

RH: Characters correlation

# **Influence of different modes of morphological character correlation on phylogenetic tree inference**

## **Supplementary material 3 - Additional results**

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SIGNAL TO NOISE RATIO

TREE RESOLUTION

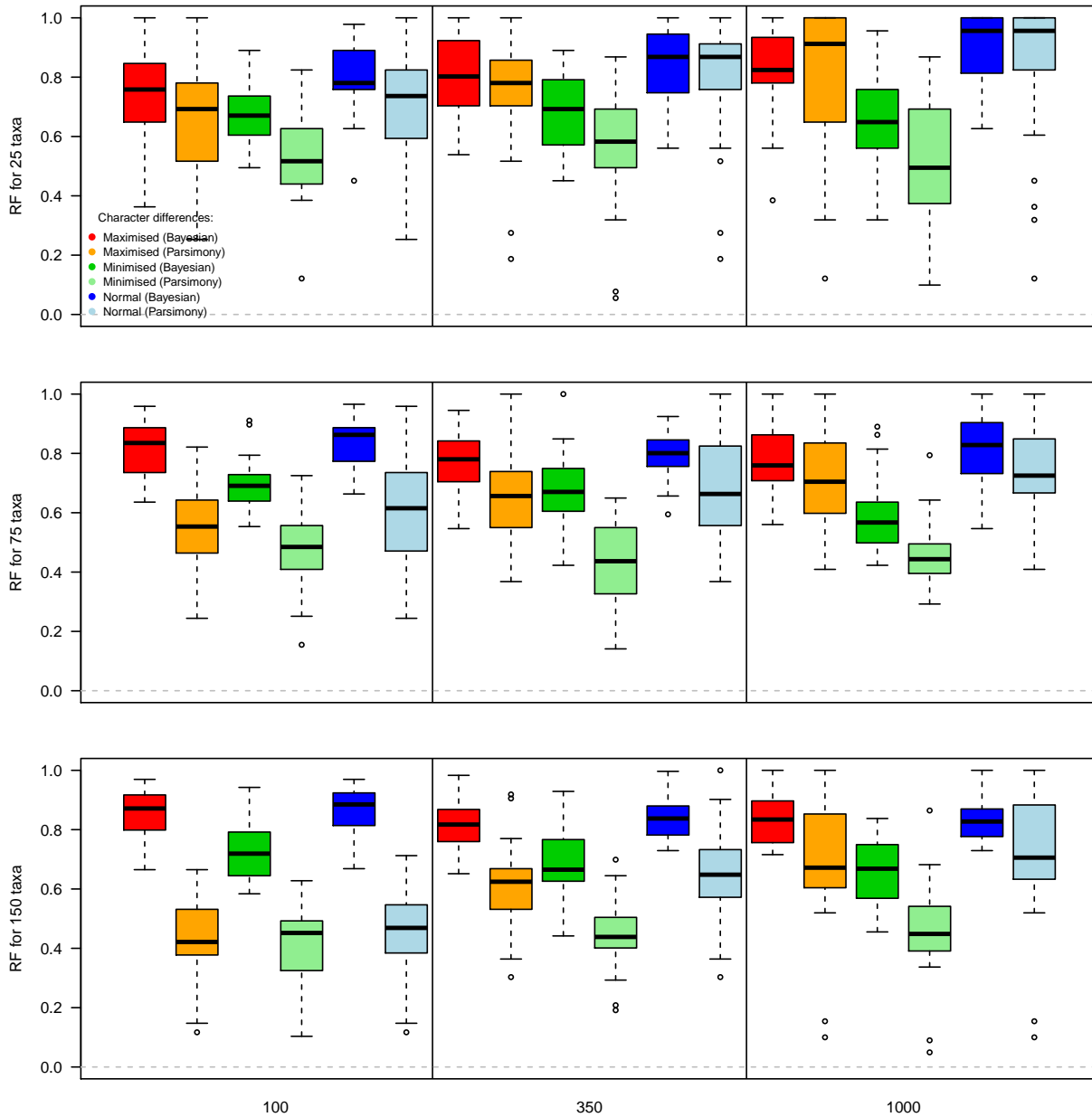


Figure 1: Effect of Character Difference on recovering the “random” topology. The y axis represents the Normalised Tree Similarity using Robinson-Foulds distance for matrices with 25, 75 and 150 taxa from top to bottom respectively. The x axis represents the different Character Difference scenarios and tree inference method with the Maximised Character Difference in Bayesian (red) and under Maximum Parsimony (orange), the Minimised Character Difference in Bayesian (dark green) and under Maximum Parsimony (light green) and the Randomised Character Difference in Bayesian (dark blue) and under Maximum Parsimony (light blue) for matrices of 100, 350 and 1000 characters in the panels from left to right.

