Supplementary figures and tables for StarBEAST2

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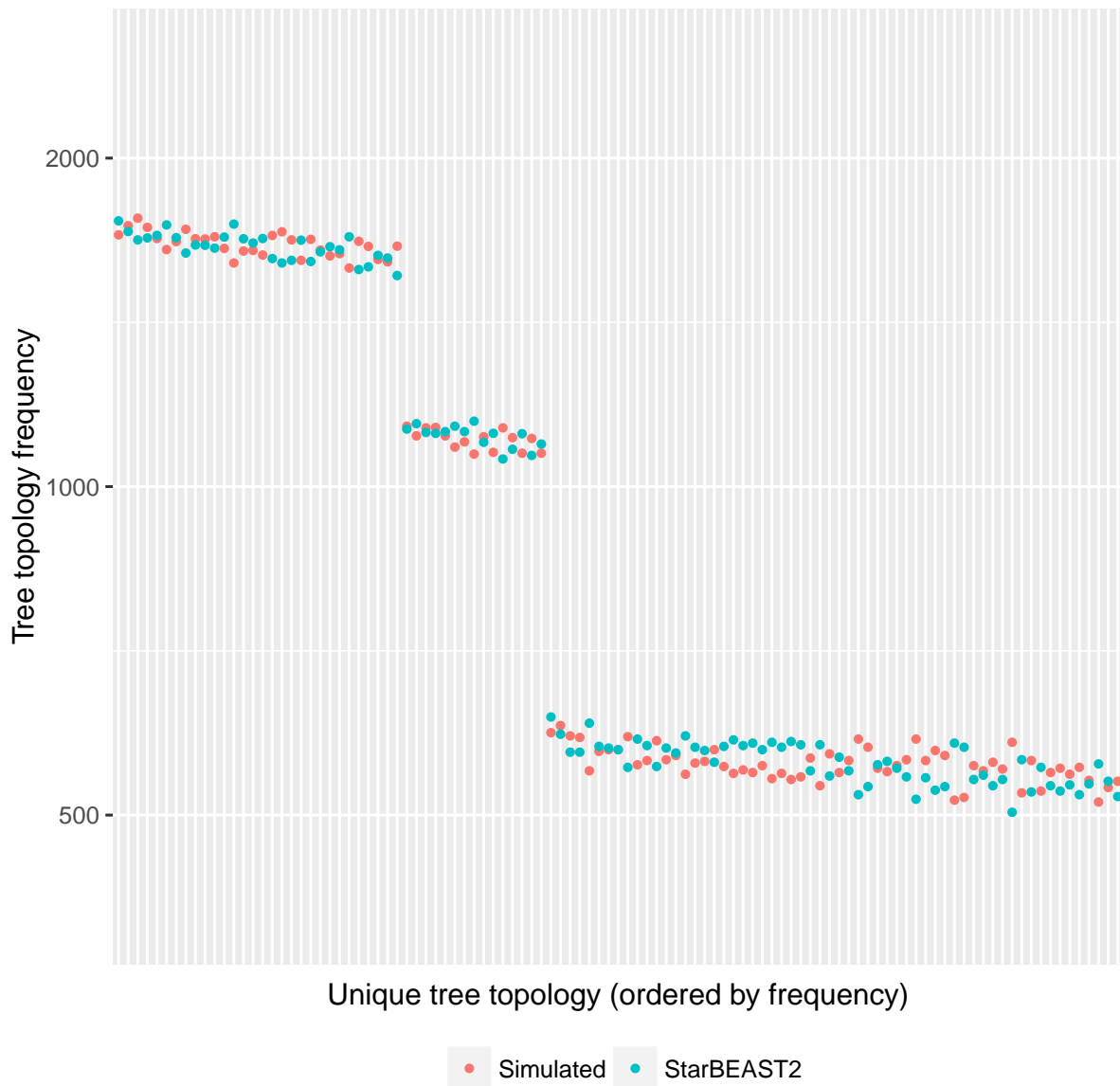August 15, 2016

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Figure S1: Frequency of five-taxon species tree topologies sampled from a birth-death prior distribution. Topologies were sampled by simulating trees using biopy (red), or by using a StarBEAST2 MCMC chain (blue). Frequencies are identical apart from noise, indicating that StarBEAST2 is mathematically correct. Three levels of probability are evident from left to right — high probability balanced topologies e.g. ((a,b),((c,d),e)), middle probability intermediate topologies e.g. (((a,b),(c,d)),e), and low probability unbalanced topologies e.g. ((((a,b),c),d),e).
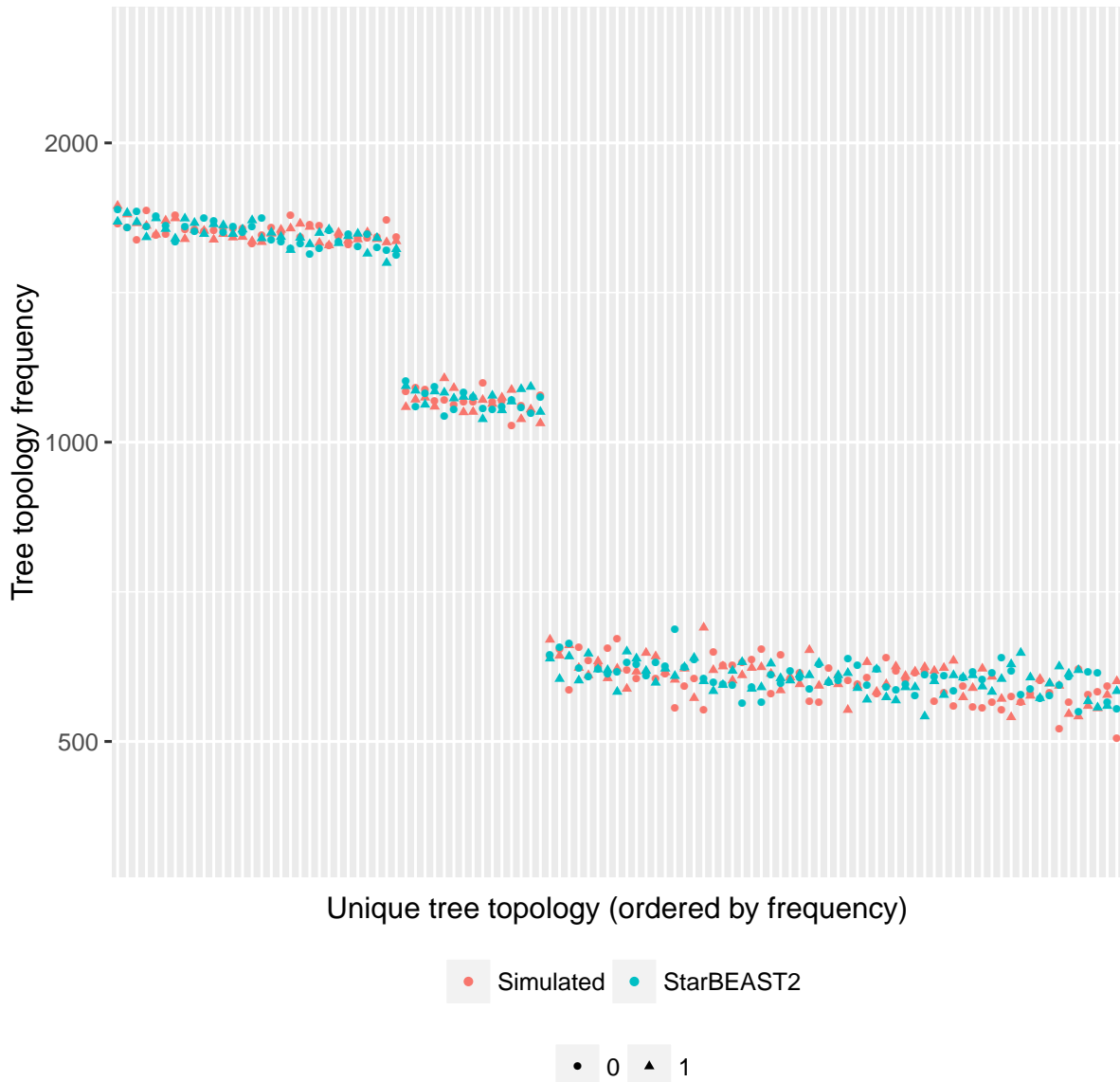
Figure S2: Frequency of five-taxon gene tree topologies sampled from a multispecies coalescent prior distribution. Topologies were sampled by simulating gene trees within species trees using biopy (red), or by using a StarBEAST2 MCMC chain (blue). Gene trees were sampled with two clock rates, 0.5 (circles) and 2.0 (triangles), although clock rate should not affect topology or node heights in units of time. Frequencies are identical apart from noise, indicating that StarBEAST2 is mathematically correct. Three levels of probability are evident from left to right — high probability balanced topologies e.g. ((a,b),((c,d),e)), middle probability intermediate topologies e.g. (((a,b),(c,d)),e), and low probability unbalanced topologies e.g. ((((a,b),c),d),e).

