

## Litter Size and Menstruation 12/3 update

Data: 1006 out of 2278 species (all species within Rodentia that I have data for) Plotted: 819 species are phylogenetically resolved, thus plotted here Consensus tree extracted from an Upham et al. paper (Jetz lab)

This version includes all families and all species that I can find. I labeled suprafamilies and a few common families (Acomys, Mus, Rattus).

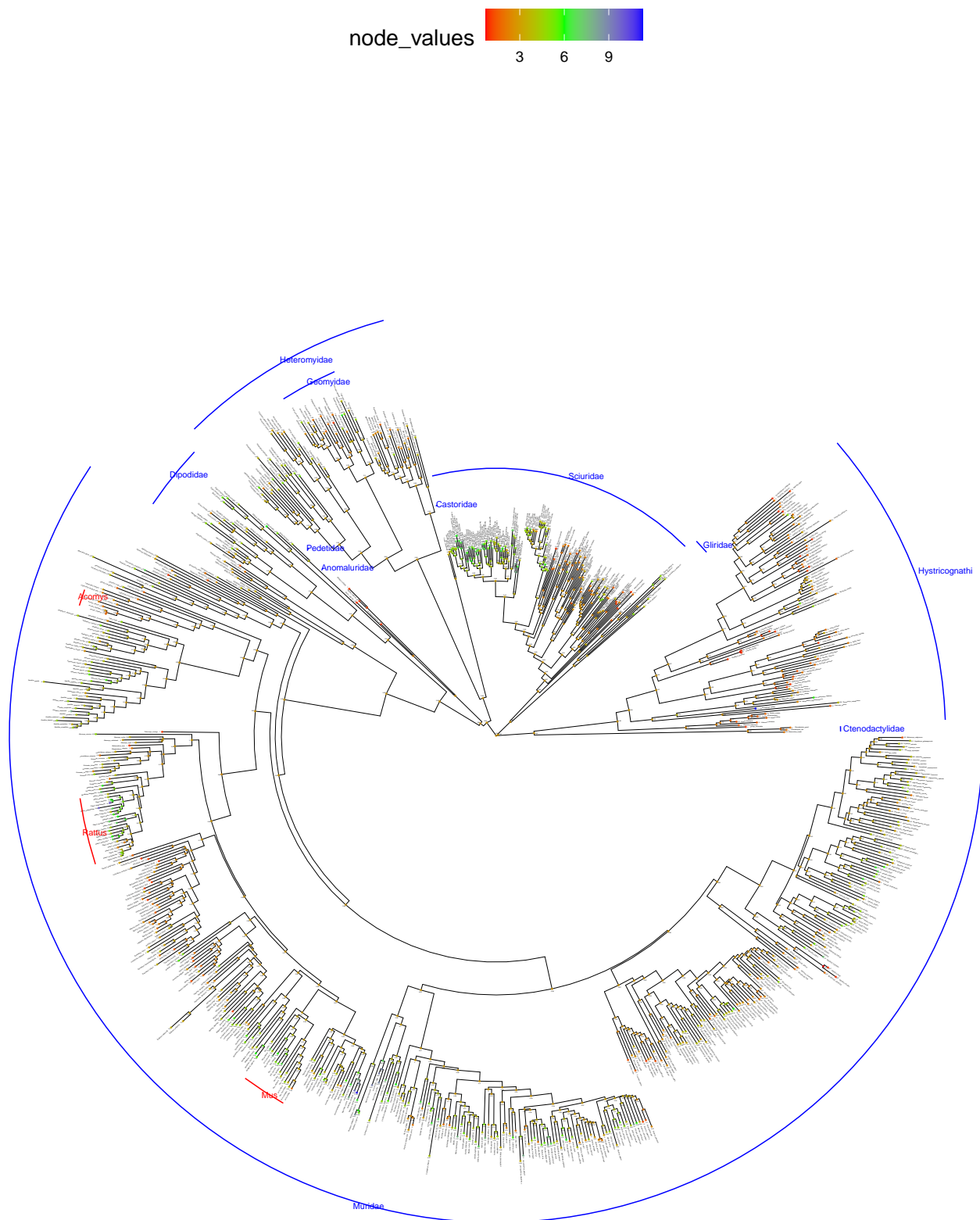
The labeling are based on this paper. There is a minor taxonomy conflict, the relationship between Heteromyidae and Geomyidae outlined by the paper is different from this tree I used. I am leaning towards the tree, as it was published in 2019, time calibrated and used 31 genes instead of 2 to construct.