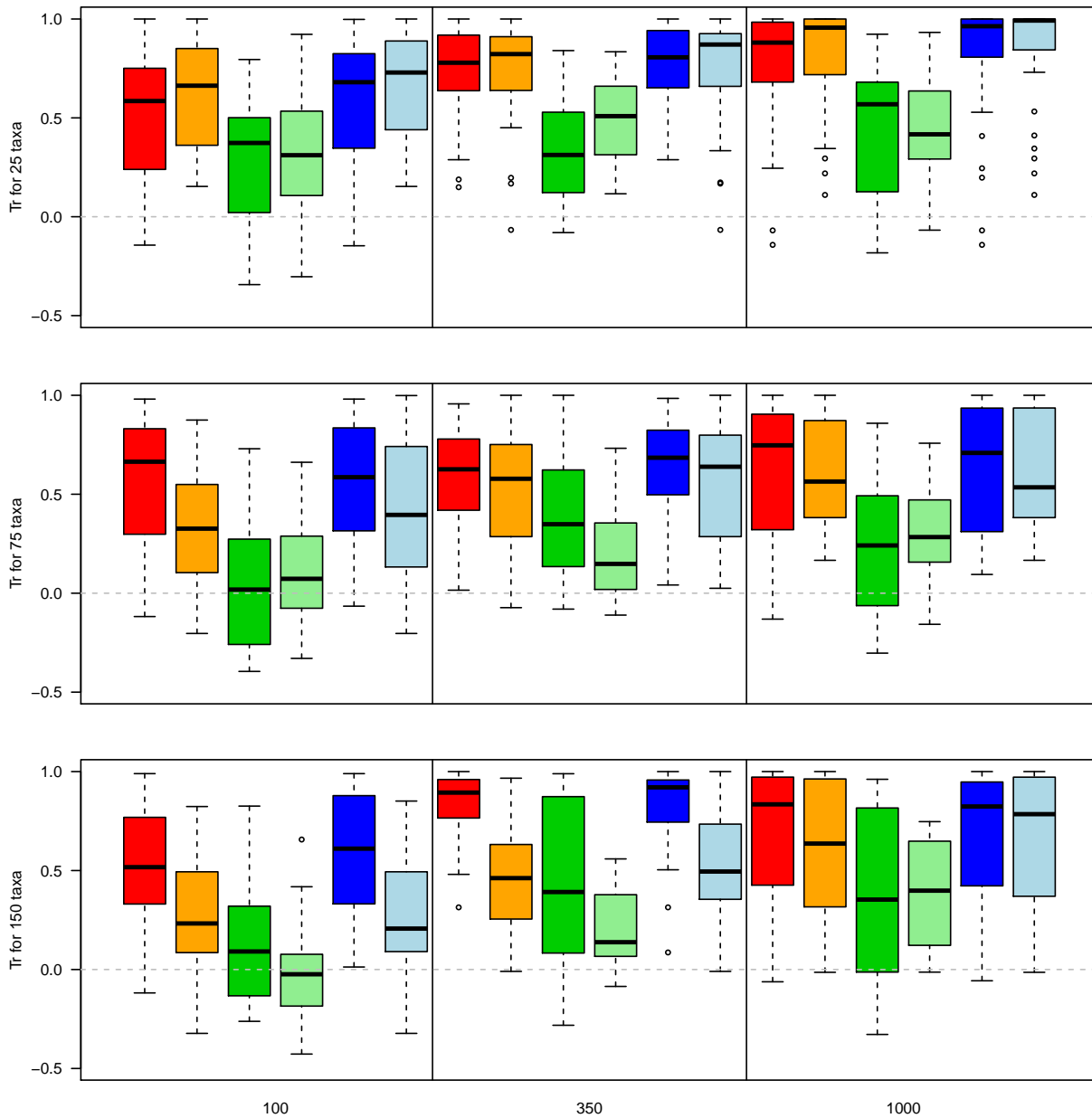


Figure 2: Effect of Character Difference on recovering the “random” topology. The axis are identical to figure 1 but y axis represents the Normalised Tree Similarity using Triplets distance.