Figure S3: Probability densities of five-taxon species tree node heights sampled from a birth-death prior distribution. Node heights were sampled by simulating trees using biopy (red), or by using a StarBEAST2 MCMC chain (blue). Probability densities are plotted separately for each ranked node giving four peaks, one for each internal node. Node height probability densities are identical apart from noise, indicating that StarBEAST2 is mathematically correct.
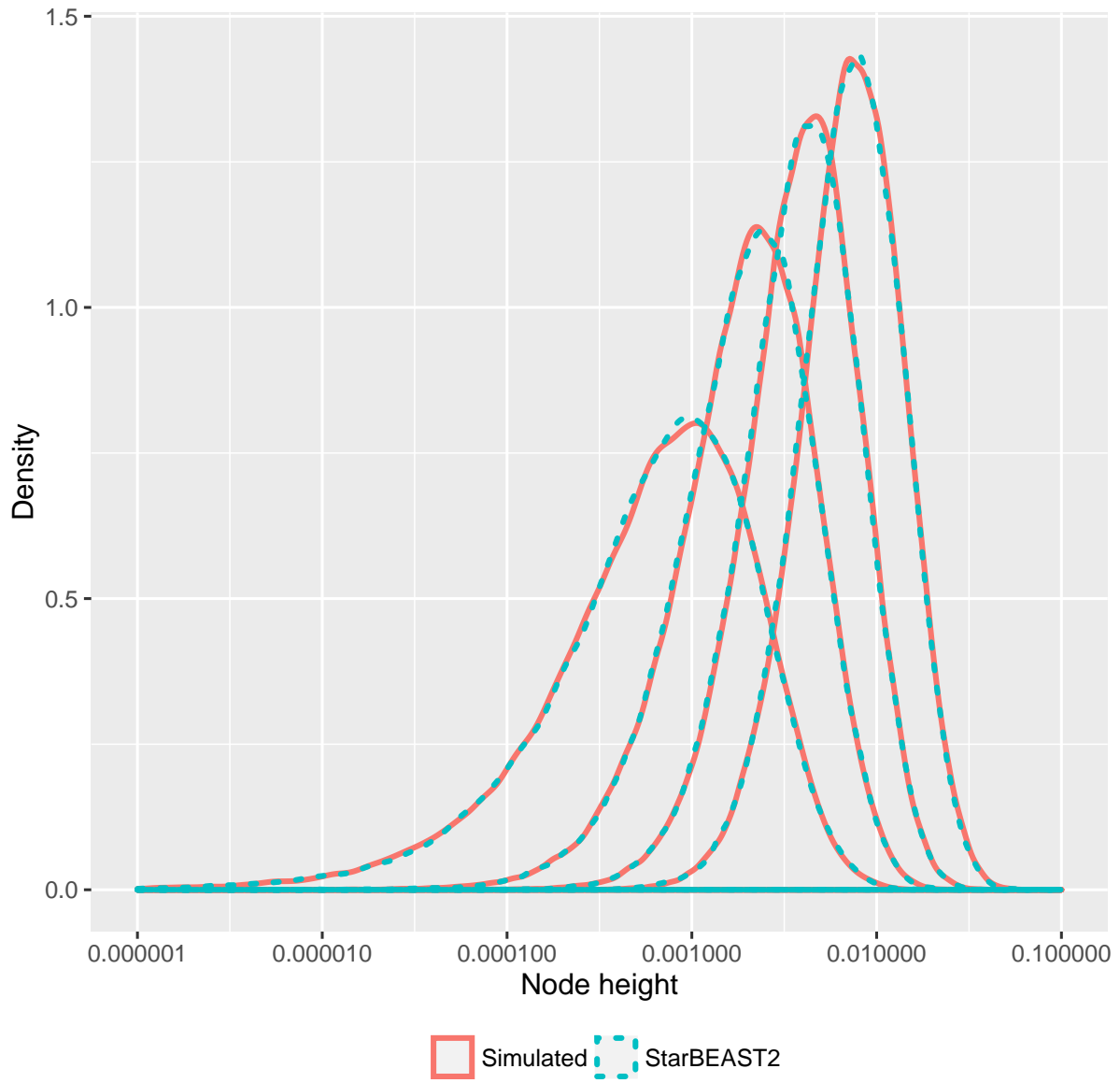
Figure S4: Probability densities of five-taxon gene tree node heights sampled from a multispecies coalescent prior distribution. Node heights were sampled by simulating gene trees within species trees using biopy (red), or by using a StarBEAST2 MCMC chain (blue). Gene trees were sampled with two clock rates, 0.5 and 2.0, and node heights from both sets of gene trees were combined as clock rate should not affect topology or node heights in units of time. Probability densities are plotted separately for each ranked node giving four peaks, one for each internal node. Node height probability densities are identical apart from noise, indicating that StarBEAST2 is mathematically correct.
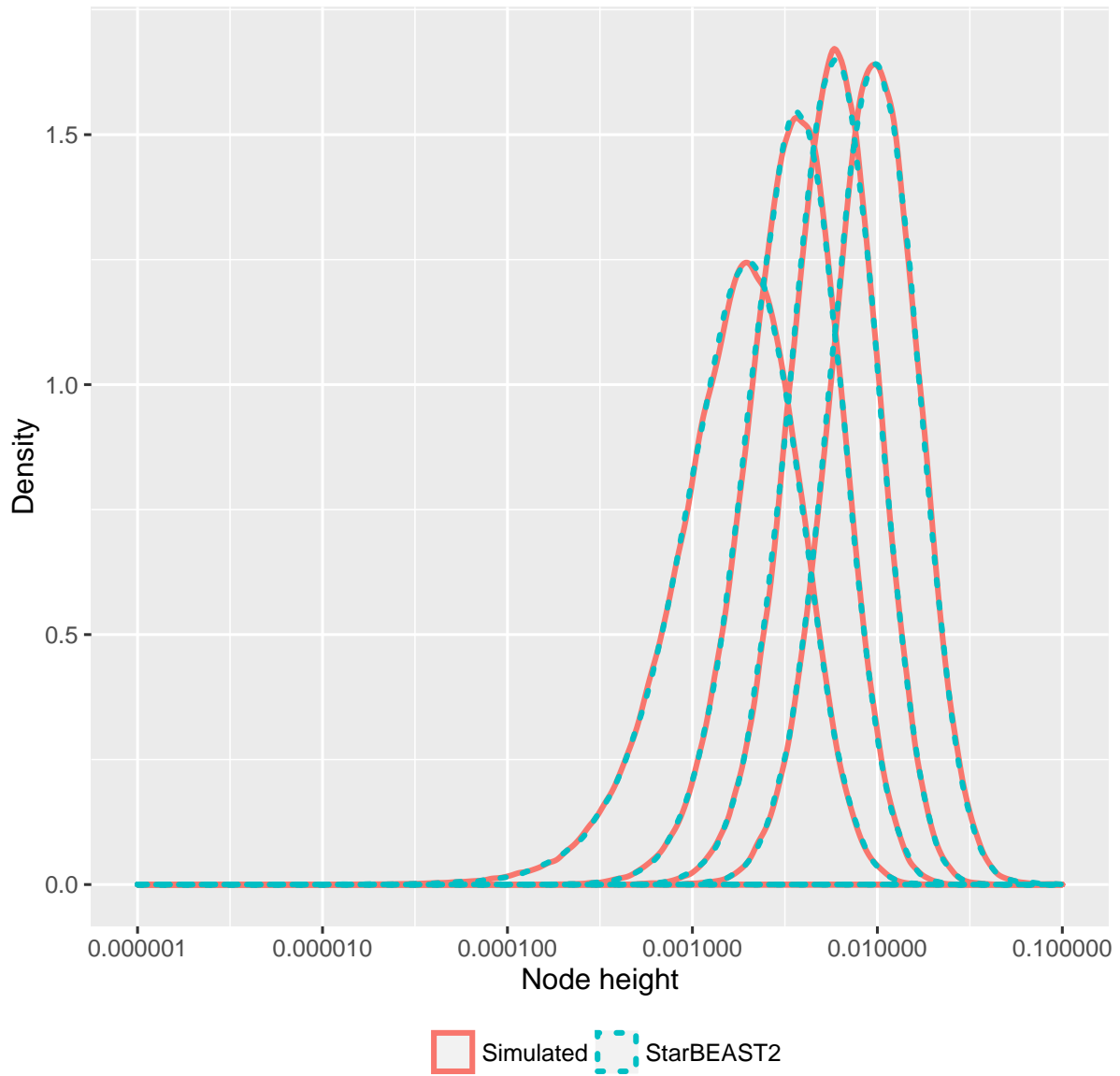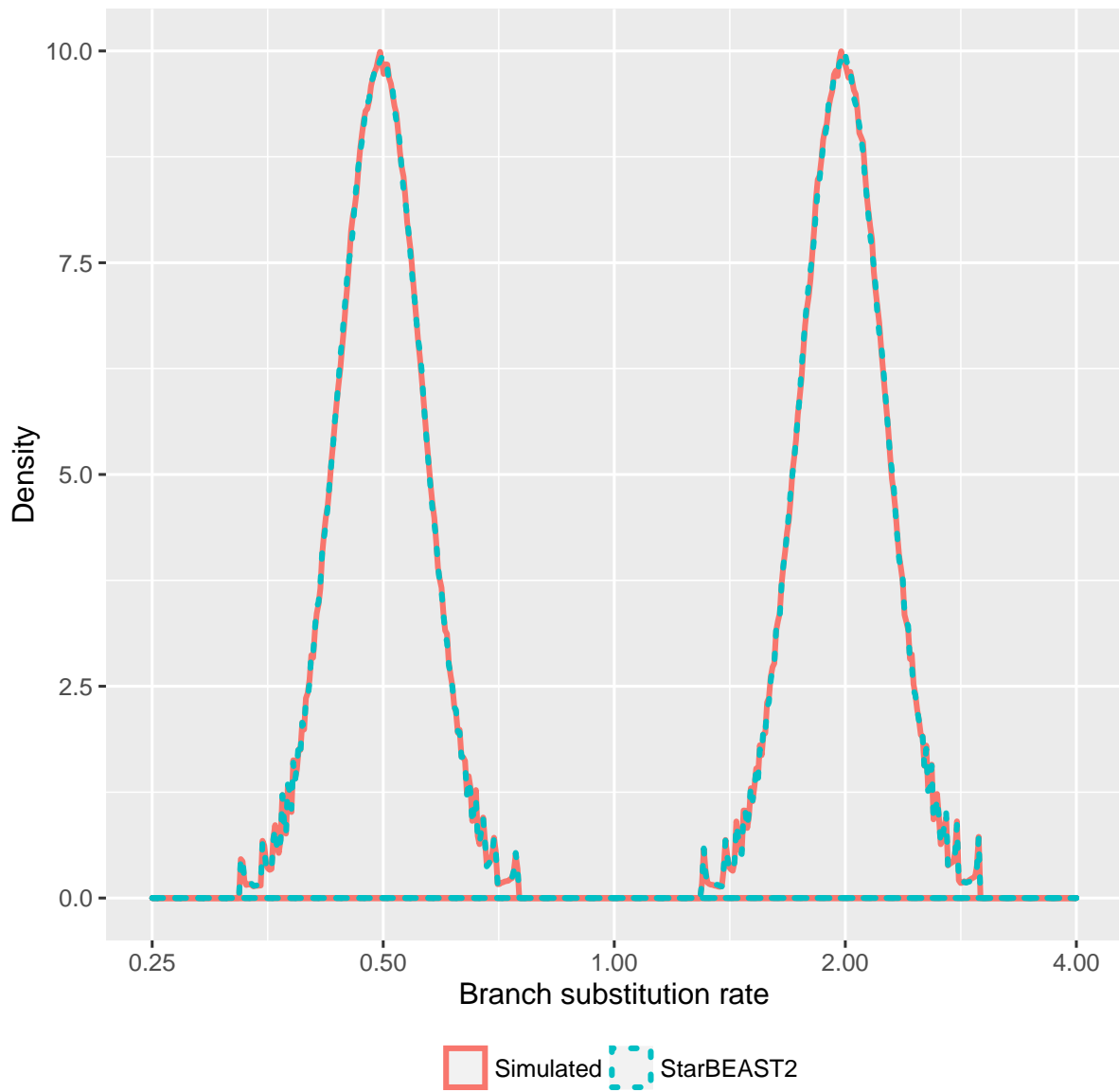
Figure S5: Probability densities of five-taxon gene tree branch rates produced by a species tree uncorrelated lognormal (UCLN) relaxed clock. Branch rates were sampled by simulating gene trees within species trees using biopy and simulating species tree branch rates using scipy (red), or by using a Star-BEAST2 MCMC chain (blue). Gene trees were sampled with two clock rates, 0.5 and 2.0, resulting in two peaks. Branch rate probability densities are identical apart from noise, indicating that StarBEAST2 is mathematically correct.
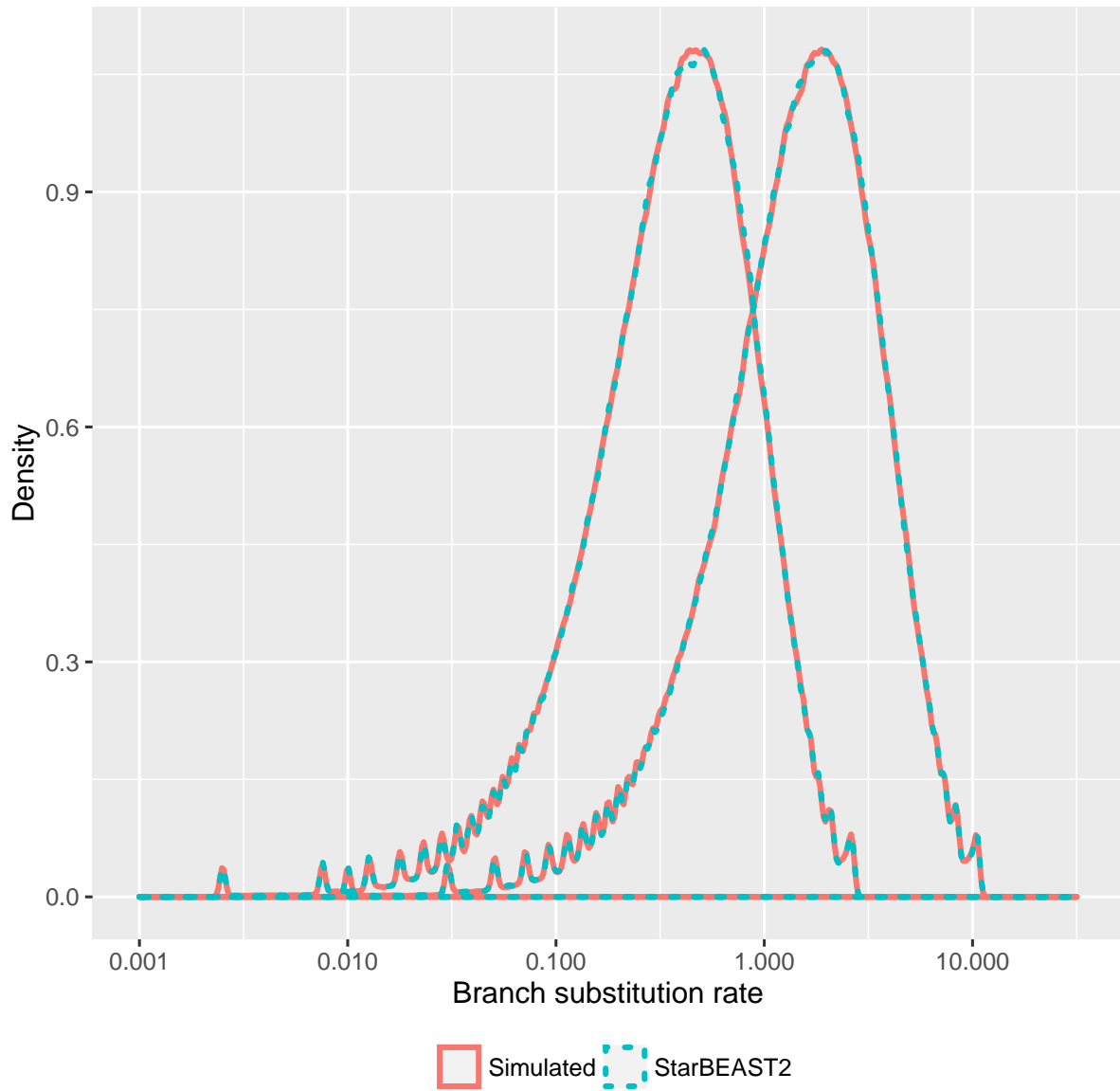
Figure S6: Probability densities of five-taxon gene tree branch rates produced by a species tree uncorrelated exponential (UCED) relaxed clock. Branch rates were sampled by simulating gene trees within species trees using biopy and simulating species tree branch rates using scipy (red), or by using a Star-BEAST2 MCMC chain (blue). Gene trees were sampled with two clock rates, 0.5 and 2.0, resulting in two peaks. Branch rate probability densities are identical apart from noise, indicating that StarBEAST2 is mathematically correct.
