

# LizardPhylogenyTb

*Glenn J Tattersall*

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## Mapping a continuous trait (field body temperature) onto a phylogeny

This example mirrors the example on bees by Dr. Richards, but these data are already in the public domain.

Libraries required:

```
library(ade4) # source of example data and tree
library(ape)  # tree handling
library(Thermimage) # for access to heat map palette
library(phytools)
```

```
## Loading required package: maps
```

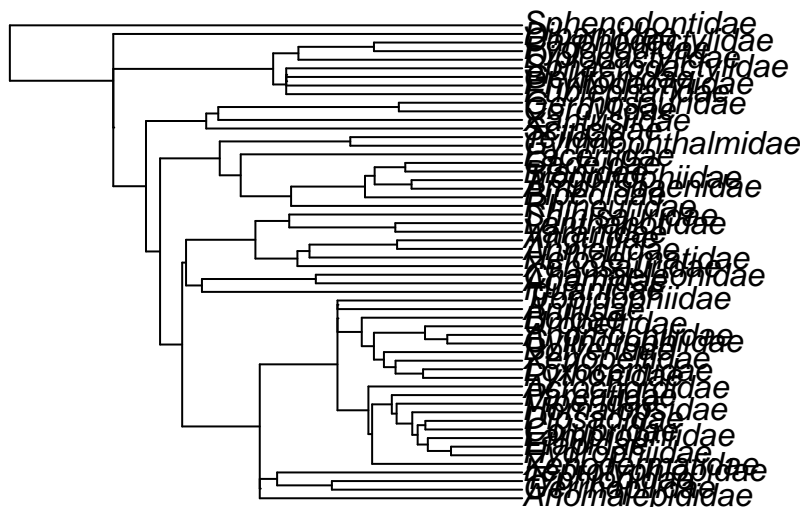
### Obtain your phylogeny

We'll use the phylogeny for Lepidosauria and then match it to our trait data.

lepidosauria\_family.nwk was derived from timetree.org by searching for Lepidosauria and selecting the tree option on the timetree.org website

```
tree<-read.tree("lepidosauria_family.nwk")
tree
```

```
##
## Phylogenetic tree with 56 tips and 55 internal nodes.
##
## Tip labels:
##  Anomalepididae, Gerrhopilidae, Typhlopidae, Leptotyphlopidae, Xenodermatidae, Hydrophiidae, ...
## Node labels:
##  , 126, 127, 110, 88, 78, ...
##
## Rooted; includes branch lengths.
plot(tree)
```



```
tree$tip.label # tip labels
```

```
## [1] "Anomalepididae" "Gerrhopilidae" "Typhlopidae"
## [4] "Leptotyphlopidae" "Xenodermatidae" "Hydrophiidae"
## [7] "Elapidae" "Lamprophiidae" "Colubridae"
## [10] "Dipsadidae" "Homalopsidae" "Viperidae"
## [13] "Pareatidae" "Acrochordidae" "Pythonidae"
## [16] "Loxocemidae" "Xenopeltidae" "Bolyeridae"
## [19] "Cyllindrophiiidae" "Anomochilidae" "Uropeltidae"
## [22] "Boidae" "Aniliidae" "Tropidophiidae"
## [25] "Iguanidae" "Agamidae" "Chamaeleonidae"
## [28] "Xenosauridae" "Helodermatidae" "Anniellidae"
## [31] "Anguidae" "Varanidae" "Lanthanotidae"
## [34] "Shinisauridae" "Rhineuridae" "Bipedidae"
## [37] "Amphisbaenidae" "Trogonophiidae" "Blanidae"
## [40] "Cadeidae" "Lacertidae" "Gymnophthalmidae"
## [43] "Teiidae" "Scincidae" "Xantusiidae"
## [46] "Cordylidae" "Gerrhosauridae" "Eublepharidae"
## [49] "Phyllodactylidae" "Gekkonidae" "Sphaerodactylidae"
## [52] "Diplodactylidae" "Pygopodidae" "Carphodactylidae"
## [55] "Dibamidae" "Sphenodontidae"
```