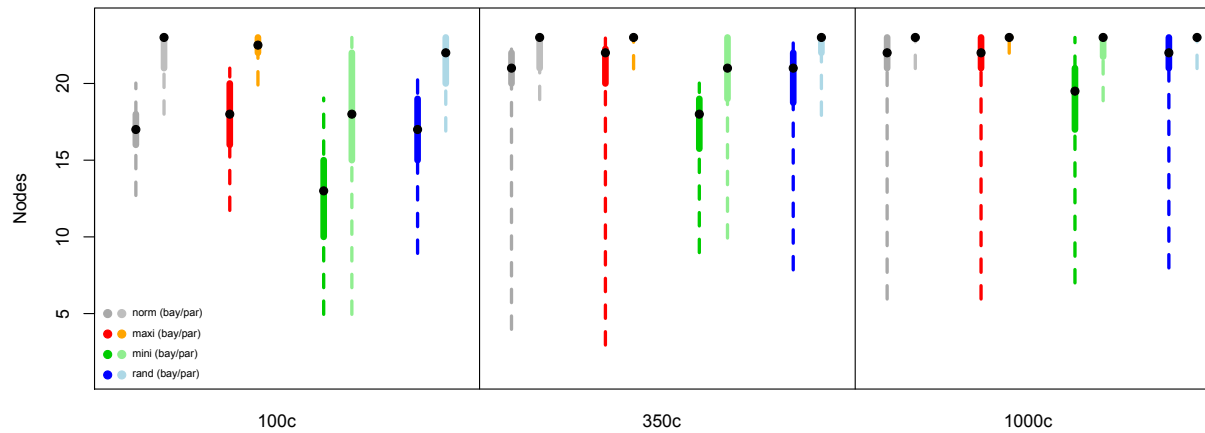


Figure 3: Node resolution for the trees with 25 taxa. The y axis represents the number of nodes in the tree. The horizontal lines are the distributions of resolved nodes per trees per number of characters (100c, 350c and 1000c), per matrix type (normal: norm, maxi: maximised, mini: minimised, rand: randomised - respectively in grey, red, green and blue) and per method (bay: Bayesian and par: maximum parsimony - respectively in dark and light colours). The black dots, thick solid lines and dashed lines represent respectively the median, 50% CI and 95% CI of the distribution.

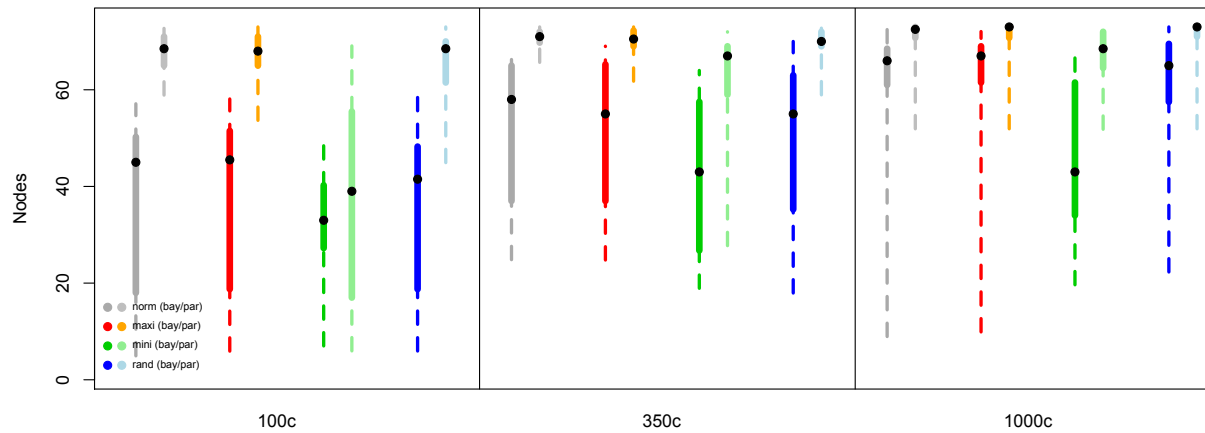


Figure 4: Node resolution for the trees with 75 taxa. The y axis represents the number of nodes in the tree. The horizontal lines are the distributions of resolved nodes per trees per number of characters (100c, 350c and 1000c), per matrix type (normal: norm, maxi: maximised, mini: minimised, rand: randomised - respectively in grey, red, green and blue) and per method (bay: Bayesian and par: maximum parsimony - respectively in dark and light colours). The black dots, thick solid lines and dashed lines represent respectively the median, 50% CI and 95% CI of the distribution.

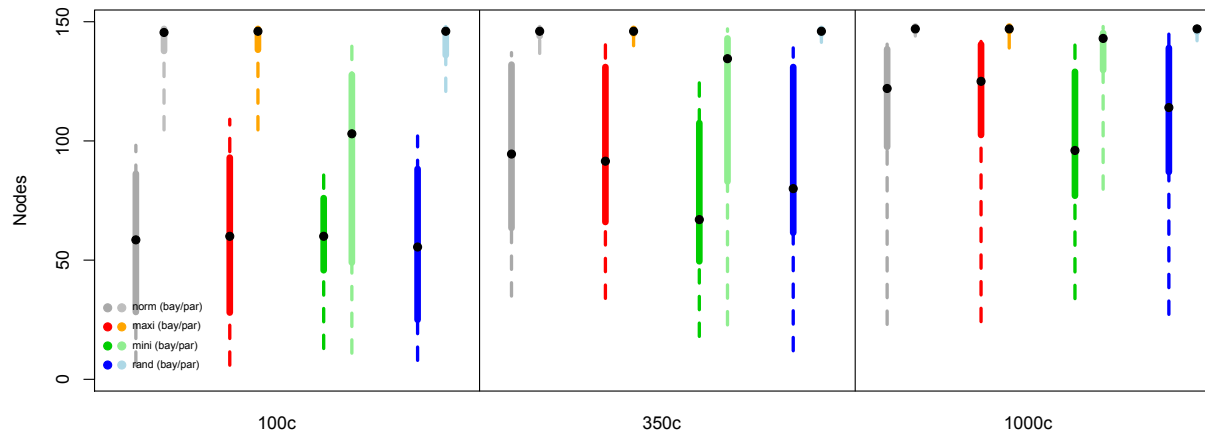


Figure 5: Node resolution for the trees with 150 taxa. The y axis represents the number of nodes in the tree. The horizontal lines are the distributions of resolved nodes per trees per number of characters (100c, 350c and 1000c), per matrix type (normal: norm, maxi: maximised, mini: minimised, rand: randomised - respectively in grey, red, green and blue) and per method (bay: Bayesian and par: maximum parsimony - respectively in dark and light colours). The black dots, thick solid lines and dashed lines represent respectively the median, 50% CI and 95% CI of the distribution.