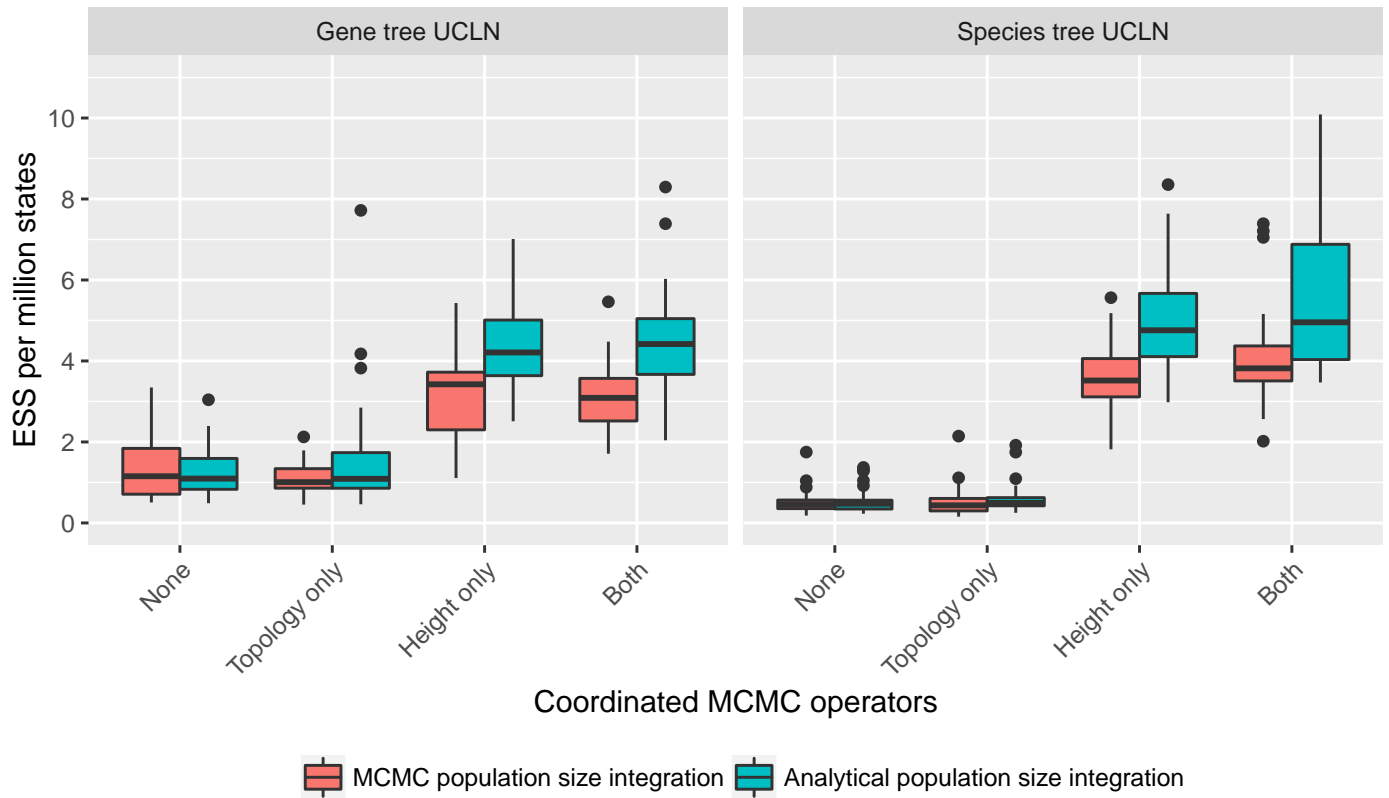
Figure S7: Impact of operators, population size integration and clock models on effective sample size (ESS) per million states of *Pseudacris* reanalyses. The estimated sample size (ESS) per hour for a given replicate used the smallest ESS out of all recorded statistics. Topology refers to the replacement of naïve nearest-neighbor interchange and subtree prune and regraft operators with coordinated operators. Height refers to the addition of operators which make coordinated changes to node heights. Uncorrelated log-normal (UCLN) relaxed clocks were applied to either each gene tree or to the species tree. N = 32.
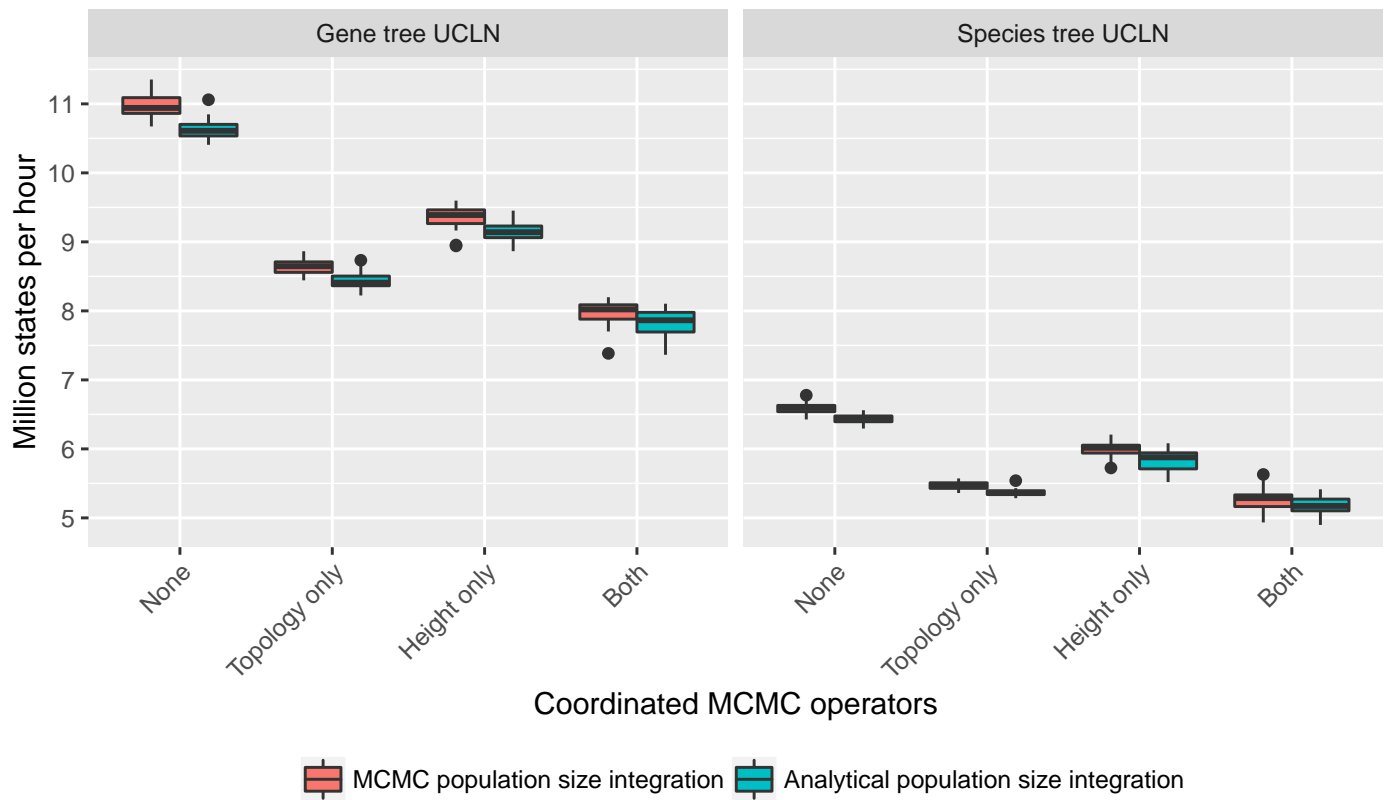
Figure S8: Impact of operators, population size integration and clock models on the calculation time for each state. The estimated sample size (ESS) per hour for a given replicate used the smallest ESS out of all recorded statistics. Topology refers to the replacement of naïve nearest-neighbor interchange and subtree prune and regraft operators with coordinated operators. Height refers to the addition of operators which make coordinated changes to node heights. Uncorrelated log-normal (UCLN) relaxed clocks were applied to either each gene tree or to the species tree. N = 32.
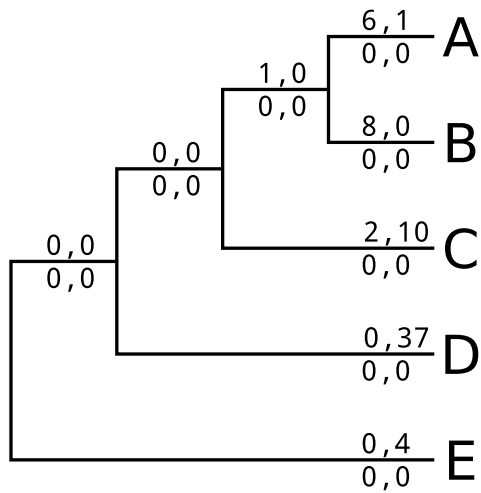
Figure S9: Number of erroneous per-species substitution rates estimated using BEAST concatenation and StarBEAST2. Erroneous branch rates are those with 95% credibility intervals which do not include the true rate of 1. Numbers above a branch are the counts of erroneous branches for concatenation, and those below are the counts for StarBEAST2, both out of 96 replicates. The first count is the number of branch rates inferred to be faster than 1, and the second is the number inferred to be slower than 1.
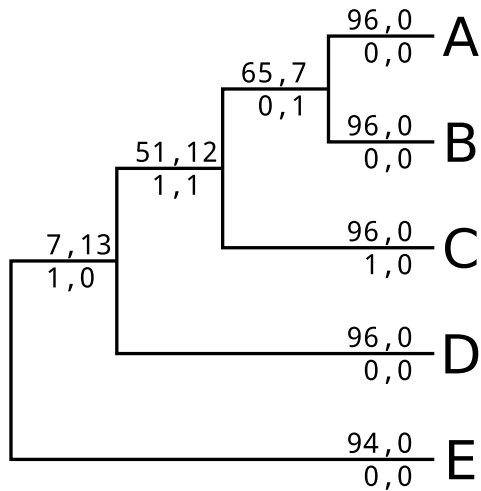
Figure S10: Number of erroneous branch lengths estimated using BEAST concatenation and StarBEAST2. Erroneous branch lengths are those with 95% credibility intervals which do not include the true simulated length for a given branch. Numbers above a branch are the counts of erroneous branches for concatenation, and those below are the counts for StarBEAST2, both out of 96 replicates. The first count is the number of branch lengths inferred to be longer than the true length, and the second is the number inferred to be shorter.

