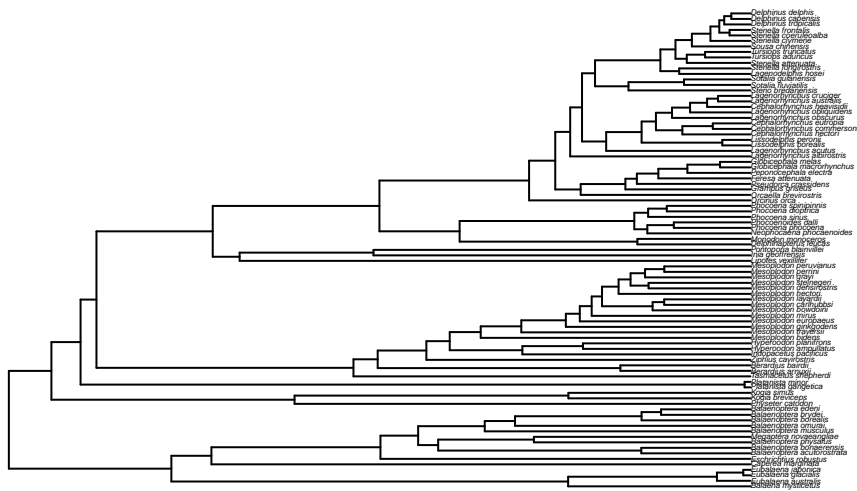# AncCond Practice

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Introduction

First let's load in an example phylogeny.

```
library(phytools)
```

```
## Loading required package: ape
```

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

```
library(diversitree)
library(geiger)
tree <- read.tree(file = 'Data/whales.tre')
plot(tree, cex = 0.25)
```

 That's a lot of whales!

Wonder how big they are, let's import thier weights.

```
load(file = 'Data/exampleSizeData.RData')
length(sizedata)
```
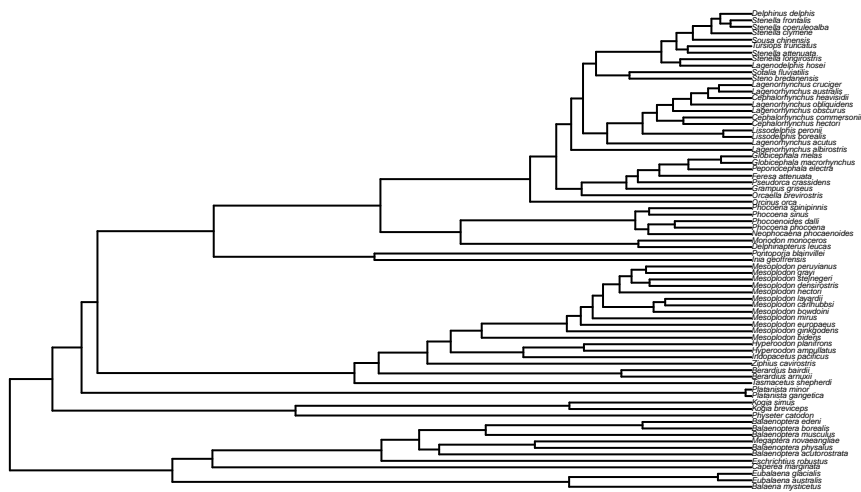
```
## [1] 74
```

