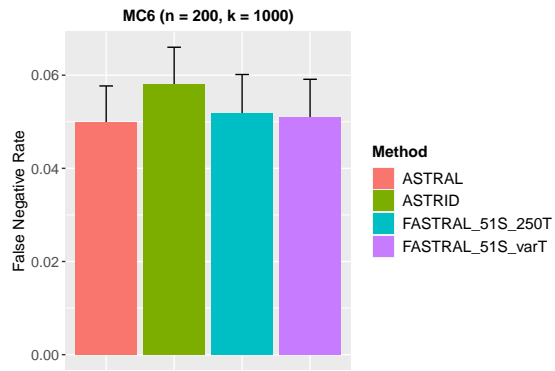


Supplementary Materials for FASTRAL

Material provided here is due to the page limit for the Bioinformatics submission.

(A) MC6



(B) MC11

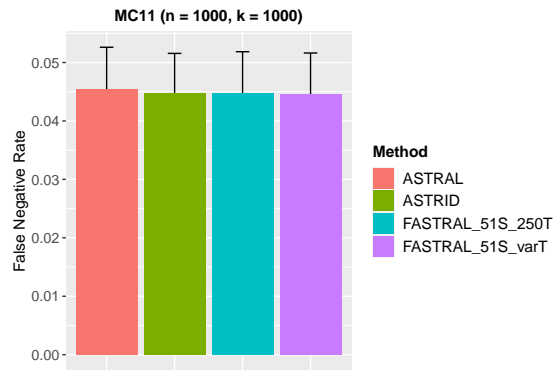


Fig. S1. Experiment 1: Impact of sampling strategy on tree error for FASTRAL and comparison to ASTRAL and ASTRID. (A) The performance of the tested methods on MC6 dataset with 1000 genes and 200 species. (B) The performance of the tested methods on MC11 dataset with 1000 genes and 1000 species. FASTRAL is tested under two parameter settings: first with 51 samples each containing 250 trees, and second with 51 samples containing variable number of trees. Error bars indicate the standard error from mean.