Table S1: Mean log(ESS per hour) for *Pseudacris* data.

	Birth-death probability	Clock rate stdev	Extinction fraction	Among-site rate variation	Transition/ Transversion κ	Phylogenetic likelihood	Minimum
◇◇◇◇	4.63 4.51−4.74	5.36 5.20−5.50	5.28 5.16−5.40	5.59 5.37−5.81	5.61 5.40−5.83	3.28 3.16−3.41	2.52 2.30−2.72
◇◇◇◆	4.86 4.78−4.93	5.66 5.60−5.72	5.39 5.36−5.42	6.27 6.17−6.37	6.35 6.24−6.47	3.50 3.35−3.62	3.33 3.21−3.44
◇◇◆◇	4.25 4.17−4.32	5.06 4.95−5.16	5.00 4.91−5.09	5.25 5.10−5.39	5.28 5.14−5.43	2.88 2.75−3.02	2.18 2.05−2.30
◇◇◆◆	4.65 4.59−4.71	5.45 5.40−5.51	5.27 5.24−5.30	6.11 6.02−6.20	6.21 6.13−6.29	3.34 3.23−3.45	3.18 3.11−3.26
◇◆◇◇	3.49 3.33−3.65	4.13 3.93−4.35	4.08 3.87−4.26	4.16 3.95−4.38	4.17 3.94−4.39	2.65 2.54−2.74	1.12 0.98−1.26
◇◆◇◆	4.49 4.45−4.54	5.42 5.37−5.48	5.09 5.05−5.13	5.91 5.81−6.02	5.98 5.85−6.09	3.10 3.00−3.20	3.03 2.95−3.11
◇◆◆◇	3.27 3.11−3.43	4.00 3.82−4.18	3.98 3.81−4.16	4.04 3.84−4.26	4.04 3.83−4.26	2.53 2.43−2.63	0.90 0.71−1.11
◇◆◆◆	4.42 4.34−4.49	5.38 5.32−5.45	4.96 4.93−5.00	5.91 5.81−6.01	5.98 5.86−6.10	3.10 3.00−3.20	3.02 2.92−3.13
◆◇◇◇	4.67 4.59−4.74	5.25 5.13−5.36	5.21 5.12−5.30	5.44 5.28−5.60	5.46 5.31−5.62	3.36 3.25−3.46	2.48 2.33−2.64
◆◇◇◆	4.96 4.91−5.01	5.73 5.68−5.78	5.47 5.44−5.50	6.45 6.36−6.54	6.59 6.50−6.68	3.71 3.63−3.81	3.66 3.59−3.74
◆◇◆◇	4.54 4.44−4.65	5.20 5.06−5.33	5.08 5.00−5.17	5.50 5.30−5.72	5.56 5.35−5.80	3.12 2.95−3.28	2.36 2.15−2.58
◆◇◆◆	4.79 4.74−4.83	5.59 5.54−5.64	5.28 5.25−5.31	6.27 6.18−6.35	6.40 6.31−6.49	3.55 3.45−3.66	3.53 3.43−3.62
◆◆◇◇	3.76 3.62−3.90	4.25 4.09−4.42	4.23 4.05−4.38	4.31 4.12−4.48	4.30 4.13−4.48	2.83 2.77−2.89	1.16 1.01−1.31
◆◆◇◆	4.60 4.54−4.66	5.56 5.50−5.62	5.11 5.07−5.15	6.15 6.07−6.23	6.27 6.17−6.36	3.39 3.28−3.48	3.36 3.28−3.46
◆◆◆◇	3.57 3.42−3.72	4.14 3.97−4.32	4.10 3.93−4.26	4.18 3.97−4.38	4.19 3.99−4.40	2.71 2.63−2.79	1.05 0.91−1.22
◆◆◆◆	4.45 4.36−4.52	5.47 5.39−5.53	4.99 4.95−5.02	6.17 6.11−6.24	6.26 6.20−6.32	3.32 3.21−3.44	3.31 3.21−3.42

