An empirical example: *Rhynoclemmys* data.

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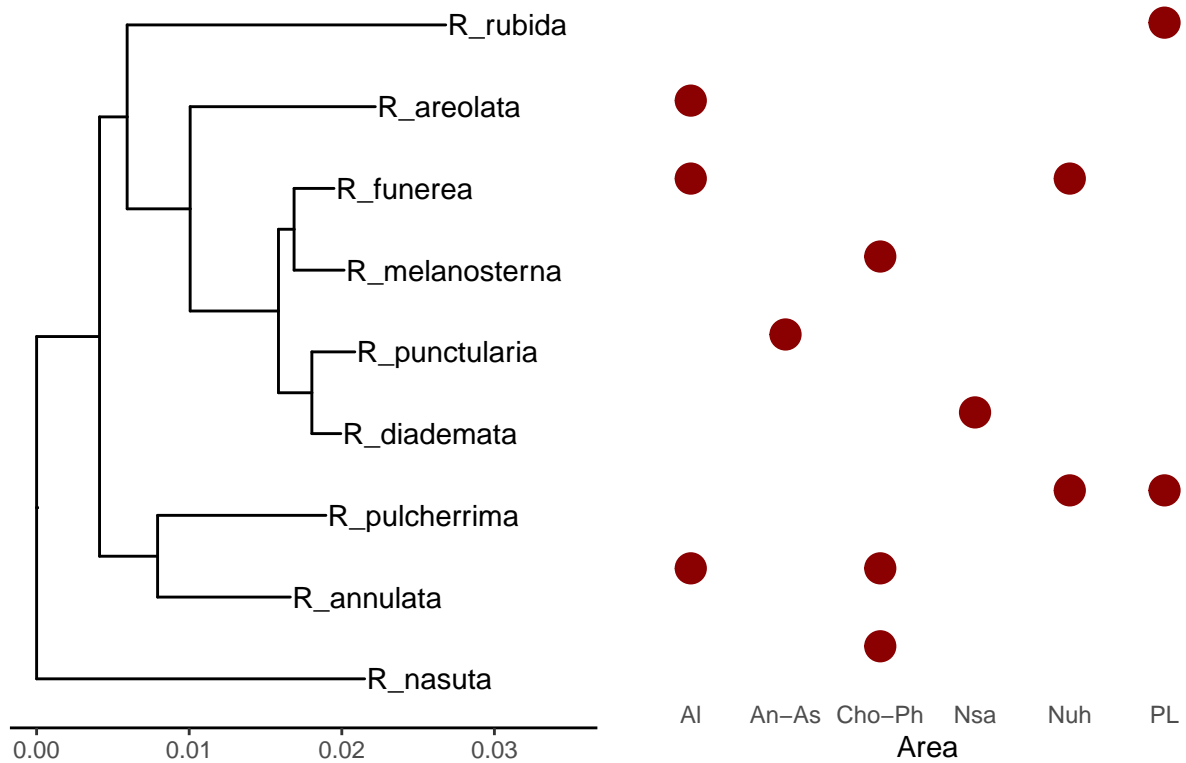
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We read the data, distribution and tree.

```
## Analyses made  with blepd version: 0 1 7 2020 10 15
```


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).

Rhinoclemmys_TE_likelihood

Branch length: internals and terminals

Rhinoclemmys_TE_likelihood

Branch length: terminals
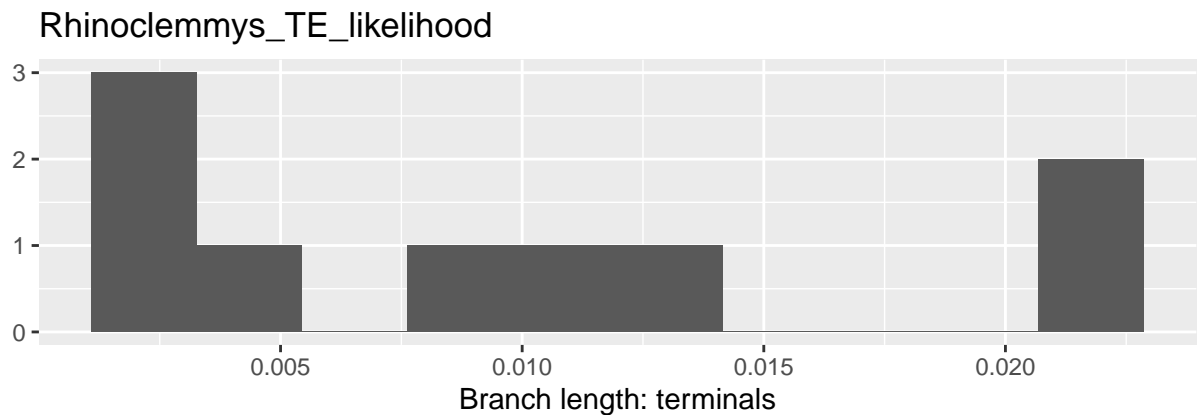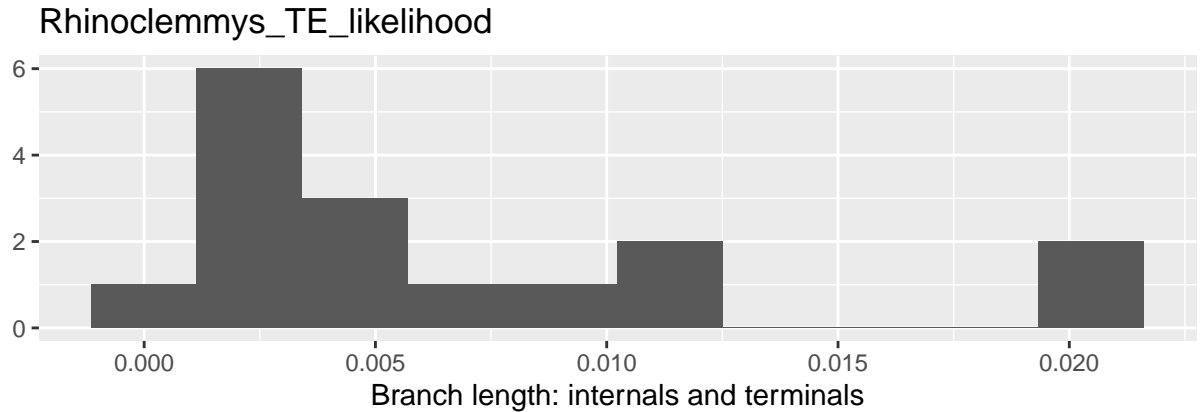
The branch length histogram and the tree plot, show there are two longer branches, *R. aerolata* (Al) and *R. rubida* (Pl), while Al and Cho-Ph are the richest.

