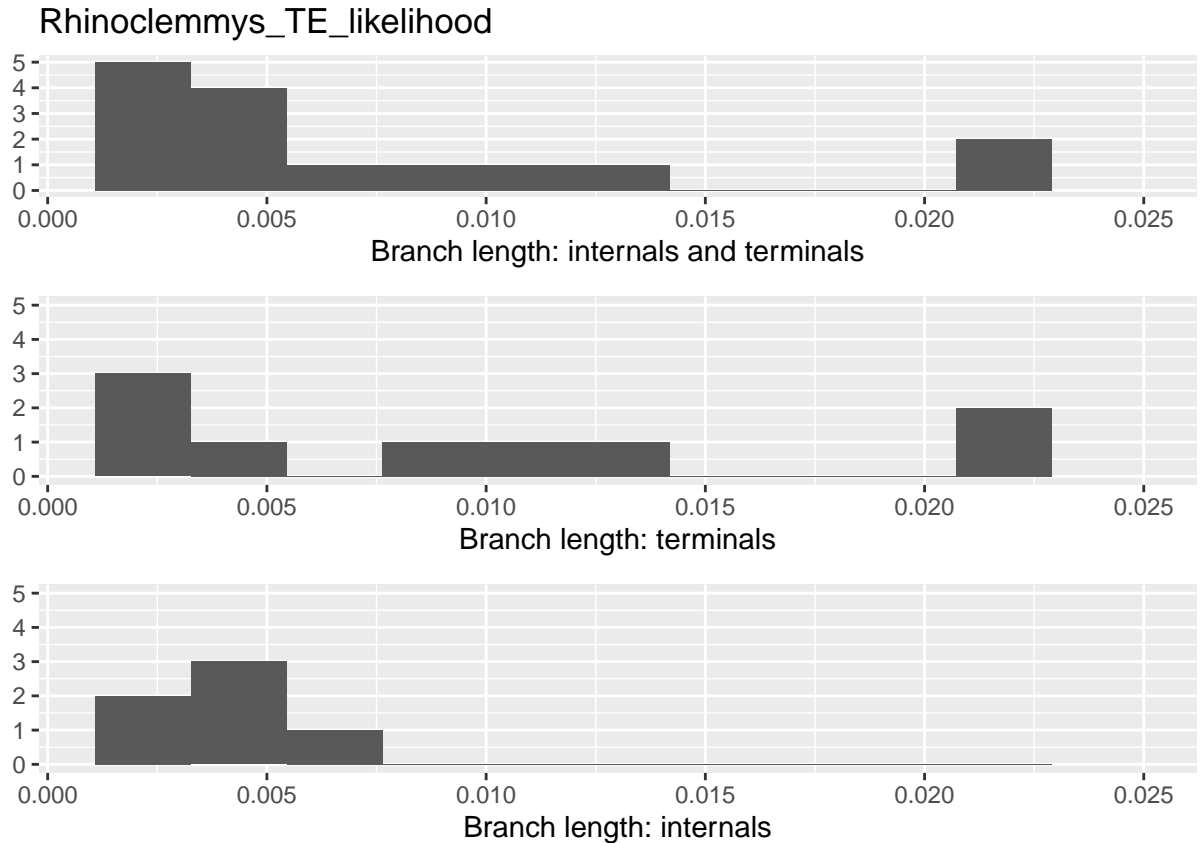

```
## Terminals, with BL larger than 0.02 =  R_nasuta R_rubida
```

The branch length histograms and the tree plot, show the internal length branches are similar, and different to terminals'; there are two longer branches (larger than 0.02), *R. nasuta* (inhabiting Cho) 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_likelihood
##   Model= simpleswap
##   Branches 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
##   Branches swapped= internals
## 
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1          Cho  100     100
## 
## 
## 
## model to test simpleswap reps 100
## 
##   Tree= Rhinoclemmys_TE_likelihood
##   Model= simpleswap
##   Branches swapped= all
## 
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al    8       8
## 2          Cho   91      91
## 3           Pl    1       1
## 
## 
## 
## model to test allswap reps 100
## 
##   Tree= Rhinoclemmys_TE_likelihood
##   Model= allswap
##   Branches swapped= terminals
## 
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al   35      35
## 2          Cho   53      53
## 3          Nuh   10      10
## 4           Pl    2       2
## 
## 
## 
## model to test allswap reps 100
## 
##   Tree= Rhinoclemmys_TE_likelihood
##   Model= allswap
```

```
##     Branches swapped= internals
##
## BestInitial:Cho
##     AreaSelected Freq Percent
## 1            Cho  100     100
##
##
##
## model to test allswap reps 100
##
##     Tree= Rhinoclemmys_TE_likelihood
##     Model= allswap
##     Branches swapped= all
##
## BestInitial:Cho
##     AreaSelected Freq Percent
## 1             Al   37      37
## 2          An-As    4       4
## 3            Cho   33      33
## 4            Nsa    4       4
## 5            Nuh   19      19
## 6             Pl    3       3
##
##
##
## model to test uniform reps 100
##
##     Tree= Rhinoclemmys_TE_likelihood
##     Model= uniform
##     Branches swapped= terminals
##
## BestInitial:Cho
##     AreaSelected Freq Percent
## 1             Al   46      46
## 2            Cho   50      50
## 3            Nuh    4       4
##
##
##
## model to test uniform reps 100
##
##     Tree= Rhinoclemmys_TE_likelihood
##     Model= uniform
##     Branches swapped= internals
##
## BestInitial:Cho
##     AreaSelected Freq Percent
## 1            Cho  100     100
##
##
##
## model to test uniform reps 100
##
##     Tree= Rhinoclemmys_TE_likelihood
```

```
##   Model= uniform
##   Branches swapped= all
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al   38      38
## 2         An-As    1       1
## 3          Cho   53      53
## 4          Nsa    1       1
## 5          Nuh    7       7
```

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 branch(es) 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          Cho    1      50
## 2          Nuh    1      50
## model to test allswap reps 4
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al    1      25
## 2          Cho    3      75
## model to test allswap reps 8
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al    2    25.0
## 2          Cho    3    37.5
## 3          Nuh    3    37.5
## model to test allswap reps 16
##
## BestInitial:Cho
##   AreaSelected Freq Percent
## 1           Al    4    25.0
## 2          Cho   10    62.5
## 3          Nuh    2    12.5
```

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.

```
##
## 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

##
## 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*.