Method: both REML and PIC, metadata attached at the end. The confidence interval for REML is quite wide. One of the Brownian motion parameter is  $\sigma^2$ , and I am still trying to figure out what that means. The two methods give very different results.

Thoughts: The earlier ancestors all have an average litter size of 2.88 or 2.89, and then evolve either into clades with higher or smaller litter size. I don't think this necessarily disqualify our hypothesis,

The sampling is not uniform, which means the constructed ancestral values lean towards available data.

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



Metadata about REML reconstruction:

- $\sigma^2$  is the estimate of the Brownian Motion parameter.
- $CI_{95}$  are the confidence intervals on the ancestral character state reconstructions.

Residual log-likelihood: -5664.2874262

Sigma2: 997.3621519, NaN

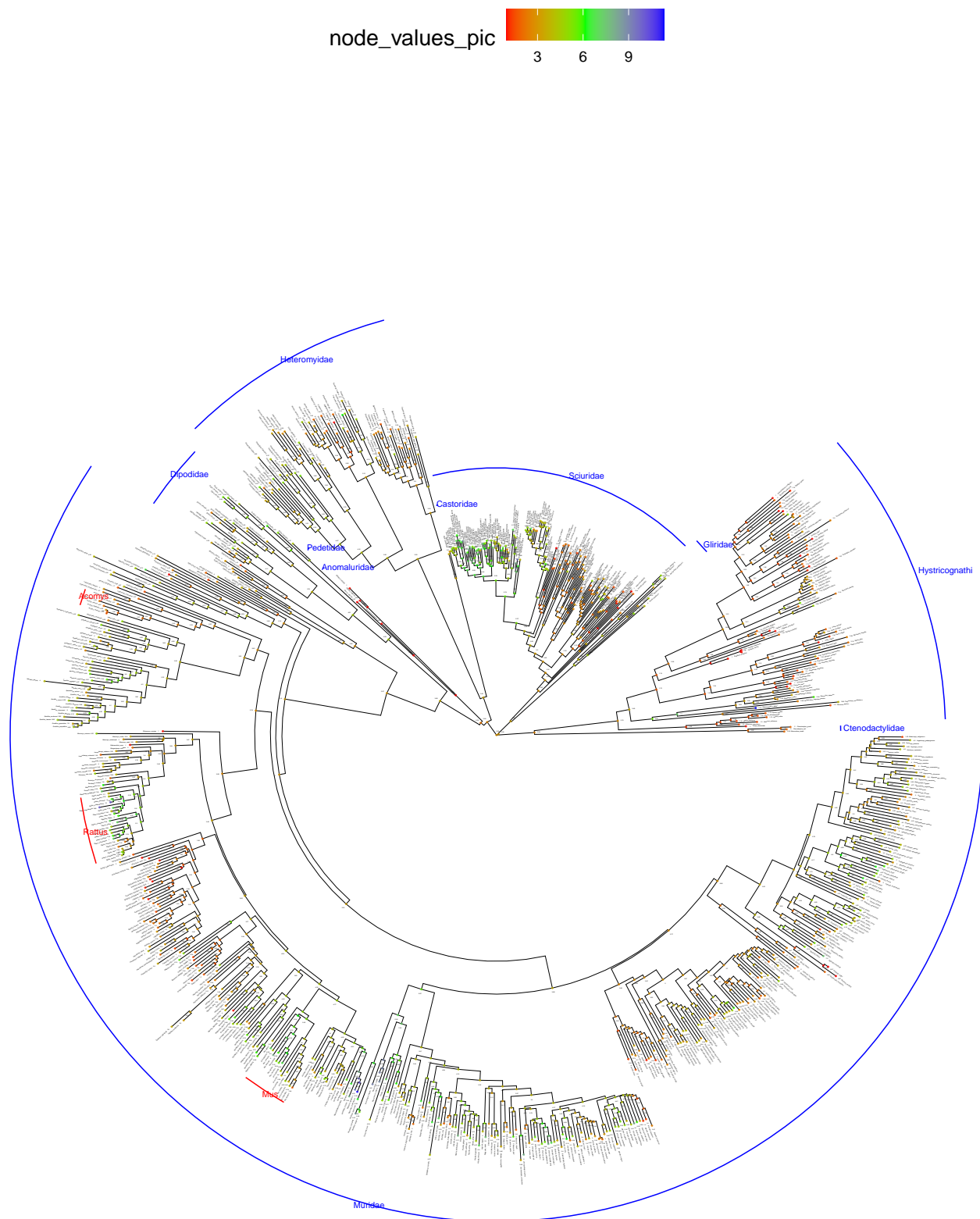
CI95:

```
kable(litter_ancestral$CI95[1:10, ], col.names = c('lower bound', 'upper bound'), caption = "sample REML confidence interval")
```