## POOLED RESULTS DISTRIBUTIONS

comp	metric	scenario	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
Best	RF	maxi	0.407	0.802	0.956	0.885	1.000	1.000
		mini	0.076	0.471	0.605	0.594	0.726	0.956
		rand	0.100	0.656	0.792	0.762	0.894	1.000
	Tr	maxi	-0.031	0.749	0.964	0.839	1.000	1.000
		mini	-0.473	0.050	0.303	0.312	0.592	0.980
		rand	-0.323	0.370	0.713	0.628	0.926	1.000
Null	RF	maxi	0.100	0.619	0.758	0.731	0.868	1.000
		mini	0.049	0.457	0.584	0.574	0.705	1.000
		norm	0.100	0.656	0.792	0.762	0.894	1.000
	Tr	maxi	-0.323	0.338	0.651	0.597	0.889	1.000
		mini	-0.427	0.027	0.276	0.284	0.535	1.000
		norm	-0.323	0.370	0.713	0.628	0.926	1.000

Table 1: Summary statistics of the normalised distances to the best or null tree for the pooled scenarios.



comp	metric	character	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
Best	RF	c100	0.107	0.583	0.758	0.730	0.892	1.000
		c350	0.077	0.623	0.773	0.745	0.912	1.000
		c1000	0.076	0.615	0.821	0.767	0.971	1.000
	Tr	c100	-0.473	0.161	0.544	0.497	0.863	1.000
		c350	-0.307	0.363	0.693	0.622	0.936	1.000
		c1000	-0.276	0.372	0.799	0.659	0.992	1.000
Null	RF	c100	0.103	0.517	0.670	0.658	0.814	1.000
		c350	0.055	0.583	0.718	0.694	0.824	1.000
		c1000	0.049	0.576	0.739	0.715	0.871	1.000
	Tr	c100	-0.427	0.076	0.368	0.375	0.677	1.000
		c350	-0.282	0.295	0.603	0.551	0.839	1.000
		c1000	-0.328	0.295	0.620	0.582	0.930	1.000

Table 2: Summary statistics of the normalised distances to the best or null tree for the pooled number of characters.

comp	metric	taxa	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
Best	RF	t25	0.077	0.648	0.802	0.772	0.934	1.000
		t75	0.155	0.595	0.760	0.737	0.904	1.000
		t150	0.076	0.578	0.763	0.732	0.915	1.000
	Tr	t25	-0.436	0.463	0.758	0.670	0.964	1.000
		t75	-0.473	0.237	0.588	0.543	0.920	1.000
		t150	-0.424	0.238	0.615	0.565	0.955	1.000
Null	RF	t25	0.055	0.605	0.758	0.729	0.890	1.000
		t75	0.141	0.548	0.691	0.672	0.814	1.000
		t150	0.049	0.533	0.689	0.667	0.827	1.000
	Tr	t25	-0.343	0.370	0.665	0.606	0.902	1.000
		t75	-0.395	0.184	0.429	0.435	0.739	1.000
		t150	-0.427	0.137	0.472	0.467	0.826	1.000

Table 3: Summary statistics of the normalised distances to the best or null tree for the pooled number of taxa.

comp	metric	method	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
Best	RF	bayesian	0.319	0.714	0.828	0.811	0.934	1.000
		parsimony	0.076	0.496	0.679	0.684	0.911	1.000
	Tr	bayesian	-0.473	0.354	0.738	0.618	0.947	1.000
		parsimony	-0.436	0.258	0.601	0.568	0.949	1.000
Null	RF	bayesian	0.319	0.684	0.780	0.770	0.871	1.000
		parsimony	0.049	0.457	0.601	0.608	0.758	1.000
	Tr	bayesian	-0.395	0.276	0.608	0.538	0.856	1.000
		parsimony	-0.427	0.194	0.468	0.468	0.750	1.000

Table 4: Summary statistics of the normalised distances to the best or null tree for the pooled methods.