	Diversification rate	Population Mean	Log-posterior	Log-prior	Species tree height	Species tree length	Coalescent probability
◇◇◇◇	5.31 5.18−5.45	3.51 3.40−3.61	3.36 3.25−3.50	3.61 3.53−3.70	2.54 2.34−2.72	4.39 4.26−4.52	3.19 3.08−3.31
◇◇◇◆	5.45 5.41−5.48	3.79 3.69−3.88	3.75 3.67−3.83	3.75 3.67−3.83	4.50 4.44−4.56	4.66 4.58−4.73	3.51 3.42−3.60
◇◇◆◇	5.03 4.93−5.13	3.23 3.17−3.30	3.13 3.04−3.21	3.29 3.20−3.38	2.20 2.07−2.32	4.07 3.99−4.15	2.95 2.85−3.04
◇◇◆◆	5.31 5.28−5.34	3.63 3.54−3.71	3.58 3.50−3.66	3.52 3.44−3.61	4.34 4.28−4.40	4.49 4.42−4.55	3.33 3.24−3.42
◇◆◇◇	4.10 3.92−4.28	3.04 2.95−3.14	2.99 2.88−3.09	2.89 2.77−2.99	1.12 0.97−1.28	3.03 2.85−3.21	2.83 2.73−2.92
◇◆◇◆	5.10 5.04−5.14	3.44 3.35−3.53	3.46 3.37−3.55	3.37 3.30−3.44	3.87 3.81−3.93	4.27 4.22−4.33	3.22 3.12−3.31
◇◆◆◇	3.94 3.76−4.13	2.84 2.76−2.93	2.79 2.69−2.91	2.78 2.69−2.88	0.90 0.71−1.10	2.78 2.55−3.00	2.67 2.58−2.75
◇◆◆◆	5.02 4.97−5.06	3.43 3.33−3.52	3.44 3.36−3.51	3.32 3.25−3.40	3.88 3.82−3.94	4.20 4.12−4.28	3.20 3.11−3.30
◆◇◇◇	5.22 5.11−5.31	3.98 3.90−4.06	3.69 3.58−3.80	5.05 4.94−5.15	2.48 2.34−2.64	4.46 4.36−4.56	3.56 3.46−3.65
◆◇◇◆	5.52 5.48−5.56	4.39 4.31−4.47	4.15 4.07−4.22	5.46 5.40−5.51	4.68 4.63−4.72	4.75 4.70−4.81	3.88 3.81−3.96
◆◇◆◇	5.12 5.02−5.21	3.83 3.71−3.95	3.51 3.35−3.67	4.98 4.86−5.09	2.40 2.17−2.66	4.32 4.19−4.44	3.42 3.29−3.55
◆◇◆◆	5.30 5.27−5.33	4.32 4.25−4.39	4.03 3.95−4.09	5.33 5.28−5.38	4.57 4.53−4.61	4.60 4.55−4.64	3.80 3.72−3.88
◆◆◇◇	4.19 4.04−4.35	3.56 3.48−3.64	3.33 3.25−3.42	4.10 3.96−4.24	1.16 1.00−1.33	3.42 3.26−3.60	3.24 3.16−3.32
◆◆◇◆	5.16 5.13−5.20	4.23 4.17−4.29	3.93 3.87−3.99	5.31 5.25−5.37	4.11 4.05−4.18	4.43 4.38−4.48	3.71 3.64−3.78
◆◆◆◇	4.08 3.92−4.25	3.35 3.25−3.45	3.18 3.09−3.27	3.93 3.75−4.11	1.05 0.89−1.22	3.01 2.81−3.22	3.09 3.01−3.16
◆◆◆◆	5.03 5.00−5.07	4.19 4.11−4.28	3.89 3.81−3.96	5.26 5.20−5.32	3.96 3.88−4.06	4.27 4.19−4.35	3.68 3.61−3.76

Bottom numbers show 95% confidence intervals for the mean calculated by bootstrapping

Filled diamonds indicate which new features are enabled. From left-to-right; analytical integration of population sizes, species tree relaxed clocks, coordinated topology operators, and coordinated height operators.

Table S2: Mean log(ESS per million states) for *Pseudacris* data.

	Birth-death probability	Clock rate stdev	Extinction fraction	Among-site rate variation	Transition/ Transversion κ	Phylogenetic likelihood	Minimum
◇◇◇◇	2.23 2.12−2.34	2.96 2.81−3.10	2.88 2.76−3.00	3.19 2.99−3.40	3.22 3.00−3.43	0.88 0.75−1.02	0.13 −0.06−0.33
◇◇◇◆	2.62 2.56−2.69	3.42 3.37−3.48	3.16 3.13−3.19	4.03 3.93−4.12	4.11 3.99−4.22	1.26 1.13−1.38	1.09 0.98−1.21
◇◇◆◇	2.09 2.02−2.16	2.90 2.79−3.00	2.85 2.75−2.93	3.09 2.95−3.25	3.13 2.97−3.28	0.73 0.59−0.85	0.02 −0.09−0.14
◇◇◆◆	2.57 2.51−2.63	3.38 3.32−3.43	3.19 3.17−3.23	4.03 3.94−4.12	4.13 4.06−4.21	1.26 1.16−1.36	1.11 1.03−1.19
◇◆◇◇	1.61 1.45−1.76	2.25 2.05−2.46	2.19 2.01−2.38	2.27 2.05−2.48	2.29 2.04−2.53	0.77 0.67−0.85	−0.77 −0.91−−0.62
◇◆◇◆	2.70 2.66−2.74	3.63 3.58−3.69	3.30 3.26−3.33	4.12 4.02−4.22	4.18 4.07−4.29	1.31 1.21−1.41	1.24 1.15−1.32
◇◆◆◇	1.57 1.41−1.74	2.30 2.13−2.49	2.28 2.10−2.45	2.34 2.13−2.57	2.34 2.14−2.54	0.83 0.73−0.93	−0.80 −1.00−−0.60
◇◆◆◆	2.76 2.69−2.82	3.72 3.66−3.79	3.31 3.27−3.34	4.25 4.15−4.35	4.32 4.20−4.43	1.44 1.34−1.54	1.36 1.27−1.46
◆◇◇◇	2.30 2.23−2.38	2.88 2.76−2.99	2.84 2.74−2.94	3.08 2.92−3.24	3.10 2.95−3.25	0.99 0.89−1.09	0.12 −0.04−0.27
◆◇◇◆	2.75 2.70−2.79	3.51 3.46−3.57	3.25 3.23−3.28	4.24 4.15−4.32	4.38 4.29−4.46	1.50 1.41−1.59	1.45 1.37−1.53
◆◇◆◇	2.41 2.30−2.51	3.07 2.95−3.19	2.95 2.87−3.04	3.37 3.17−3.56	3.43 3.22−3.66	0.99 0.84−1.15	0.23 0.03−0.46
◆◇◆◆	2.73 2.68−2.77	3.53 3.47−3.59	3.22 3.19−3.25	4.21 4.12−4.30	4.35 4.26−4.43	1.49 1.39−1.60	1.47 1.38−1.56
◆◆◇◇	1.90 1.75−2.05	2.39 2.22−2.55	2.36 2.19−2.54	2.44 2.26−2.60	2.43 2.26−2.61	0.97 0.91−1.03	−0.70 −0.85−−0.55
◆◆◇◆	2.84 2.78−2.90	3.79 3.73−3.86	3.35 3.30−3.38	4.39 4.30−4.46	4.50 4.41−4.59	1.62 1.52−1.73	1.60 1.51−1.69
◆◆◆◇	1.89 1.74−2.02	2.46 2.29−2.64	2.42 2.25−2.58	2.50 2.31−2.70	2.51 2.29−2.73	1.03 0.96−1.11	−0.63 −0.77−−0.47
◆◆◆◆	2.81 2.72−2.88	3.82 3.74−3.90	3.34 3.30−3.38	4.53 4.46−4.59	4.61 4.55−4.67	1.67 1.57−1.78	1.66 1.56−1.78