## Mapping Tb trait onto tree

Load in trait data, and assign the family names (column 1) as row.names

```
lizards <- read.csv("Clusella Trullas Review Table 1.csv", row.names=1)
lizards
```

```
##           Tb TbSD TbN   Tp TpSD TpN
## Agamidae    33.9 3.50  23 35.2  3.3  20
## Amphisbaenidae 23.6  NA   1 21.3  0.1   2
## Anguidae    27.4 5.20   6 30.0   NA   2
## Anniellidae  21.0  NA   1 24.5   NA   1
## Carphodactylidae 23.4 2.95  5 26.1  1.6   2
## Chamaeleonidae 28.0 3.70 10 31.1  2.4  11
## Cordylidae   28.4 0.90   5 32.7  0.9   7
## Corytophanidae 30.8 4.50   3  NA   NA   NA
```

```
## Crotophytidae      37.8 0.30   3 33.5   NA   1
## Diplodactylidae    25.4 5.10  15 31.9   3.6   6
## Eublepharidae      26.1 2.10   5 27.0   3.4   9
## Gekkonidae          28.5 4.90  13 29.8   3.3  15
## Gerrhosauridae     32.2 1.90   3  NA    NA   NA
## Gymnophthalmidae   27.0 2.60   9  NA    NA   NA
## Helodermatidae     29.8 0.60   2 28.7   NA   1
## Iguanidae           37.5 1.80   7 35.8   2.6   7
## Lacertidae          34.9 2.90  31 34.1   1.7  24
## Lanthanotidae      28.0  NA    1  NA    NA   NA
## Leiocephalidae     36.3  NA    1  NA    NA   NA
## Liolaemidae         33.8 2.40  74 34.3   2.1  13
## Opluridae           38.2 2.20   2  NA    NA   NA
## Phrynosomatidae     34.9 2.10  59 35.1   2.2  20
## Phyllodactylidae    25.7 4.40  11 31.5   1.9   5
## Polychrotidae       29.4 2.60  44 29.3   2.7  10
## Pygopodidae         24.9  NA    1  NA    NA   NA
## Scincidae           31.4 4.00  72 31.0   3.3  58
## Sphaerodactylidae   30.4 4.20   9  NA    NA   NA
## Sphenodontidae      14.5  NA    1  NA    NA   NA
## Teiidae             37.7 2.30  36 37.0   2.2   7
## Trogonophiidae      22.0  NA    1 22.5   NA   1
## Tropiduridae        33.6 2.70  21 34.6   1.6  11
## Varanidae           35.0 2.70  19 35.0   1.6   8
## Xantusiidae         23.6 3.10   4 28.9   2.0   3
## Xenosauridae        23.0 1.90   4  NA    NA   NA
```

```
sort(tree$tip.label)
```

```
## [1] "Acrochordidae"      "Agamidae"           "Amphisbaenidae"
## [4] "Anguidae"           "Aniliidae"          "Anniellidae"
## [7] "Anomalepididae"     "Anomochilidae"     "Bipedidae"
## [10] "Blaniidae"          "Boidae"             "Bolyeridae"
## [13] "Cadeidae"           "Carphodactylidae"  "Chamaeleonidae"
## [16] "Colubridae"         "Cordylidae"         "Cylindrophidae"
## [19] "Dibamidae"          "Diplodactylidae"    "Dipsadidae"
## [22] "Elapidae"           "Eublepharidae"     "Gekkonidae"
## [25] "Gerrhopilidae"      "Gerrhosauridae"     "Gymnophthalmidae"
## [28] "Helodermatidae"     "Homalopsidae"       "Hydrophiidae"
## [31] "Iguanidae"          "Lacertidae"         "Lamprophiidae"
## [34] "Lanthanotidae"      "Leptotyphlopidae"   "Loxocemidae"
## [37] "Pareatidae"         "Phyllodactylidae"   "Pygopodidae"
## [40] "Pythonidae"         "Rhineuridae"        "Scincidae"
## [43] "Shinisauridae"      "Sphaerodactylidae"  "Sphenodontidae"
## [46] "Teiidae"            "Trogonophiidae"     "Tropidophiidae"
## [49] "Typhlopidae"        "Uropeltidae"        "Varanidae"
## [52] "Viperidae"          "Xantusiidae"        "Xenodermatidae"
## [55] "Xenopeltidae"       "Xenosauridae"
```

```
length(tree$tip.label)
```

```
## [1] 56
```

```
rownames(lizards)
```

```
## [1] "Agamidae"           "Amphisbaenidae"     "Anguidae"
```

```
## [4] "Anniellidae"      "Carphodactylidae" "Chamaeleonidae"
## [7] "Cordylidae"       "Corytophanidae"   "Crotaphytidae"
## [10] "Diplodactylidae"  "Eublepharidae"    "Gekkonidae"
## [13] "Gerrhosauridae"   "Gymnophthalmidae" "Helodermatidae"
## [16] "Iguanidae"        "Lacertidae"       "Lanthanotidae"
## [19] "Leiocephalidae"   "Liolaemidae"      "Opluridae"
## [22] "Phrynosomatidae"  "Phyllodactylidae" "Polychrotidae"
## [25] "Pygopodidae"      "Scincidae"        "Sphaerodactylidae"
## [28] "Sphenodontidae"   "Teiidae"          "Trogonophiidae"
## [31] "Tropiduridae"     "Varanidae"        "Xantusiidae"
## [34] "Xenosauridae"
```

```
nrow(lizards)
```

```
## [1] 34
```