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

```
## [1] 87
```

We dont have size data for all of the species!
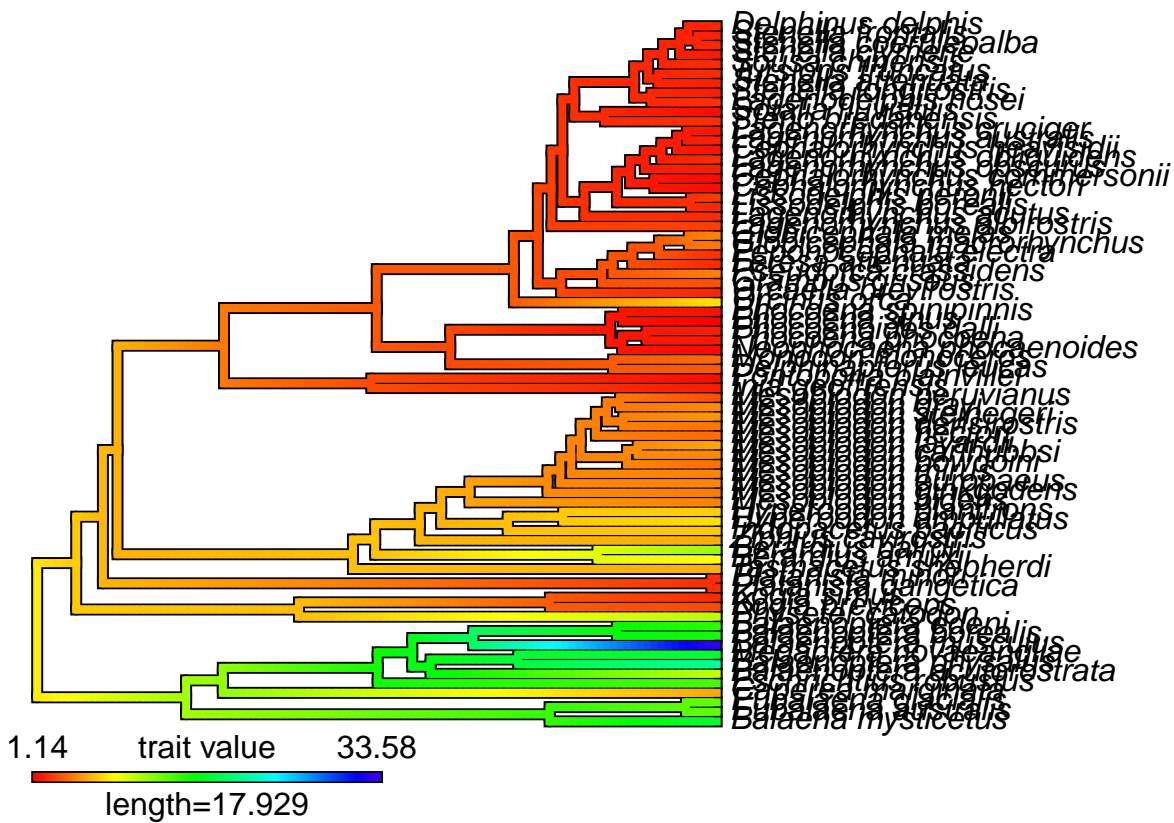
lets fix that

```
tree <- keep.tip(tree, names(sizedata))
plot(tree, cex = 0.25)
```

The sizes are our continious trait.

Lets perform an ancestral state estimation on the size data of extant whales.
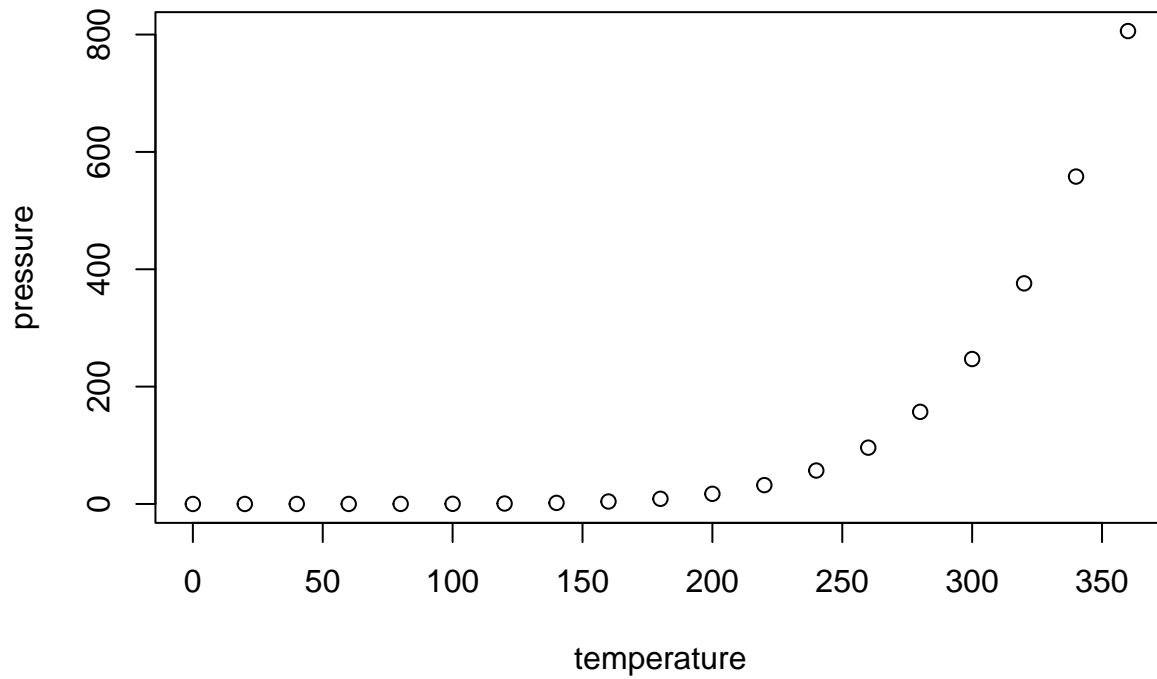
```
contMap(tree,sizedata, cex = 0.05)
```



```
# , ftype = 'off', legend = F, lims = c(.24,2), plot = F)
# n<-length(smp$cols)
# smp$cols[1:n]<-rainbow(n, end = 4/6)
# plot(smp, legend = F,ftype = 'off')
```

Including Plots

You can also embed plots, for example:

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.