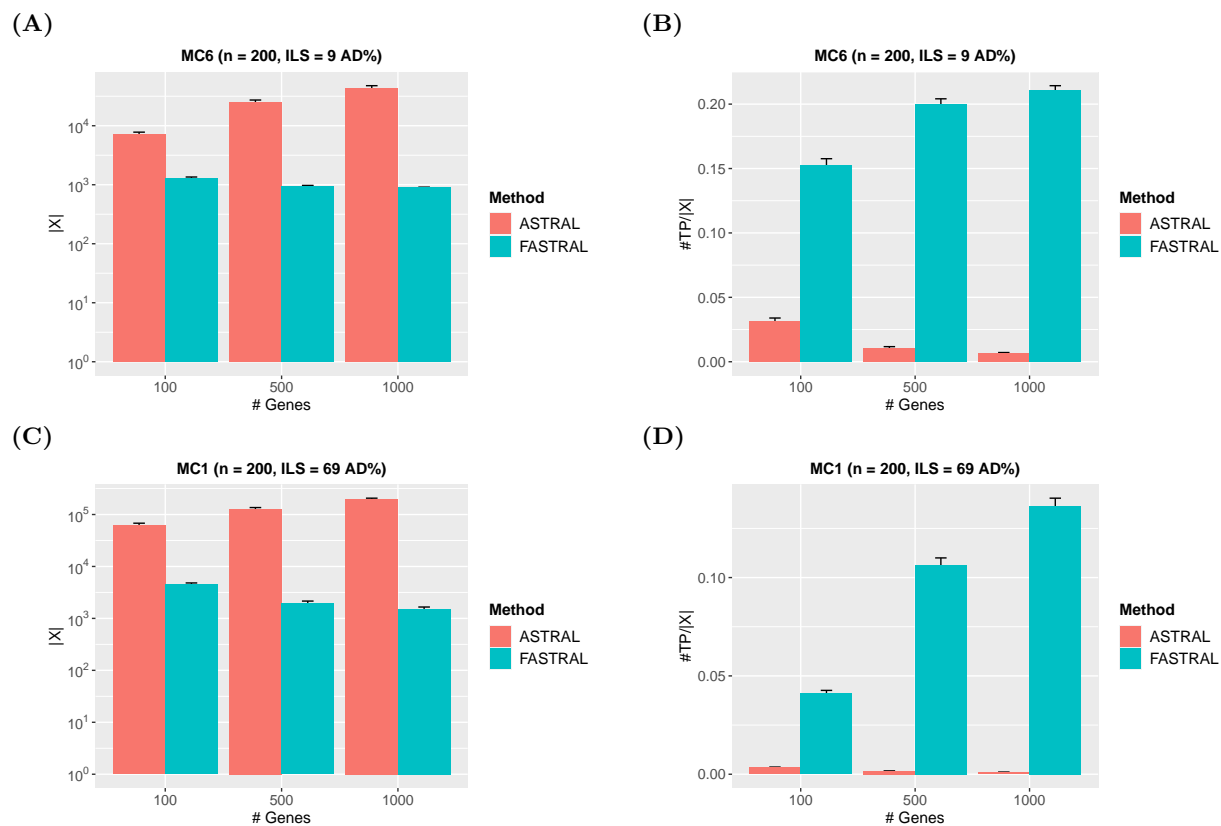


Fig. S2. Understanding the impact of FASTRAL’s strategy on the constrained search (MC6 and MC1). (A, C): Comparing size of set X between ASTRAL and FASTRAL on MC6 (low ILS) and MC1 (high ILS) datasets with 1000 genes (note that the y-axis is logarithmically scaled). (B, D): The density of the true species tree bipartitions in the set X (i.e., space efficiency) for ASTRAL and FASTRAL on MC6 and MC1 datasets with 1000 genes and 200 species. Error bars represent standard error.

Figure S2 shows the impact of FASTRAL’s strategy for defining the set X compared to ASTRAL, on the MC6 and MC1 model conditions. The same trends hold here as for MC11: as the number of genes increase, the size of the set X increases for ASTRAL but not for FASTRAL, and the density of the true species tree bipartitions increase for FASTRAL but not for ASTRAL. Thus, this trend holds for low and high ILS as well as for moderate ILS.

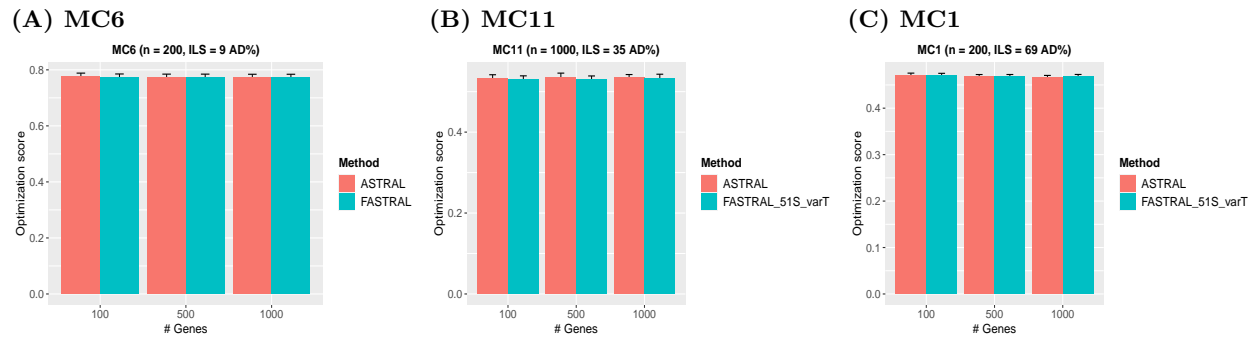


Fig. S3. Experiment 2: Maximum Quartet Support Supertree (MQSST) scores (averaged across 50 replicates) for FASTRAL and ASTRAL; larger is better. A: MC6 datasets (low ILS, 200 species, 1000 genes). B: MC11 datasets (moderate ILS, 1000 species, 1000 genes). C: MC1 datasets (high ILS, 200 species, 1000 genes). Error bars represent standard error.