	Diversification rate	Population Mean	Log-posterior	Log-prior	Species tree height	Species tree length	Coalescent probability
◇◇◇◇	2.91 2.77−3.03	1.11 1.01−1.20	0.97 0.85−1.09	1.22 1.14−1.29	0.14 −0.05−0.32	2.00 1.87−2.12	0.80 0.68−0.92
◇◇◇◆	3.21 3.18−3.24	1.56 1.46−1.65	1.51 1.44−1.59	1.51 1.44−1.59	2.27 2.20−2.33	2.42 2.35−2.48	1.28 1.18−1.37
◇◇◆◇	2.88 2.77−2.97	1.08 1.02−1.13	0.97 0.89−1.05	1.14 1.04−1.22	0.04 −0.09−0.16	1.91 1.84−1.99	0.79 0.70−0.88
◇◇◆◆	3.23 3.20−3.27	1.55 1.46−1.63	1.50 1.42−1.59	1.45 1.37−1.53	2.26 2.20−2.32	2.41 2.35−2.47	1.25 1.16−1.34
◇◆◇◇	2.21 2.01−2.39	1.15 1.05−1.25	1.10 1.00−1.22	1.01 0.90−1.11	−0.77 −0.92−−0.60	1.15 0.98−1.34	0.95 0.85−1.03
◇◆◇◆	3.31 3.26−3.35	1.65 1.56−1.73	1.67 1.58−1.76	1.58 1.51−1.65	2.08 2.01−2.15	2.48 2.43−2.53	1.43 1.34−1.52
◇◆◆◇	2.24 2.07−2.41	1.14 1.05−1.23	1.09 1.00−1.21	1.08 0.99−1.18	−0.80 −1.01−−0.60	1.08 0.83−1.32	0.97 0.89−1.04
◇◆◆◆	3.36 3.32−3.40	1.77 1.67−1.85	1.78 1.71−1.84	1.66 1.59−1.73	2.22 2.16−2.27	2.54 2.47−2.61	1.54 1.45−1.63
◆◇◇◇	2.85 2.75−2.95	1.62 1.54−1.70	1.33 1.22−1.43	2.69 2.59−2.79	0.12 −0.03−0.28	2.10 2.00−2.20	1.20 1.11−1.28
◆◇◇◆	3.31 3.26−3.35	2.18 2.10−2.25	1.94 1.86−2.01	3.24 3.19−3.30	2.46 2.42−2.51	2.54 2.49−2.59	1.67 1.59−1.75
◆◇◆◇	2.99 2.88−3.09	1.70 1.58−1.81	1.38 1.20−1.54	2.85 2.74−2.95	0.27 0.04−0.52	2.19 2.07−2.30	1.28 1.15−1.42
◆◇◆◆	3.24 3.21−3.28	2.26 2.19−2.33	1.97 1.90−2.04	3.27 3.22−3.32	2.51 2.47−2.54	2.54 2.50−2.58	1.74 1.67−1.82
◆◆◇◇	2.33 2.17−2.47	1.70 1.62−1.77	1.47 1.38−1.55	2.24 2.08−2.37	−0.70 −0.86−−0.53	1.56 1.39−1.72	1.38 1.30−1.45
◆◆◇◆	3.40 3.36−3.44	2.47 2.40−2.53	2.17 2.11−2.23	3.55 3.49−3.61	2.35 2.28−2.41	2.66 2.61−2.71	1.95 1.88−2.01
◆◆◆◇	2.40 2.22−2.57	1.67 1.57−1.78	1.50 1.41−1.59	2.25 2.07−2.41	−0.63 −0.78−−0.46	1.33 1.11−1.55	1.41 1.33−1.48
◆◆◆◆	3.39 3.35−3.42	2.55 2.47−2.63	2.25 2.17−2.32	3.61 3.55−3.67	2.32 2.22−2.41	2.63 2.55−2.71	2.04 1.96−2.12

Bottom numbers show 95% confidence intervals for the mean calculated by bootstrapping
Filled diamonds indicate which new features are enabled. From left-to-right; analytical integration of population sizes, species tree relaxed clocks, coordinated topology operators, and coordinated height operators.

Table S3: Standard deviation of log(ESS per hour) for *Pseudacris* data.

	Birth-death probability	Clock rate stdev	Extinction fraction	Among-site rate variation	Transition/ Transversion κ	Phylogenetic likelihood	Minimum
◇◇◇◇	0.33 0.25−0.39	0.44 0.34−0.51	0.37 0.26−0.45	0.63 0.53−0.72	0.64 0.53−0.73	0.38 0.26−0.47	0.55 0.45−0.63
◇◇◇◆	0.20 0.13−0.25	0.16 0.11−0.19	0.09 0.07−0.10	0.29 0.22−0.35	0.34 0.26−0.41	0.39 0.27−0.49	0.34 0.25−0.42
◇◇◆◇	0.22 0.16−0.26	0.31 0.24−0.38	0.28 0.19−0.35	0.44 0.32−0.55	0.45 0.33−0.57	0.40 0.30−0.48	0.36 0.26−0.44
◇◇◆◆	0.17 0.14−0.20	0.16 0.12−0.20	0.08 0.06−0.10	0.27 0.20−0.31	0.24 0.17−0.27	0.31 0.24−0.38	0.23 0.17−0.29
◇◆◇◇	0.46 0.33−0.56	0.63 0.44−0.79	0.56 0.40−0.71	0.64 0.45−0.81	0.67 0.44−0.85	0.28 0.16−0.40	0.44 0.29−0.56
◇◆◇◆	0.13 0.10−0.15	0.16 0.12−0.20	0.11 0.08−0.13	0.30 0.22−0.37	0.34 0.27−0.42	0.29 0.21−0.35	0.24 0.17−0.29
◇◆◆◇	0.47 0.35−0.57	0.53 0.40−0.63	0.51 0.38−0.61	0.62 0.42−0.75	0.60 0.41−0.72	0.29 0.20−0.37	0.58 0.42−0.70
◇◆◆◆	0.21 0.15−0.27	0.19 0.15−0.23	0.11 0.08−0.13	0.30 0.24−0.35	0.35 0.29−0.40	0.31 0.22−0.37	0.29 0.19−0.37
◆◇◇◇	0.22 0.16−0.28	0.34 0.24−0.43	0.28 0.21−0.35	0.47 0.35−0.58	0.45 0.34−0.55	0.28 0.22−0.34	0.44 0.34−0.53
◆◇◇◆	0.13 0.10−0.16	0.15 0.11−0.19	0.09 0.07−0.10	0.25 0.20−0.29	0.25 0.19−0.30	0.26 0.19−0.32	0.23 0.17−0.28
◆◇◆◇	0.30 0.24−0.34	0.38 0.30−0.44	0.26 0.21−0.29	0.58 0.46−0.66	0.63 0.49−0.74	0.45 0.32−0.55	0.63 0.43−0.80
◆◇◆◆	0.13 0.09−0.17	0.16 0.13−0.19	0.09 0.07−0.10	0.26 0.20−0.30	0.25 0.22−0.28	0.30 0.20−0.39	0.28 0.19−0.35
◆◆◇◇	0.42 0.33−0.49	0.47 0.36−0.55	0.48 0.38−0.57	0.52 0.39−0.63	0.54 0.42−0.63	0.18 0.13−0.21	0.47 0.33−0.55
◆◆◇◆	0.16 0.13−0.19	0.17 0.13−0.20	0.11 0.07−0.14	0.21 0.16−0.26	0.26 0.17−0.32	0.30 0.22−0.35	0.26 0.20−0.31
◆◆◆◇	0.42 0.33−0.49	0.52 0.36−0.65	0.49 0.35−0.61	0.58 0.39−0.72	0.62 0.40−0.79	0.23 0.17−0.28	0.47 0.31−0.60
◆◆◆◆	0.24 0.16−0.31	0.22 0.13−0.31	0.11 0.08−0.14	0.20 0.15−0.24	0.19 0.14−0.22	0.32 0.25−0.37	0.31 0.24−0.36

	Diversification rate	Population Mean	Log-posterior	Log-prior	Species tree height	Species tree length	Coalescent probability
◇◇◇◇	0.38 0.29−0.46	0.31 0.23−0.36	0.35 0.26−0.42	0.24 0.19−0.28	0.56 0.46−0.63	0.38 0.30−0.45	0.34 0.26−0.40
◇◇◇◆	0.10 0.07−0.12	0.27 0.19−0.33	0.23 0.17−0.28	0.22 0.17−0.25	0.18 0.13−0.23	0.20 0.15−0.24	0.27 0.21−0.32
◇◇◆◇	0.29 0.21−0.38	0.17 0.14−0.20	0.24 0.16−0.30	0.25 0.14−0.34	0.37 0.27−0.45	0.23 0.17−0.27	0.27 0.18−0.34
◇◇◆◆	0.10 0.07−0.12	0.25 0.17−0.29	0.24 0.18−0.30	0.23 0.18−0.27	0.17 0.14−0.20	0.18 0.14−0.21	0.26 0.17−0.34
◇◆◇◇	0.56 0.40−0.69	0.28 0.19−0.36	0.31 0.22−0.39	0.32 0.21−0.40	0.44 0.29−0.57	0.52 0.37−0.63	0.27 0.19−0.34
◇◆◇◆	0.14 0.09−0.19	0.27 0.21−0.32	0.25 0.19−0.30	0.20 0.15−0.24	0.20 0.14−0.25	0.15 0.12−0.18	0.26 0.20−0.32
◇◆◆◇	0.51 0.39−0.61	0.25 0.17−0.32	0.31 0.18−0.42	0.27 0.21−0.33	0.58 0.42−0.72	0.65 0.48−0.77	0.24 0.15−0.32
◇◆◆◆	0.12 0.09−0.15	0.27 0.16−0.37	0.22 0.16−0.27	0.23 0.16−0.29	0.17 0.12−0.21	0.22 0.15−0.28	0.27 0.18−0.36
◆◇◇◇	0.30 0.22−0.37	0.23 0.18−0.28	0.32 0.21−0.40	0.30 0.22−0.36	0.44 0.33−0.53	0.29 0.21−0.35	0.25 0.16−0.31
◆◇◇◆	0.13 0.07−0.18	0.22 0.17−0.26	0.22 0.15−0.27	0.15 0.10−0.19	0.13 0.10−0.16	0.15 0.11−0.17	0.22 0.16−0.27
◆◇◆◇	0.29 0.23−0.32	0.33 0.24−0.41	0.47 0.32−0.60	0.33 0.25−0.39	0.69 0.47−0.87	0.35 0.27−0.41	0.37 0.26−0.47
◆◇◆◆	0.10 0.08−0.12	0.22 0.16−0.26	0.21 0.16−0.24	0.14 0.11−0.17	0.11 0.08−0.14	0.12 0.09−0.15	0.22 0.17−0.26
◆◆◇◇	0.45 0.35−0.53	0.22 0.16−0.28	0.24 0.19−0.28	0.41 0.32−0.50	0.47 0.34−0.55	0.47 0.37−0.56	0.23 0.17−0.27
◆◆◇◆	0.11 0.08−0.12	0.18 0.14−0.21	0.18 0.14−0.21	0.18 0.14−0.22	0.19 0.13−0.23	0.15 0.11−0.19	0.19 0.15−0.23
◆◆◆◇	0.49 0.34−0.61	0.30 0.21−0.37	0.27 0.20−0.32	0.50 0.35−0.62	0.47 0.30−0.59	0.62 0.48−0.73	0.22 0.17−0.25
◆◆◆◆	0.11 0.09−0.13	0.24 0.18−0.28	0.22 0.16−0.26	0.18 0.13−0.21	0.27 0.20−0.34	0.24 0.16−0.31	0.23 0.17−0.28

Bottom numbers show 95% confidence intervals for the standard deviation calculated by bootstrapping

Filled diamonds indicate which new features are enabled. From left-to-right; analytical integration of population sizes, species tree relaxed clocks, coordinated topology operators, and coordinated height operators.

