# Litter Size Evolution

Consensus tree extracted from an Upham et al. paper (Jetz lab)
Data: 1006 out of 2278 species

```
## Warning in sqrt(1/out$hessian): NaNs produced
```

```
##
## 4.86 5.94 5.17 4.99 4.99 4.86 4.99 6.15 5.34 5.53 5.28 5.29 4.86 5.15 5.00 4.99
##
## 6.00 5.47 5.04 5.36 4.86 5.18 4.86 5.30 4.91 6.27 5.00 5.90 6.24 6.97 5.34 5.00
##
## 4.95 4.77 5.44 7.50 5.18 4.76 5.99 4.86 6.28 8.47 5.48 7.14 4.99 5.71 6.06 5.20
##
## 8.99 8.79 9.01 6.55 5.01 4.83 5.37 6.90 5.60 7.77 5.83 5.51 6.14 4.99 5.06 5.54
##
## 5.16 4.73 5.93 8.10 8.00 5.34 5.49 7.89 6.80 5.62 7.50 4.76 5.25 5.10 6.39 6.86
##         82   83   84   85   86   87   88   89   90   91   92   93   94   95   96
## 4.80 5.35 5.34 5.39 5.17 5.00 5.37 5.33 5.27 5.40 5.36 5.38 5.44 5.37 5.35 5.17
##   97   98   99  100  101  102  103  104  105  106  107  108  109  110  111  112
## 5.12 5.03 5.68 5.36 5.26 5.90 5.88 5.65 5.44 5.14 5.11 5.45 5.52 5.71 5.68 5.42
##  113  114  115  116  117  118  119  120  121  122  123  124  125  126  127  128
## 5.82 5.98 6.07 5.03 4.94 5.77 5.85 5.38 5.40 6.00 6.65 6.41 6.35 6.82 6.21 6.31
##  129  130  131  132  133  134  135  136  137  138  139  140  141  142  143  144
## 6.07 6.01 8.60 8.83 5.77 5.84 5.84 5.89 5.79 5.88 5.67 5.39 5.75 5.94 5.97 6.04
##  145  146  147  148  149  150  151  152  153  154  155  156  157  158  159  160
## 5.94 5.63 5.71 5.94 5.59 5.45 5.42 6.08 6.10 5.97 6.01 6.18 6.98 5.95 5.66 5.72
##  161
## 5.35
```
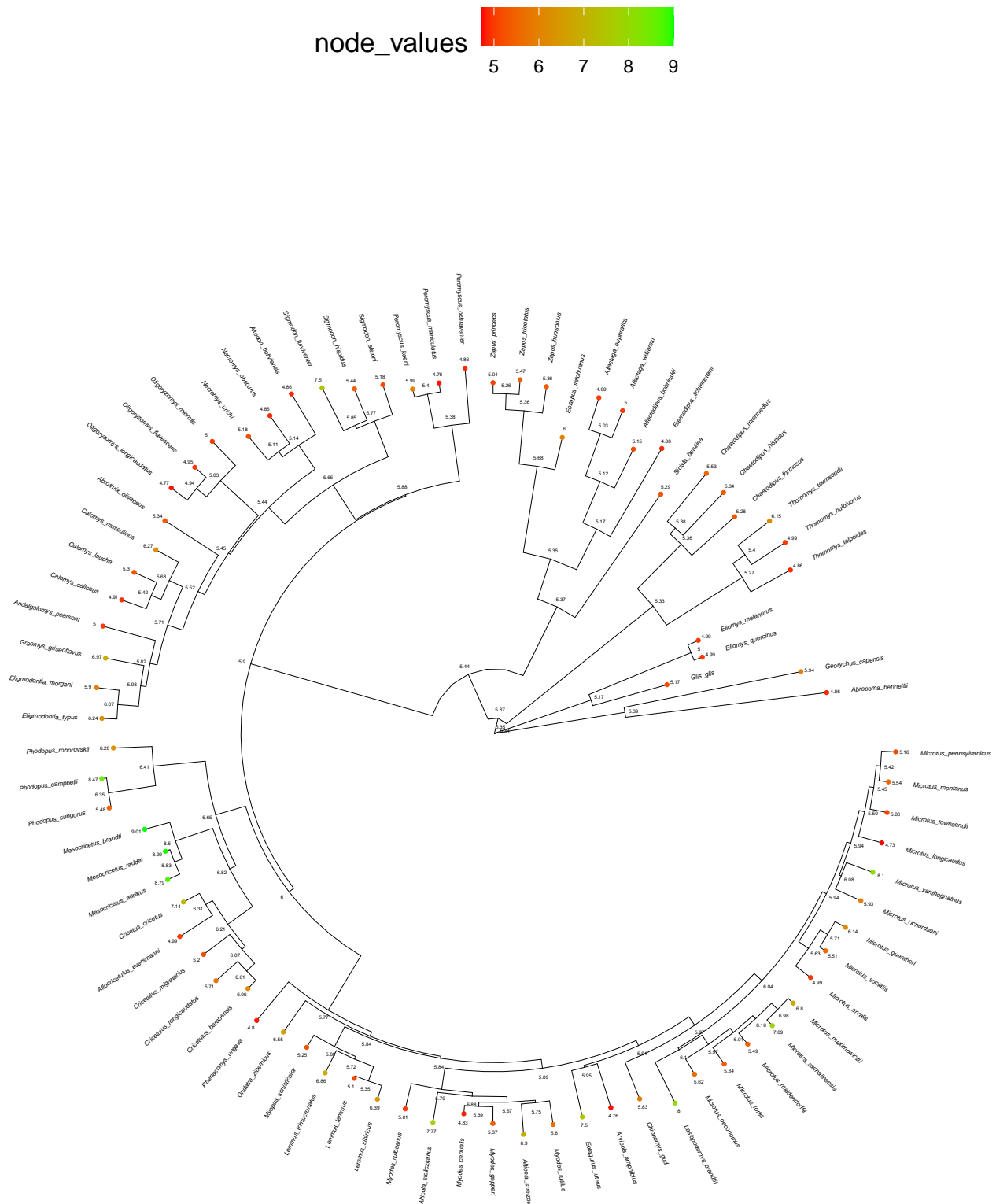
This gives us a variety of information about the ancestral character reconstructions:

- `$ace` contains the reconstructed ancestral character states. There is one value per internal node, and they are in the order that the internal nodes are numbered in.
- `$sigma2` is the estimate of the Brownian Motion parameter.
- `$CI95` are the confidence intervales on the ancestral character state reconstructions.