## POOLED TESTS RESULTS

comp	metric	test	bhatt.coeff	statistic	p.value
Best	RF	maxi:mini	0.573	356436.000	0.000
		maxi:rand	0.873	287225.000	0.000
		mini:rand	0.856	95841.500	0.000
	Tr	maxi:mini	0.614	358800.000	0.000
		maxi:rand	0.908	288223.500	0.000
		mini:rand	0.858	98507.500	0.000
Null	RF	maxi:mini	0.874	295590.000	0.000
		maxi:norm	0.993	176071.000	0.006
		mini:norm	0.830	83672.000	0.000
	Tr	maxi:mini	0.869	298342.000	0.000
		maxi:norm	0.994	185972.500	0.640
		mini:norm	0.841	90617.000	0.000

Table 5: Difference between the pooled scenarios. Bhatt.coeff is the Bhattacharrya Co-efficient (probability of overlap), the statistic and the p.value are from a non-parametric wilcoxon test (with Bonferonni-Holm correciton)

comp	metric	test	bhatt.coeff	statistic	p.value
Best	RF	c100:c350	0.990	190357.500	1.000
		c100:c1000	0.980	174085.500	0.002
		c350:c1000	0.984	180460.000	0.063
	Tr	c100:c350	0.961	166609.500	0.000
		c100:c1000	0.956	151389.500	0.000
		c350:c1000	0.981	178793.500	0.028
Null	RF	c100:c350	0.975	177982.000	0.018
		c100:c1000	0.951	164880.000	0.000
		c350:c1000	0.971	183201.000	0.218
	Tr	c100:c350	0.940	143165.000	0.000
		c100:c1000	0.939	133257.000	0.000
		c350:c1000	0.965	181479.000	0.103

Table 6: Difference between the pooled number of characters. Bhatt.coeff is the Bhattacharrya Coefficient (probability of overlap), the statistic and the p.value are from a non-parametric wilcoxon test (with Bonferonni-Holm correciton)

comp	metric	test	bhatt.coeff	statistic	p.value
Best	RF	t25:t75	0.976	218421.000	0.023
		t25:t150	0.988	220529.000	0.007
		t75:t150	0.990	201037.000	1.000
	Tr	t25:t75	0.976	233282.000	0.000
		t25:t150	0.978	227288.000	0.000
		t75:t150	0.992	194201.000	1.000
Null	RF	t25:t75	0.959	237247.000	0.000
		t25:t150	0.978	234937.000	0.000
		t75:t150	0.983	196946.000	1.000
	Tr	t25:t75	0.961	255239.000	0.000
		t25:t150	0.969	242327.000	0.000
		t75:t150	0.986	188297.000	1.000

Table 7: Difference between the pooled number of taxa. Bhatt.coeff is the Bhattacharyya Coefficient (probability of overlap), the statistic and the p.value are from a non-parametric wilcoxon test (with Bonferonni-Holm correciton)

comp	metric	test	bhatt.coeff	statistic	p.value
Best	RF	bayesian:parsimony	0.891	579437.500	0.000
		bayesian:parsimony	0.984	470621.500	0.168
	Tr	bayesian:parsimony	0.847	657875.500	0.000
		bayesian:parsimony	0.975	499754.000	0.000
Null	RF	bayesian:parsimony	0.891	579437.500	0.000
		bayesian:parsimony	0.984	470621.500	0.168
	Tr	bayesian:parsimony	0.847	657875.500	0.000
		bayesian:parsimony	0.975	499754.000	0.000

Table 8: Difference between the pooled methods. Bhatt.coeff is the Bhattacharrya Coefficient (probability of overlap), the statistic and the p.value are from a non-parametric wilcoxon test (with Bonferonni-Holm correciton)

## FULL RESULTS

method	taxa	characters	scenario	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
bayesian	25	100	maxi	0.561	0.780	0.868	0.862	0.956	1.000
			mini	0.451	0.659	0.714	0.722	0.813	0.868
			rand	0.451	0.758	0.780	0.804	0.890	0.978
	350	100	maxi	0.539	0.692	0.890	0.834	0.967	1.000
			mini	0.407	0.561	0.736	0.692	0.791	0.934
			rand	0.561	0.747	0.868	0.832	0.945	1.000
	1000	100	maxi	0.407	0.868	0.934	0.896	1.000	1.000
			mini	0.319	0.561	0.692	0.675	0.769	0.956
			rand	0.627	0.813	0.956	0.901	1.000	1.000
	75	100	maxi	0.650	0.849	0.986	0.919	0.993	1.000
			mini	0.553	0.646	0.718	0.720	0.777	0.938
			rand	0.663	0.773	0.863	0.843	0.887	0.966
350		100	maxi	0.574	0.863	0.945	0.905	0.990	1.000
			mini	0.402	0.615	0.698	0.677	0.766	0.856
			rand	0.595	0.756	0.801	0.796	0.845	0.924
1000		100	maxi	0.574	0.825	0.904	0.900	0.986	1.000
			mini	0.430	0.502	0.581	0.607	0.670	0.945
			rand	0.546	0.732	0.828	0.816	0.904	1.000
150	100	maxi	0.756	0.958	0.993	0.959	0.997	1.000	