Table S4: Standard deviation of log(ESS per million states) for *Pseudacris* data.

	Birth-death probability	Clock rate stdev	Extinction fraction	Among-site rate variation	Transition/Transversion κ	Phylogenetic likelihood	Minimum
◇◇◇◇	0.32 0.25−0.38	0.43 0.34−0.50	0.36 0.26−0.44	0.62 0.51−0.71	0.63 0.52−0.71	0.37 0.27−0.46	0.54 0.45−0.61
◇◇◇♦	0.20 0.13−0.25	0.15 0.11−0.19	0.09 0.06−0.10	0.28 0.21−0.34	0.33 0.26−0.39	0.38 0.26−0.48	0.34 0.25−0.42
◇◇♦◇	0.21 0.16−0.26	0.31 0.23−0.37	0.27 0.19−0.35	0.44 0.31−0.54	0.45 0.33−0.56	0.40 0.30−0.49	0.36 0.26−0.44
◇◇♦♦	0.17 0.14−0.20	0.16 0.11−0.20	0.08 0.06−0.10	0.26 0.20−0.30	0.23 0.17−0.26	0.31 0.23−0.37	0.23 0.17−0.29
◇♦◇◇	0.45 0.33−0.55	0.62 0.44−0.78	0.56 0.40−0.71	0.64 0.44−0.80	0.67 0.47−0.84	0.28 0.16−0.38	0.43 0.29−0.56
◇♦◇♦	0.13 0.10−0.15	0.16 0.12−0.20	0.10 0.08−0.13	0.30 0.22−0.37	0.34 0.27−0.41	0.28 0.20−0.34	0.23 0.16−0.29
◇♦♦◇	0.47 0.36−0.57	0.53 0.39−0.65	0.51 0.39−0.61	0.61 0.44−0.77	0.60 0.42−0.73	0.29 0.20−0.37	0.58 0.42−0.71
◇♦♦♦	0.20 0.14−0.25	0.18 0.14−0.21	0.10 0.08−0.11	0.29 0.23−0.34	0.33 0.28−0.38	0.29 0.21−0.34	0.28 0.18−0.34
♦◇◇◇	0.22 0.15−0.27	0.33 0.24−0.42	0.27 0.20−0.34	0.47 0.36−0.57	0.45 0.33−0.55	0.28 0.21−0.34	0.44 0.33−0.52
♦◇◇♦	0.14 0.10−0.17	0.15 0.11−0.19	0.09 0.07−0.10	0.25 0.19−0.29	0.25 0.19−0.30	0.26 0.19−0.32	0.23 0.17−0.27
♦◇♦◇	0.29 0.23−0.34	0.38 0.30−0.44	0.25 0.21−0.29	0.58 0.46−0.66	0.63 0.48−0.73	0.45 0.31−0.56	0.63 0.44−0.78
♦◇♦♦	0.13 0.09−0.17	0.15 0.12−0.18	0.08 0.06−0.09	0.25 0.20−0.29	0.24 0.21−0.27	0.29 0.18−0.39	0.27 0.18−0.34
♦♦◇◇	0.42 0.33−0.48	0.46 0.37−0.55	0.48 0.38−0.57	0.52 0.40−0.62	0.54 0.43−0.63	0.18 0.13−0.22	0.47 0.34−0.56
♦♦◇♦	0.17 0.13−0.20	0.18 0.13−0.21	0.10 0.07−0.13	0.21 0.15−0.25	0.26 0.17−0.32	0.30 0.22−0.35	0.26 0.20−0.30
♦♦♦◇	0.41 0.31−0.49	0.51 0.37−0.63	0.49 0.35−0.60	0.57 0.39−0.73	0.61 0.39−0.78	0.23 0.17−0.28	0.46 0.30−0.59
♦♦♦♦	0.24 0.16−0.30	0.22 0.12−0.31	0.11 0.07−0.14	0.19 0.14−0.23	0.17 0.12−0.20	0.31 0.24−0.36	0.30 0.23−0.35

	Diversification rate	Population Mean	Log-posterior	Log-prior	Species tree height	Species tree length	Coalescent probability
◇◇◇◇	0.37 0.29−0.46	0.30 0.23−0.35	0.34 0.26−0.41	0.24 0.19−0.28	0.55 0.46−0.62	0.37 0.29−0.44	0.33 0.24−0.39
◇◇◇♦	0.10 0.07−0.12	0.27 0.20−0.32	0.23 0.17−0.28	0.22 0.17−0.26	0.18 0.13−0.22	0.19 0.14−0.24	0.27 0.21−0.32
◇◇♦◇	0.29 0.20−0.37	0.17 0.14−0.19	0.24 0.17−0.30	0.25 0.14−0.34	0.37 0.27−0.44	0.23 0.18−0.27	0.27 0.19−0.34
◇◇♦♦	0.10 0.08−0.12	0.25 0.18−0.30	0.24 0.17−0.30	0.23 0.18−0.27	0.18 0.14−0.21	0.18 0.14−0.21	0.26 0.17−0.33
◇♦◇◇	0.55 0.40−0.69	0.28 0.19−0.35	0.31 0.21−0.39	0.31 0.22−0.39	0.43 0.28−0.57	0.52 0.39−0.63	0.27 0.18−0.33
◇♦◇♦	0.13 0.08−0.18	0.26 0.20−0.31	0.25 0.19−0.31	0.21 0.15−0.25	0.20 0.15−0.25	0.16 0.12−0.18	0.26 0.19−0.32
◇♦♦◇	0.51 0.40−0.60	0.25 0.17−0.32	0.31 0.18−0.43	0.27 0.21−0.32	0.58 0.42−0.70	0.65 0.48−0.77	0.24 0.15−0.32
◇♦♦♦	0.11 0.09−0.13	0.26 0.15−0.36	0.20 0.15−0.25	0.22 0.15−0.27	0.16 0.12−0.19	0.20 0.14−0.26	0.26 0.17−0.34
♦◇◇◇	0.29 0.22−0.37	0.23 0.17−0.27	0.32 0.21−0.40	0.29 0.22−0.36	0.44 0.33−0.53	0.29 0.21−0.35	0.24 0.16−0.31
♦◇◇♦	0.13 0.08−0.18	0.22 0.18−0.26	0.21 0.15−0.26	0.15 0.10−0.20	0.13 0.10−0.16	0.15 0.11−0.17	0.22 0.16−0.27
♦◇♦◇	0.28 0.22−0.32	0.34 0.24−0.42	0.48 0.32−0.60	0.33 0.25−0.39	0.68 0.46−0.88	0.35 0.27−0.41	0.38 0.27−0.47
♦◇♦♦	0.09 0.07−0.11	0.21 0.16−0.25	0.20 0.16−0.24	0.14 0.10−0.16	0.11 0.08−0.13	0.12 0.09−0.15	0.22 0.17−0.26
♦♦◇◇	0.45 0.35−0.53	0.22 0.16−0.27	0.24 0.19−0.27	0.41 0.32−0.50	0.47 0.34−0.56	0.47 0.37−0.56	0.22 0.16−0.27
♦♦◇♦	0.11 0.09−0.13	0.17 0.13−0.21	0.18 0.14−0.21	0.19 0.14−0.23	0.19 0.13−0.24	0.16 0.12−0.19	0.19 0.15−0.23
♦♦♦◇	0.49 0.35−0.61	0.29 0.20−0.37	0.26 0.20−0.31	0.49 0.35−0.61	0.46 0.32−0.58	0.62 0.47−0.73	0.21 0.17−0.25
♦♦♦♦	0.10 0.08−0.12	0.23 0.17−0.27	0.20 0.15−0.25	0.18 0.13−0.22	0.27 0.19−0.34	0.23 0.15−0.31	0.22 0.16−0.26

Bottom numbers show 95% confidence intervals for the standard deviation calculated by bootstrapping
Filled diamonds indicate which new features are enabled. From left-to-right; analytical integration of population sizes, species tree relaxed clocks, coordinated topology operators, and coordinated height operators.

Table S5: Mean log(ESS per hour) convergence for simulated data.