We have 56 taxa in the phylogeny, but only 34 data points in file for temperature data. Lepidosauria include lizards, snakes, tuatara, whereas the data file from Clusella-Trullas et al (2008) focused on lizard families, but has multiple subtaxa within the Iguanidae, so the intersection of the two data sets will be smaller than 34, and we will lose data for these extra taxa.

Create a variable called **both** that describes which taxa are found in both:

```
both <- intersect(tree$tip.label, rownames(lizards))
both
```

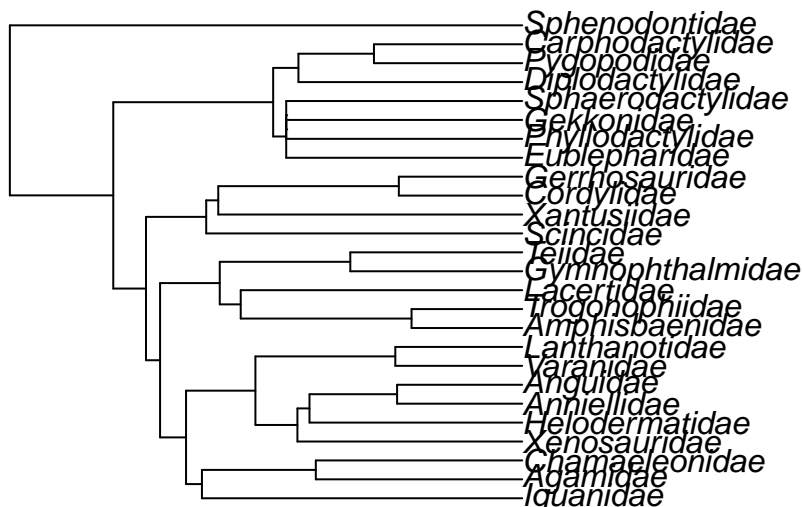
```
## [1] "Iguanidae"      "Agamidae"        "Chamaeleonidae"
## [4] "Xenosauridae"   "Helodermatidae"  "Anniellidae"
## [7] "Anguidae"       "Varanidae"       "Lanthanotidae"
## [10] "Amphisbaenidae" "Trogonophiidae"  "Lacertidae"
## [13] "Gymnophthalmidae" "Teiidae"         "Scincidae"
## [16] "Xantusiidae"    "Cordylidae"      "Gerrhosauridae"
## [19] "Eublepharidae"  "Phyllodactylidae" "Gekkonidae"
## [22] "Sphaerodactylidae" "Diplodactylidae" "Pygopodidae"
## [25] "Carphodactylidae" "Sphenodontidae"
```

Create a tree that is matched to the data by only selecting those found in both:

```
tree.matched <- root(drop.tip(tree, setdiff(tree$tip.label, both)), outgroup="Sphenodontidae")
tree.matched
```

```
##
## Phylogenetic tree with 26 tips and 25 internal nodes.
##
## Tip labels:
## Iguanidae, Agamidae, Chamaeleonidae, Xenosauridae, Helodermatidae, Anniellidae, ...
## Node labels:
## , 127, 110, 88, 64, 54, ...
##
## Rooted; includes branch lengths.
```

```
plot(tree.matched)
```