			mini	0.594	0.674	0.750	0.756	0.831	0.942
			rand	0.668	0.814	0.885	0.860	0.924	0.970
		350	maxi	0.672	0.922	0.976	0.940	0.990	1.000
			mini	0.459	0.631	0.679	0.697	0.775	0.915
			rand	0.729	0.782	0.838	0.834	0.880	0.997
		1000	maxi	0.780	0.883	0.973	0.933	0.992	0.997
			mini	0.455	0.580	0.662	0.677	0.800	0.919
			rand	0.729	0.777	0.827	0.832	0.870	1.000
parsimony	25	100	maxi	0.517	0.725	0.824	0.830	1.000	1.000
			mini	0.121	0.495	0.561	0.579	0.670	0.824
			rand	0.253	0.594	0.736	0.699	0.824	1.000
		350	maxi	0.648	0.824	0.912	0.889	1.000	1.000
			mini	0.077	0.473	0.605	0.583	0.703	0.912
			rand	0.187	0.758	0.868	0.799	0.912	1.000
		1000	maxi	0.605	0.956	1.000	0.940	1.000	1.000
			mini	0.121	0.363	0.495	0.507	0.692	0.912
			rand	0.121	0.824	0.956	0.854	1.000	1.000
	75	100	maxi	0.492	0.715	0.904	0.842	1.000	1.000
			mini	0.210	0.426	0.471	0.494	0.543	0.876
			rand	0.244	0.471	0.615	0.599	0.735	0.959
		350	maxi	0.608	0.705	0.979	0.861	1.000	1.000

			mini	0.155	0.330	0.437	0.450	0.588	0.718
			rand	0.368	0.557	0.663	0.680	0.825	1.000
		1000	maxi	0.546	0.997	1.000	0.943	1.000	1.000
			mini	0.279	0.399	0.443	0.474	0.495	0.890
			rand	0.409	0.667	0.725	0.747	0.849	1.000
150	100		maxi	0.479	0.567	0.706	0.760	1.000	1.000
			mini	0.107	0.349	0.459	0.439	0.528	0.679
			rand	0.117	0.384	0.469	0.459	0.547	0.712
		350	maxi	0.533	0.677	0.807	0.824	1.000	1.000
			mini	0.198	0.379	0.442	0.470	0.533	0.797
			rand	0.303	0.572	0.648	0.647	0.733	1.000
		1000	maxi	0.608	0.819	0.936	0.895	1.000	1.000
			mini	0.076	0.398	0.449	0.481	0.552	0.861
			rand	0.100	0.633	0.706	0.717	0.883	1.000

Table 9: Summary statistics of the normalised Robinson-Fould distance to the best tree.

method	taxa	characters	scenario	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
bayesian	25	100	maxi	-0.014	0.642	0.860	0.783	0.977	1.000
			mini	-0.389	0.075	0.371	0.335	0.628	0.838
			rand	-0.147	0.347	0.680	0.583	0.825	0.998
		350	maxi	0.176	0.709	0.916	0.824	0.981	1.000

		mini	-0.183	0.074	0.345	0.353	0.597	0.874
		rand	0.288	0.652	0.806	0.761	0.942	1.000
	1000	maxi	0.371	0.845	0.978	0.897	1.000	1.000
		mini	-0.213	0.264	0.530	0.481	0.742	0.923
		rand	-0.142	0.807	0.963	0.815	1.000	1.000
75	100	maxi	0.004	0.611	0.965	0.805	0.998	1.000
		mini	-0.473	-0.269	-0.058	0.086	0.479	0.901
		rand	-0.066	0.315	0.586	0.542	0.835	0.981
	350	maxi	0.113	0.741	0.945	0.824	0.994	1.000
		mini	-0.307	0.223	0.347	0.407	0.683	0.927
		rand	0.042	0.497	0.685	0.635	0.824	0.984
	1000	maxi	0.225	0.659	0.896	0.798	0.998	1.000
		mini	-0.276	-0.027	0.358	0.300	0.608	0.857
		rand	0.095	0.311	0.709	0.630	0.935	1.000
150	100	maxi	0.520	0.867	0.996	0.914	0.999	1.000
		mini	-0.397	-0.056	0.151	0.225	0.580	0.971
		rand	0.013	0.332	0.611	0.592	0.878	0.990
	350	maxi	0.032	0.951	0.987	0.910	0.999	1.000
		mini	-0.174	0.151	0.425	0.447	0.807	0.980
		rand	0.086	0.745	0.920	0.814	0.957	1.000
	1000	maxi	0.048	0.855	0.957	0.851	0.998	1.000