Statistic	Concatenation	Concatenation 10X	*BEAST	StarBEAST2 GT-UCLN	StarBEAST2 ST-UCLN
Birth-death probability	6.76 (6.67–6.85)	3.06 (2.97–3.14)	4.55 (4.46–4.64)	5.14 (5.08–5.20)	4.80 (4.73–4.86)
Clock rates σ	7.16 (7.04–7.25)	3.86 (3.82–3.90)	5.05 (4.92–5.16)	5.69 (5.60–5.76)	5.59 (5.54–5.65)
Coalescent probability	NA	NA	3.25 (3.17–3.32)	4.07 (4.00–4.15)	3.92 (3.85–4.00)
Extinction fraction	6.72 (6.68–6.76)	4.41 (4.37–4.45)	5.03 (4.91–5.14)	5.48 (5.46–5.51)	5.21 (5.18–5.24)
Log-posterior	6.75 (6.63–6.83)	2.26 (2.22–2.30)	3.36 (3.29–3.43)	4.19 (4.12–4.27)	4.06 (3.98–4.13)
Log-prior	7.14 (6.99–7.25)	3.04 (2.99–3.09)	3.60 (3.53–3.66)	5.41 (5.32–5.50)	5.43 (5.37–5.49)
Minimum	6.36 (6.24–6.45)	1.99 (1.90–2.06)	2.18 (2.04–2.32)	4.01 (3.92–4.09)	3.74 (3.66–3.84)
Net diversification rate	6.80 (6.74–6.84)	4.38 (4.31–4.43)	5.04 (4.92–5.15)	5.50 (5.47–5.53)	5.22 (5.18–5.25)
Phylogenetic likelihood	6.78 (6.73–6.82)	2.26 (2.22–2.29)	4.10 (4.00–4.20)	4.84 (4.79–4.90)	4.42 (4.35–4.49)
Population mean	NA	NA	3.50 (3.42–3.57)	4.60 (4.51–4.67)	4.43 (4.35–4.49)
Species tree height	6.65 (6.56–6.74)	2.25 (2.12–2.38)	2.20 (2.04–2.36)	4.75 (4.63–4.84)	4.13 (4.00–4.25)
Species tree length	6.59 (6.50–6.68)	2.29 (2.19–2.39)	4.22 (4.10–4.33)	4.95 (4.89–5.01)	4.55 (4.47–4.63)
Substitution model α	7.98 (7.89–8.06)	5.01 (4.92–5.10)	5.30 (5.14–5.45)	6.67 (6.61–6.73)	6.42 (6.36–6.47)
Substitution model κ	8.36 (8.29–8.42)	5.15 (5.05–5.25)	5.32 (5.16–5.48)	6.84 (6.77–6.90)	6.57 (6.51–6.64)

Numbers in parentheses show 95% confidence intervals calculated by bootstrapping

Table S6: Mean log(ESS per million states) convergence for simulated data.

Statistic	Concatenation	Concatenation 10X	*BEAST	StarBEAST2 GT-UCLN	StarBEAST2 ST-UCLN
Birth-death probability	5.28 (5.20–5.36)	3.69 (3.62–3.77)	2.12 (2.03–2.21)	2.89 (2.83–2.95)	2.96 (2.89–3.02)
Clock rates σ	5.68 (5.56–5.78)	4.50 (4.46–4.54)	2.62 (2.48–2.74)	3.43 (3.36–3.50)	3.75 (3.70–3.80)
Coalescent probability	NA	NA	0.81 (0.74–0.89)	1.82 (1.75–1.89)	2.08 (2.00–2.14)
Extinction fraction	5.24 (5.20–5.28)	5.05 (5.02–5.09)	2.60 (2.49–2.71)	3.23 (3.20–3.26)	3.37 (3.34–3.39)
Log-posterior	5.27 (5.16–5.36)	2.90 (2.87–2.93)	0.93 (0.85–1.00)	1.94 (1.87–2.01)	2.21 (2.13–2.28)
Log-prior	5.66 (5.52–5.77)	3.68 (3.64–3.72)	1.17 (1.10–1.23)	3.16 (3.06–3.25)	3.59 (3.52–3.65)
Minimum	4.88 (4.76–4.98)	2.62 (2.55–2.70)	-0.25 (−0.40–−0.11)	1.75 (1.67–1.84)	1.90 (1.81–1.99)
Net diversification rate	5.32 (5.27–5.36)	5.02 (4.97–5.06)	2.61 (2.50–2.71)	3.25 (3.21–3.28)	3.37 (3.34–3.40)
Phylogenetic likelihood	5.30 (5.25–5.34)	2.89 (2.86–2.92)	1.66 (1.57–1.76)	2.59 (2.54–2.65)	2.58 (2.51–2.64)
Population mean	NA	NA	1.06 (0.99–1.13)	2.34 (2.26–2.43)	2.58 (2.50–2.65)
Species tree height	5.18 (5.09–5.26)	2.89 (2.77–3.00)	-0.23 (−0.39–−0.08)	2.50 (2.39–2.60)	2.28 (2.15–2.40)
Species tree length	5.12 (5.04–5.20)	2.93 (2.84–3.01)	1.79 (1.67–1.90)	2.70 (2.63–2.76)	2.70 (2.63–2.78)
Substitution model α	6.50 (6.40–6.59)	5.65 (5.58–5.73)	2.87 (2.72–3.01)	4.42 (4.36–4.48)	4.57 (4.51–4.63)
Substitution model κ	6.89 (6.81–6.94)	5.79 (5.71–5.87)	2.89 (2.72–3.04)	4.59 (4.52–4.65)	4.73 (4.66–4.79)

Numbers in parentheses show 95% confidence intervals calculated by bootstrapping

Table S7: Standard deviation of log(ESS per hour) convergence for simulated data.

Statistic	Concatenation	Concatenation 10X	*BEAST	StarBEAST2 GT-UCLN	StarBEAST2 ST-UCLN
Birth-death probability	0.46 (0.39–0.53)	0.45 (0.40–0.51)	0.46 (0.37–0.55)	0.33 (0.28–0.37)	0.33 (0.29–0.36)
Clock rates σ	0.51 (0.23–0.76)	0.19 (0.16–0.21)	0.63 (0.52–0.73)	0.38 (0.27–0.51)	0.26 (0.19–0.32)
Coalescent probability	NA	NA	0.36 (0.31–0.40)	0.38 (0.33–0.43)	0.36 (0.30–0.40)
Extinction fraction	0.22 (0.17–0.27)	0.24 (0.20–0.28)	0.56 (0.44–0.68)	0.15 (0.12–0.18)	0.15 (0.12–0.19)
Log-posterior	0.52 (0.15–0.83)	0.19 (0.17–0.22)	0.37 (0.32–0.42)	0.38 (0.33–0.43)	0.38 (0.32–0.43)
Log-prior	0.65 (0.25–0.97)	0.25 (0.21–0.30)	0.34 (0.28–0.39)	0.45 (0.29–0.60)	0.32 (0.24–0.41)
Minimum	0.57 (0.29–0.80)	0.42 (0.35–0.48)	0.73 (0.61–0.84)	0.44 (0.34–0.55)	0.46 (0.39–0.52)
Net diversification rate	0.25 (0.20–0.31)	0.28 (0.23–0.31)	0.57 (0.43–0.67)	0.16 (0.12–0.19)	0.18 (0.14–0.22)
Phylogenetic likelihood	0.23 (0.16–0.32)	0.19 (0.17–0.21)	0.48 (0.40–0.54)	0.28 (0.24–0.32)	0.33 (0.28–0.39)
Population mean	NA	NA	0.36 (0.30–0.41)	0.42 (0.35–0.47)	0.36 (0.31–0.41)
Species tree height	0.45 (0.38–0.52)	0.64 (0.56–0.71)	0.77 (0.64–0.88)	0.53 (0.39–0.69)	0.61 (0.52–0.68)
Species tree length	0.45 (0.38–0.52)	0.49 (0.42–0.55)	0.58 (0.48–0.66)	0.31 (0.27–0.35)	0.37 (0.33–0.41)
Substitution model α	0.42 (0.32–0.54)	0.43 (0.37–0.49)	0.76 (0.63–0.88)	0.30 (0.20–0.42)	0.30 (0.24–0.35)
Substitution model κ	0.34 (0.14–0.52)	0.49 (0.42–0.55)	0.78 (0.64–0.89)	0.33 (0.22–0.44)	0.33 (0.27–0.39)

Numbers in parentheses show 95% confidence intervals calculated by bootstrapping

Table S8: Standard deviation of log(ESS per million states) convergence for simulated data.

Statistic	Concatenation	Concatenation 10X	*BEAST	StarBEAST2 GT-UCLN	StarBEAST2 ST-UCLN
Birth-death probability	0.43 (0.35–0.49)	0.38 (0.33–0.43)	0.45 (0.36–0.53)	0.32 (0.28–0.37)	0.32 (0.28–0.36)
Clock rates σ	0.54 (0.25–0.79)	0.19 (0.16–0.21)	0.63 (0.52–0.73)	0.38 (0.26–0.50)	0.26 (0.19–0.33)
Coalescent probability	NA	NA	0.36 (0.31–0.40)	0.38 (0.33–0.42)	0.35 (0.29–0.40)
Extinction fraction	0.20 (0.14–0.27)	0.18 (0.15–0.21)	0.55 (0.43–0.67)	0.15 (0.12–0.17)	0.15 (0.11–0.18)
Log-posterior	0.53 (0.13–0.84)	0.15 (0.13–0.16)	0.37 (0.32–0.41)	0.38 (0.33–0.42)	0.37 (0.31–0.43)
Log-prior	0.67 (0.27–1.01)	0.19 (0.15–0.23)	0.33 (0.27–0.38)	0.45 (0.28–0.60)	0.31 (0.23–0.42)
Minimum	0.57 (0.26–0.85)	0.35 (0.29–0.41)	0.72 (0.61–0.83)	0.44 (0.35–0.54)	0.45 (0.38–0.51)
Net diversification rate	0.24 (0.17–0.31)	0.22 (0.18–0.26)	0.56 (0.43–0.67)	0.15 (0.12–0.19)	0.17 (0.13–0.20)
Phylogenetic likelihood	0.23 (0.14–0.35)	0.15 (0.13–0.17)	0.47 (0.40–0.53)	0.28 (0.24–0.32)	0.33 (0.28–0.39)
Population mean	NA	NA	0.35 (0.30–0.39)	0.41 (0.35–0.47)	0.35 (0.31–0.39)
Species tree height	0.41 (0.35–0.47)	0.57 (0.50–0.63)	0.76 (0.64–0.87)	0.54 (0.40–0.70)	0.60 (0.50–0.67)
Species tree length	0.42 (0.35–0.47)	0.41 (0.35–0.46)	0.57 (0.48–0.66)	0.31 (0.27–0.35)	0.36 (0.31–0.39)
Substitution model α	0.46 (0.36–0.60)	0.38 (0.32–0.43)	0.75 (0.63–0.87)	0.30 (0.20–0.41)	0.28 (0.22–0.35)
Substitution model κ	0.34 (0.10–0.55)	0.43 (0.37–0.48)	0.77 (0.64–0.88)	0.33 (0.22–0.44)	0.32 (0.25–0.39)

Numbers in parentheses show 95% confidence intervals calculated by bootstrapping