Table 1: sample REML confidence interval

	lower bound	upper bound
820	-11.170629	16.942259
821	-11.075762	16.847165
822	-14.542507	20.307337
823	-11.577820	17.328727
824	-10.482808	16.261825
825	-9.168933	14.914383
826	-9.050760	14.727896
827	-7.636693	11.102322
828	-1.464976	3.070575
829	-9.671487	15.420109

Ancestral Reconstruction using Phylogenetic Independent Contrast



Metadata about PIC reconstruction:

Residual log-likelihood:

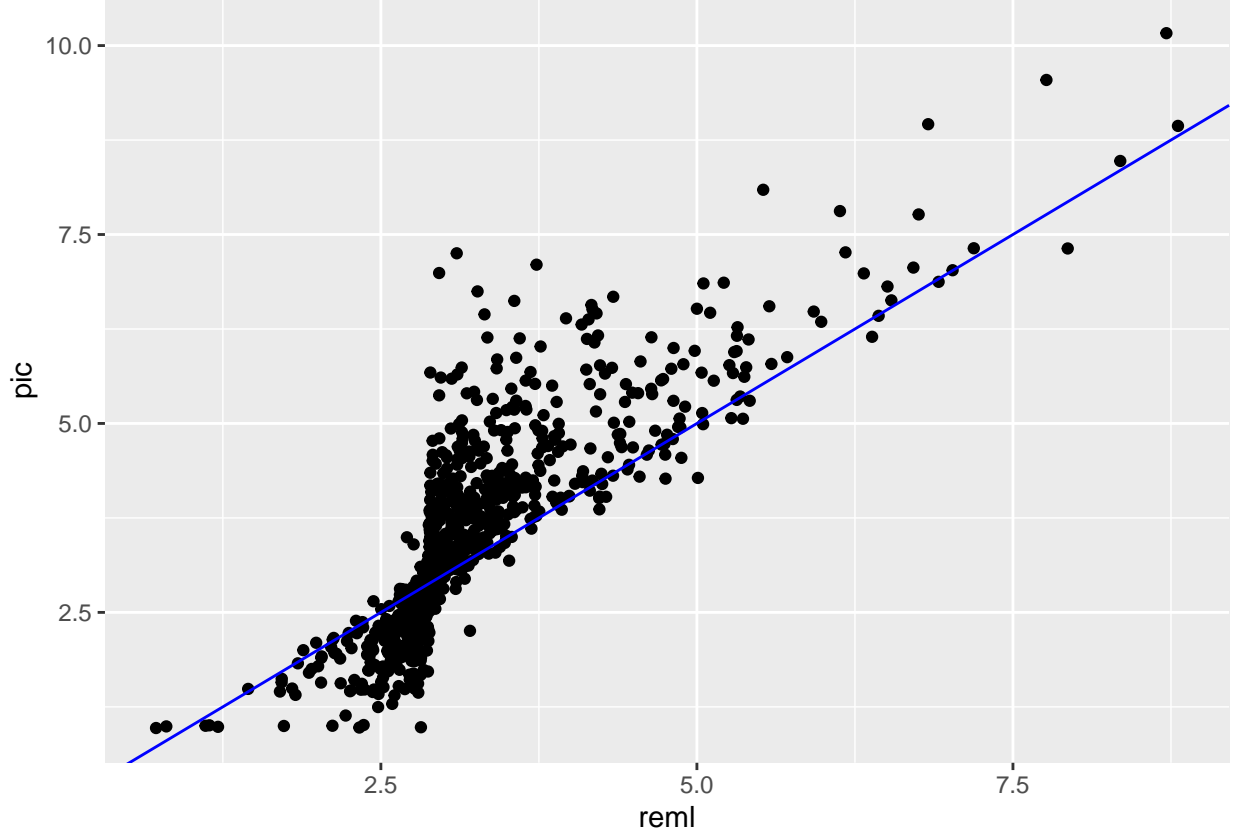
Sigma2:

CI95:

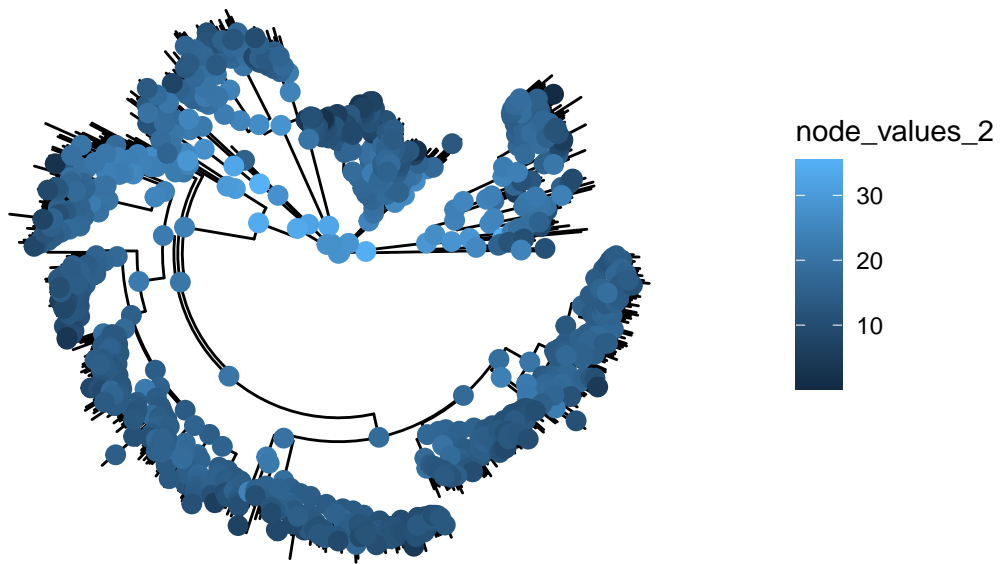
Table 2: sample PIC confidence interval

	lower bound	upper bound
820	2.0001156	3.771613
821	1.8748948	4.297813
822	0.8110138	4.270835
823	1.7176718	3.872031
824	2.4806467	4.499565
825	0.7682447	2.667815
826	0.7397868	2.736672
827	0.3333333	1.660659
828	0.8454750	1.137609
829	1.1800702	3.378577

Plotting the values of PIC over REML – RMEL definitely gives a narrower range of ancestral litter size.



Plotting the confidence interval on the tree – the further back in time, the larger the CI. REML



PIC