			mini	-0.208	0.046	0.356	0.412	0.793	0.974
			rand	-0.057	0.423	0.824	0.661	0.947	1.000
parsimony	25	100	maxi	0.207	0.722	0.930	0.826	1.000	1.000
			mini	-0.436	0.156	0.468	0.390	0.638	0.916
			rand	0.153	0.440	0.729	0.659	0.889	1.000
		350	maxi	0.334	0.779	0.943	0.881	1.000	1.000
			mini	-0.011	0.289	0.483	0.481	0.666	0.889
			rand	-0.067	0.659	0.871	0.749	0.926	1.000
		1000	maxi	0.457	0.982	1.000	0.949	1.000	1.000
			mini	-0.093	0.269	0.417	0.440	0.636	0.932
			rand	0.110	0.844	0.992	0.852	1.000	1.000
	75	100	maxi	0.158	0.547	0.944	0.770	1.000	1.000
			mini	-0.335	-0.102	0.023	0.079	0.215	0.833
			rand	-0.203	0.132	0.396	0.410	0.741	0.999
		350	maxi	0.226	0.689	0.990	0.819	1.000	1.000
			mini	-0.055	0.091	0.172	0.253	0.398	0.729
			rand	0.025	0.286	0.639	0.567	0.799	1.000
		1000	maxi	0.522	0.993	1.000	0.943	1.000	1.000
			mini	-0.119	0.123	0.275	0.305	0.443	0.848
			rand	0.166	0.382	0.535	0.601	0.936	1.000
	150	100	maxi	-0.031	0.419	0.716	0.677	1.000	1.000

		mini	-0.424	-0.163	0.018	0.005	0.141	0.475
		rand	-0.323	0.090	0.207	0.269	0.494	0.851
	350	maxi	0.047	0.573	0.847	0.767	1.000	1.000
		mini	-0.053	0.030	0.184	0.207	0.397	0.590
		rand	-0.009	0.355	0.495	0.503	0.735	1.000
	1000	maxi	0.103	0.844	0.972	0.865	1.000	1.000
		mini	-0.007	0.164	0.454	0.403	0.612	0.766
		rand	-0.014	0.370	0.785	0.658	0.972	1.000

Table 10: Summary statistics of the normalised Triplets distance to the best tree.

method	taxa	characters	scenario	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
bayesian	25	100	norm	0.451	0.758	0.780	0.804	0.890	0.978
			maxi	0.363	0.648	0.758	0.752	0.846	1.000
			mini	0.495	0.605	0.670	0.669	0.736	0.890
	350		norm	0.561	0.747	0.868	0.832	0.945	1.000
			maxi	0.539	0.703	0.802	0.807	0.923	1.000
			mini	0.451	0.572	0.692	0.677	0.791	0.890
	1000		norm	0.627	0.813	0.956	0.901	1.000	1.000
			maxi	0.385	0.780	0.824	0.826	0.934	1.000
			mini	0.319	0.561	0.648	0.658	0.758	0.956
75	100	norm	0.663	0.773	0.863	0.843	0.887	0.966	

			maxi	0.636	0.735	0.835	0.813	0.887	0.959
			mini	0.553	0.639	0.691	0.691	0.729	0.911
		350	norm	0.595	0.756	0.801	0.796	0.845	0.924
			maxi	0.546	0.705	0.780	0.765	0.842	0.945
			mini	0.423	0.605	0.670	0.670	0.749	1.000
		1000	norm	0.546	0.732	0.828	0.816	0.904	1.000
			maxi	0.560	0.708	0.760	0.783	0.863	1.000
			mini	0.423	0.498	0.567	0.588	0.636	0.890
150	100		norm	0.668	0.814	0.885	0.861	0.924	0.970
			maxi	0.665	0.799	0.871	0.847	0.917	0.970
			mini	0.584	0.645	0.719	0.730	0.792	0.942
		350	norm	0.729	0.782	0.838	0.834	0.880	0.997
			maxi	0.652	0.760	0.817	0.822	0.868	0.983
			mini	0.442	0.626	0.665	0.689	0.767	0.929
		1000	norm	0.729	0.777	0.827	0.832	0.870	1.000
			maxi	0.716	0.756	0.834	0.838	0.897	1.000
			mini	0.455	0.569	0.668	0.657	0.750	0.838
parsimony	25	100	norm	0.253	0.594	0.736	0.699	0.824	1.000
			maxi	0.253	0.517	0.692	0.654	0.780	1.000
			mini	0.121	0.440	0.517	0.544	0.627	0.824
		350	norm	0.187	0.758	0.868	0.799	0.912	1.000

		maxi	0.187	0.703	0.780	0.760	0.857	1.000
		mini	0.055	0.495	0.583	0.574	0.692	0.868
	1000	norm	0.121	0.824	0.956	0.854	1.000	1.000
		maxi	0.121	0.648	0.912	0.808	1.000	1.000
		mini	0.099	0.374	0.495	0.502	0.692	0.868
75	100	norm	0.244	0.471	0.615	0.599	0.735	0.959
		maxi	0.244	0.464	0.553	0.559	0.643	0.821
		mini	0.155	0.409	0.485	0.475	0.557	0.725
	350	norm	0.368	0.557	0.663	0.680	0.825	1.000
		maxi	0.368	0.550	0.656	0.643	0.739	1.000
		mini	0.141	0.327	0.437	0.435	0.550	0.650
	1000	norm	0.409	0.667	0.725	0.747	0.849	1.000
		maxi	0.409	0.598	0.705	0.728	0.835	1.000
		mini	0.292	0.395	0.443	0.456	0.495	0.794
150	100	norm	0.117	0.384	0.469	0.459	0.547	0.712
		maxi	0.117	0.377	0.421	0.436	0.531	0.665
		mini	0.103	0.325	0.452	0.410	0.492	0.628
	350	norm	0.303	0.572	0.648	0.647	0.733	1.000
		maxi	0.303	0.531	0.624	0.611	0.668	0.919
		mini	0.191	0.401	0.438	0.450	0.504	0.699
	1000	norm	0.100	0.633	0.706	0.717	0.883	1.000

maxi	0.100	0.604	0.672	0.702	0.853	1.000
mini	0.049	0.391	0.449	0.462	0.542	0.865