Data in the lizards data frame is not in the same order as the tips from tree, so create a data.frame, **dat** that extracts only the data that corresponds to the taxa in **both**:

```
dat <- lizards[both, ]
rownames(dat)
```

```
## [1] "Iguanidae"      "Agamidae"       "Chamaeleonidae"
## [4] "Xenosauridae"   "Helodermatidae" "Anniellidae"
## [7] "Anguillidae"    "Varanidae"      "Lanthanotidae"
## [10] "Amphisbaenidae" "Trogonophiidae" "Lacertidae"
## [13] "Gymnophthalmidae" "Teiidae"        "Scincidae"
## [16] "Xantusiidae"    "Cordylidae"     "Gerrhosauridae"
## [19] "Eublepharidae" "Phyllodactylidae" "Gekkonidae"
## [22] "Sphaerodactylidae" "Diplodactylidae" "Pygopodidae"
## [25] "Carphodactylidae" "Sphenodontidae"
```

## Plot continuous trait onto phylogeny

First, create a vector corresponding to the trait Tb and assign the names to this vector:

```
Tb<-dat$Tb
names(Tb)<-tree.matched$tip.label
```

Use the contMap function to create an object that is your plot, but we need to make further adjustments below, so set plot=F initially.

```
objTb<-contMap(tree.matched, Tb, plot=F, type="fan", invert=T, res=300,
               lims=c(22,38))
```

Invert refers to the colour palette direction. We set this to FALSE to change the direction from the normal (warm temperatures will then be a warm colour).

The res value above sets the resolution of the colour mapping onto the continuous trait. A higher res will create a smoother gradient, but colour palettes are sometimes simply a limited number of values and we need to upsample any palette we use to the number of required colour values in the continuous trait.

In this case objTb\$cols has a length of 1001, so we need to create a colour palette that is that length by filling in values derived from the selected colour palette.

```

phylopalette<-ironbowpal
n<-length(objTb$cols)
paln<-length(phylopalette)
ind<-floor(seq(1, paln, paln/(n+floor(n/paln))))
objTb$cols[1:n]<-phylopalette[ind]

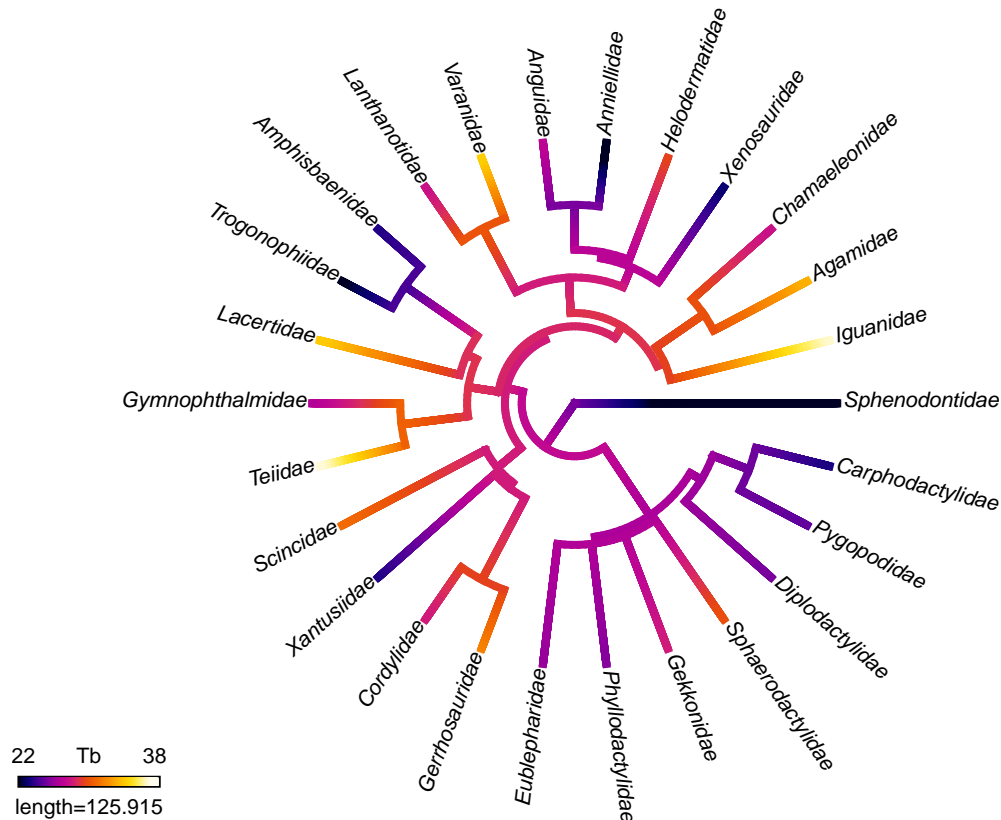
```