We examined the Maximum Quartet Support Supertree (MQSST) scores produced by ASTRAL and FASTRAL, as the two methods differ only in how they constrain the search space. As seen in Figure S3, FASTRAL and ASTRAL are nearly identical on these model conditions, showing that the change in the constraint space used by FASTRAL is not detrimental.

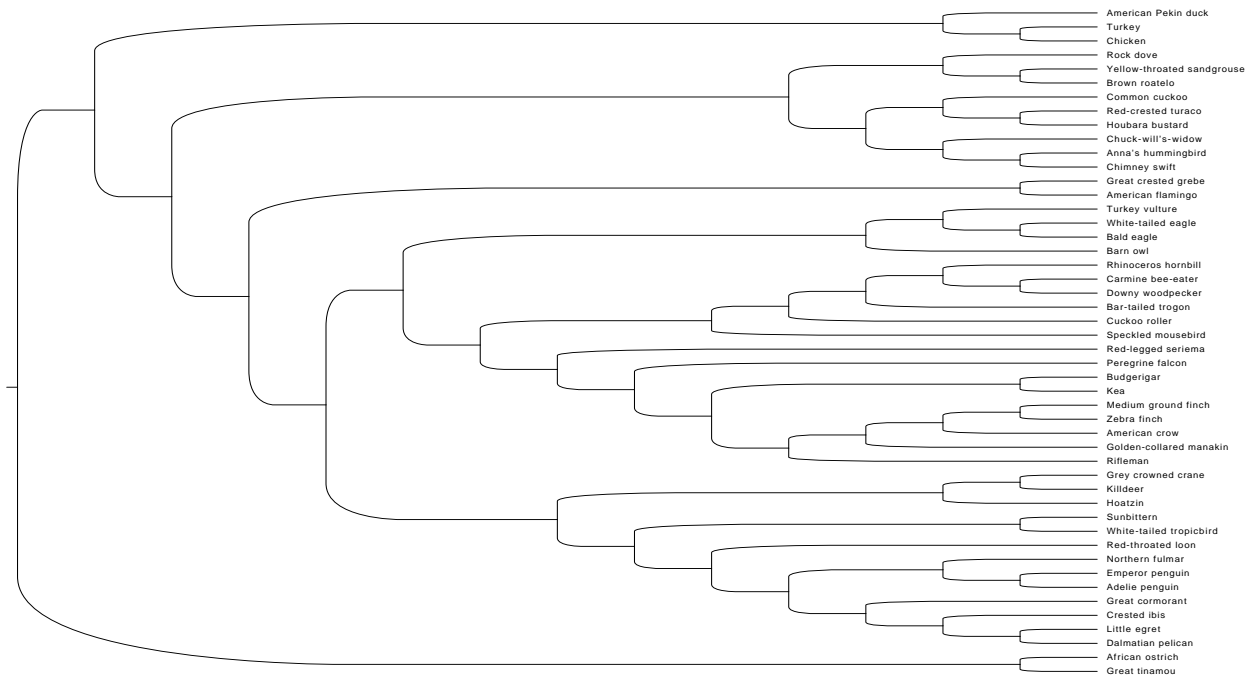


Fig. S4. Experiment 4: ASTRID tree on the Avian phylogenomic dataset

Figure S4 presents the ASTRID (version 1.4) tree on the Avian Phylogenomics project dataset, which is the same dataset as analyzed in Figure 5. Note that the ASTRID tree is quite different from the other two trees: the RF distance between the ASTRID and ASTRAL trees is 9 and between the ASTRID and FASTRAL trees is 8.

