

**S4 Table. Comparison of bias estimates across methods in large families with variation (i.e. not all ergative or all non-ergative), using AUTOTYP taxonomies**

	majority value	majority proportion	Set-based		Tree-based			
			$P_{\text{Binom. test}}$	$P_{\text{LR test}}$	ML	ML	ML	MCMC
					fitDiscrete	BayesTraits	BayesTraits	log BF
					$P_{\text{LR test}}$	$P_{\text{LR test}}$		
Oceanic	A	0.889	0.001	0.311	0.120	0.120	8.202	
Cariban	none	NA	0.500	0.705	0.705	0.705	-0.972	
Chimbu-Wahgi	none	NA	0.145	0.434	0.192	0.192	0.521	
Eastern Highlands	none	NA	0.363	0.259	0.482	0.482	-0.502	
Finisterre-Huon	none	NA	0.773	0.705	0.705	0.705	-0.563	
Binanderean	none	NA	0.500	0.654	0.654	0.654	-0.625	
Gunwingguan	none	NA	0.656	1.000	1.000	1.000	-0.947	
Indo-European	A	0.770	0.000	0.000	0.000	0.000	19.098	
Koian	none	NA	0.109	0.547	0.198	0.198	0.685	
Madang	A	0.875	0.035	0.330	0.212	0.212	2.475	
Nakh-Daghestanian	none	NA	0.868	0.369	0.369	0.369	-0.593	
Pama-Nyungan	none	NA	0.734	0.617	0.617	0.617	-1.149	
Pano-Tacanan	none	NA	0.891	0.410	0.410	0.410	-0.496	
Sino-Tibetan	none	NA	0.944	0.147	0.147	0.147	0.525	

The results from a Bayes Factor analysis of MCMC models of transitions rates agree with the results from a simple binomial tests. The only divergences in the results is found with ML models in the case of the Oceanic and Madang families.