Then plot the Phylogram of Tb onto the Lizard Family phylogeny, either using a fan or a phylogram facing rightwards:

```

plot(objTb, type="fan", fsize=0.7, outline=F, leg.txt="Tb", offset=1,
Vars=T)

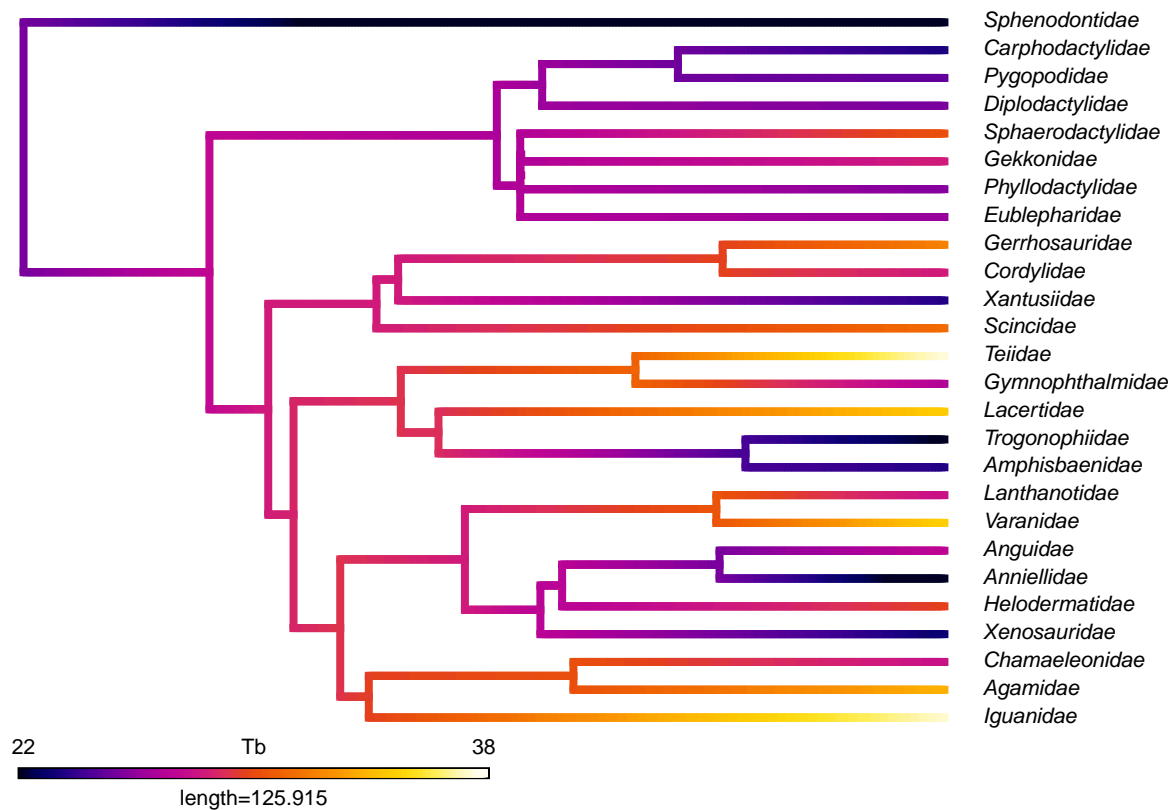
```



```

plot(objTb, type="phylogram", direction="rightwards", fsize=0.7, outline=F, leg.txt="Tb", offset=1,
Vars=T)

```



## Warning

This field is not my area of expertise, so use the above example merely as an introduction to this topic. Feel free to make suggestions or improvements.

## Reference

Data on Tb were obtained from Clusella-Trullas et al 2008:

Clusella-Trullas, S., J. S. Terblanche, T. M. Blackburn, and S. L. Chown. 2008. Testing the thermal melanism hypothesis: A macrophysiological approach. *Functional Ecology* 22:232–238. doi: 10.1111/j.1365-2435.2007.01377.x.