

TABLE 3: The posterior predictive analysis of the penguin data for branch length and tree shape statistics indicating no significant difference in the posterior and posterior predictive tree distributions for model 2 (in Table 2)

Description	Notation	p_B -value ^{a,b}
Branch length distribution statistics		
The total length of all branches in the tree	T	0.83
The ratio of the length of the subtree induced by extant taxa and the total tree length	ρ_{trunk}^T	0.33
Genealogical Fu and Li's D calculated as the normalized difference between external branch length in the tree with suppressed sampled ancestor nodes and total tree length.	D_F	0.5
The time of the MRCA of all taxa	t_{MRCA}	0.57
The time of the MRCA of all extant taxa	t_{EMRCA}	0.46
Tree shape statistics		
The maximum number of bifurcation nodes between a bifurcation node and the leaves summed over all bifurcation nodes except for the root	B_1	0.75
Coless's tree imbalance index calculated as the difference between the numbers of leaves on two sides of a node summed over all internal bifurcation nodes and divided by the total number of leaves	I_c	0.28
The number of cherries (two terminal nodes forming a monophyletic clade, sampled ancestors are suppressed)	C_n	0.54
The number of sampled ancestors	SA	0.26

^a A p_B value is the proportion of times a given test statistic for the simulated tree exceeds the value of that statistic for the tree from the posterior