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.

```
##         V1       V2       V3       V4       V5      V6
## 1 0.044127 0.020853 0.019937 0.034323 0.041646 0.05415
```

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

```
## model to test simpleswap reps 100
##
## Tree= Rhinoclemmys_TE_likelihood     Model= simpleswap    Branchs swapped= terminals
##
## BestInitial:Cho-Ph
##    AreaSelected Freq
## 1           Al   22
## 2       Cho-Ph   78
##
##
##
## model to test simpleswap reps 100
##
## Tree= Rhinoclemmys_TE_likelihood     Model= simpleswap    Branchs swapped= internals
##
## BestInitial:Cho-Ph
##    AreaSelected Freq
```

```
## 1        Cho-Ph   100
##
##
##
## model to test allswap reps 100
##
## Tree= Rhinoclemmys_TE_likelihood    Model= allswap  Branchs swapped= terminals
##
## BestInitial:Cho-Ph
##   AreaSelected Freq
## 1           Al   37
## 2        Cho-Ph   45
## 3          Nsa    2
## 4          Nuh   11
## 5           PL    5
##
##
##
## model to test allswap reps 100
##
## Tree= Rhinoclemmys_TE_likelihood    Model= allswap  Branchs swapped= internals
##
## BestInitial:Cho-Ph
##   AreaSelected Freq
## 1        Cho-Ph   100
##
##
##
## model to test uniform reps 100
##
## Tree= Rhinoclemmys_TE_likelihood    Model= uniform  Branchs swapped= terminals
##
## BestInitial:Cho-Ph
##   AreaSelected Freq
## 1           Al   47
## 2        Cho-Ph   45
## 3          Nuh    5
## 4           PL    3
##
##
##
## model to test uniform reps 100
##
## Tree= Rhinoclemmys_TE_likelihood    Model= uniform  Branchs swapped= internals
##
## BestInitial:Cho-Ph
##   AreaSelected Freq
## 1        Cho-Ph   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 changes from XXXX to YYY. As the terminal branch lengths are distributed unequally, we might suspect that the results depend heavily on the longest branches that inhabit the area A.

```
##
```

```
## 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-Ph  Al
## 0      R_annulata      Cho-Ph  Cho-Ph
## 0      R_pulcherrima  Cho-Ph  Cho-Ph
## 0      R_diademata     Cho-Ph  Cho-Ph
## 0      R_punctularia  Cho-Ph  Cho-Ph
## 0      R_melanosterna      Cho-Ph  Cho-Ph
## 0      R_funerea  Cho-Ph  Cho-Ph
## 0      R_areolata      Cho-Ph  Cho-Ph
## 0      R_rubida   Cho-Ph  Cho-Ph

##
## 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-Ph  Cho-Ph
## 0      R_annulata      Cho-Ph  Cho-Ph
## 116.077   R_pulcherrima  Cho-Ph  PL
## 1819.587       R_diademata     Cho-Ph  Nsa
## 1202.589       R_punctularia  Cho-Ph  An-As
## 0      R_melanosterna      Cho-Ph  Cho-Ph
## 391.0172       R_funerea  Cho-Ph  Al
## 84.9473   R_areolata      Cho-Ph  Al
## 61.3246   R_rubida   Cho-Ph  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 evalTerminalvsInternal.

```
## 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-Ph
##   AreaSelected Freq
## 1      AlCho-Ph  100
## Evaluated: All equal      Branch swapped: internals
```

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```
## 
## BestInitial:AlCho-Ph
##   AreaSelected Freq
## 1     AlCho-Ph  100
## Evaluated: Terminals     Branch swapped: terminals
## 
## BestInitial:AlCho-Ph
##   AreaSelected Freq
## 1     AlCho-Ph  100
## Evaluated: Terminals     Branch swapped: internals
## 
## BestInitial:AlCho-Ph
##   AreaSelected Freq
## 1          Al   44
## 2     AlCho-Ph   48
## 3       Cho-Ph    8
## Evaluated: Internals     Branch swapped: terminals
## 
## BestInitial:Cho-Ph
##   AreaSelected Freq
## 1          Al   50
## 2       Cho-Ph   37
## 3          Nuh   13
## Evaluated: Internals     Branch swapped: internals
## 
## BestInitial:Cho-Ph
##   AreaSelected Freq
## 1       Cho-Ph  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*.