Table 11: Summary statistics of the normalised Robinson-Fould distance to the null tree.

method	taxa	characters	scenario	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
bayesian	25	100	norm	-0.147	0.347	0.680	0.583	0.825	0.998
			maxi	-0.144	0.239	0.585	0.526	0.751	1.000
			mini	-0.343	0.021	0.373	0.292	0.501	0.795
	350	1000	norm	0.288	0.652	0.806	0.761	0.942	1.000
			maxi	0.149	0.637	0.779	0.732	0.918	1.000
			mini	-0.080	0.122	0.312	0.339	0.529	0.840
	75	100	norm	-0.142	0.807	0.963	0.815	1.000	1.000
			maxi	-0.142	0.681	0.881	0.767	0.984	1.000
			mini	-0.183	0.126	0.569	0.429	0.680	0.923
	350	1000	norm	-0.066	0.315	0.586	0.542	0.835	0.981
			maxi	-0.118	0.298	0.664	0.529	0.831	0.981
			mini	-0.395	-0.259	0.018	0.037	0.273	0.730
1000	1000	norm	0.042	0.497	0.685	0.635	0.824	0.984	
		maxi	0.015	0.419	0.626	0.582	0.779	0.957	
		mini	-0.080	0.134	0.349	0.392	0.623	1.000	
			norm	0.095	0.311	0.709	0.630	0.935	1.000



			maxi	-0.131	0.321	0.747	0.622	0.905	1.000
			mini	-0.303	-0.063	0.241	0.235	0.492	0.859
	150	100	norm	0.013	0.332	0.611	0.592	0.878	0.990
			maxi	-0.118	0.331	0.517	0.536	0.769	0.990
			mini	-0.262	-0.133	0.091	0.135	0.320	0.826
		350	norm	0.086	0.745	0.920	0.814	0.957	1.000
			maxi	0.314	0.765	0.894	0.838	0.960	1.000
			mini	-0.282	0.083	0.391	0.436	0.873	0.989
		1000	norm	-0.057	0.423	0.824	0.661	0.947	1.000
			maxi	-0.062	0.426	0.834	0.668	0.972	1.000
			mini	-0.328	-0.013	0.353	0.390	0.816	0.961
parsimony	25	100	norm	0.153	0.440	0.729	0.659	0.889	1.000
			maxi	0.153	0.361	0.663	0.609	0.851	1.000
			mini	-0.303	0.107	0.311	0.329	0.534	0.922
		350	norm	-0.067	0.659	0.871	0.749	0.926	1.000
			maxi	-0.067	0.639	0.823	0.729	0.911	1.000
			mini	0.116	0.313	0.509	0.480	0.660	0.834
		1000	norm	0.110	0.844	0.992	0.852	1.000	1.000
			maxi	0.110	0.719	0.956	0.809	1.000	1.000
			mini	-0.068	0.292	0.417	0.458	0.636	0.932
	75	100	norm	-0.203	0.132	0.396	0.410	0.741	0.999

		maxi	-0.203	0.104	0.326	0.350	0.549	0.875
		mini	-0.329	-0.076	0.073	0.105	0.288	0.662
	350	norm	0.025	0.286	0.639	0.567	0.799	1.000
		maxi	-0.073	0.286	0.578	0.513	0.751	1.000
		mini	-0.111	0.019	0.148	0.204	0.355	0.732
	1000	norm	0.166	0.382	0.535	0.601	0.936	1.000
		maxi	0.166	0.382	0.564	0.587	0.872	1.000
		mini	-0.157	0.157	0.284	0.296	0.471	0.758
150	100	norm	-0.323	0.090	0.207	0.269	0.494	0.851
		maxi	-0.323	0.085	0.233	0.273	0.494	0.823
		mini	-0.427	-0.185	-0.024	-0.017	0.077	0.657
	350	norm	-0.009	0.355	0.495	0.503	0.735	1.000
		maxi	-0.009	0.255	0.462	0.463	0.632	0.967
		mini	-0.085	0.067	0.138	0.188	0.378	0.559
	1000	norm	-0.014	0.370	0.785	0.658	0.972	1.000
		maxi	-0.014	0.317	0.636	0.613	0.963	1.000
		mini	-0.013	0.122	0.398	0.390	0.648	0.747

Table 12: Summary statistics of the normalised Triplets distance to the null tree.