Method	No. Genes / Model Condition								
	100			500			1000		
	MC1	MC6	MC11	M1	MC6	MC11	M1	MC6	MC11
ASTRAL vs. FASTRAL	0.669	0.479	0.948	0.063	0.199	0.966	0.047	0.175	0.932
ASTRID vs. ASTRAL	0.000	0.000	0.642	0.554	0.000	0.958	0.371	0.000	0.943
ASTRID vs. FASTRAL	0.000	0.000	0.694	0.833	0.000	0.924	0.749	0.001	0.987

Table S1: Experiment 2: We show the p-value of a two-sided paired t-test, applied to compare the tree topology accuracy of different methods on the 50 replicates of MC6 (low ILS, 200 taxa), MC11 (moderate ILS, 1000 taxa), and MC1 (High ILS, 200 taxa) model conditions. FASTRAL uses the variable sampling method. Results that are significant at the 0.050 level are boldfaced.

As seen in Table S1, ASTRAL and FASTRAL are statistically significantly different ($p < 0.05$) under the MC1 model condition (high ILS) when given 1000 genes, and almost significant given 500 genes; as seen in Figure 2, this is a condition where FASTRAL is more accurate than ASTRAL. There are no other conditions where the ASTRAL and FASTRAL are statistically significantly different.

Dataset	Method	No. genes	Avg. FN rate	FN rate SE	Avg. time (secs)	time SE
MC6	ASTRAL	100	0.061	0.008	36.901	5.843
MC6	ASTRAL	500	0.051	0.008	179.078	21.479
MC6	ASTRAL	1000	0.050	0.008	371.036	62.201
MC6	FASTRAL	100	0.062	0.008	134.828	7.638
MC6	FASTRAL	500	0.052	0.008	121.127	3.705
MC6	FASTRAL	1000	0.051	0.008	182.291	9.286
MC6	ASTRID	100	0.071	0.009	0.841	0.015
MC6	ASTRID	500	0.061	0.009	1.447	0.028
MC6	ASTRID	1000	0.058	0.008	2.191	0.041
MC11	ASTRAL	100	0.077	0.007	1959.494	188.096
MC11	ASTRAL	500	0.051	0.007	7499.401	836.874
MC11	ASTRAL	1000	0.045	0.007	20124.711	2409.155
MC11	FASTRAL	100	0.078	0.008	1251.484	17.748
MC11	FASTRAL	500	0.050	0.007	2157.487	74.476
MC11	FASTRAL	1000	0.045	0.007	2190.731	145.442
MC11	ASTRID	100	0.082	0.007	15.517	0.365
MC11	ASTRID	500	0.051	0.007	32.700	0.939
MC11	ASTRID	1000	0.045	0.007	50.502	1.324
MC1	ASTRAL	100	0.162	0.016	688.091	156.573
MC1	ASTRAL	500	0.086	0.011	2317.441	219.788
MC1	ASTRAL	1000	0.067	0.009	4293.490	190.043
MC1	FASTRAL	100	0.162	0.016	120.761	6.580
MC1	FASTRAL	500	0.084	0.011	120.700	2.481
MC1	FASTRAL	1000	0.064	0.009	152.801	3.876
MC1	ASTRID	100	0.177	0.015	0.815	0.014
MC1	ASTRID	500	0.083	0.009	1.409	0.025
MC1	ASTRID	1000	0.063	0.006	2.093	0.037

Table S2: Experiment 2: Average tree error (and standard error) for ASTRAL, ASTRID, and FASTRAL (using variable sampling) on the MC6 (low ILS, 200 taxa), MC11 (moderate ILS, 1000 taxa), and MC1 (high ILS, 200 taxa) model conditions with up to 1000 genes. FASTRAL is run with the variable sampling approach. Results shown are based on 50 replicates.