

Table A.

Average topological distances from the true tree (d_T) (\pm SE) of trees inferred according to JC, Kimura and HKY+ Γ models under the ML criteria (24 taxa data sets generated according to HKY+ Γ model with $\kappa=5$ and based on CR topology).

Gamma parameter	JC			Kimura			HKY+ Γ		
	SA	SA+NNI	SA+TBR	SA	SA+NNI	SA+TBR	SA	SA+NNI	SA+TBR
300 nucleotides									
0.1	22.1 \pm 0.5	22.1 \pm 0.5	20.3 \pm 0.6	22.7 \pm 0.6	24.3 \pm 0.5	23.0 \pm 0.6	21.7 \pm 0.6	21.6 \pm 0.7	18.1 \pm 0.6
0.2	14.0 \pm 0.5	14.2 \pm 0.5	12.9 \pm 0.6	13.8 \pm 0.6	13.0 \pm 0.6	12.5 \pm 0.6	14.3 \pm 0.7	12.0 \pm 0.6	10.7 \pm 0.8
0.3	13.7 \pm 0.4	11.5 \pm 0.5	10.8 \pm 0.5	12.4 \pm 0.6	10.7 \pm 0.6	9.9 \pm 0.6	14.2 \pm 0.6	10.5 \pm 0.6	8.3 \pm 0.7
1.0	8.2 \pm 0.5	5.5 \pm 0.5	5.4 \pm 0.5	5.8 \pm 0.6	5.1 \pm 0.6	4.8 \pm 0.6	6.6 \pm 0.6	8.1 \pm 0.7	6.9 \pm 0.7
1000 nucleotides									
0.1	10.1 \pm 0.5	7.8 \pm 0.5	7.4 \pm 0.5	9.8 \pm 0.5	8.0 \pm 0.5	7.3 \pm 0.6	8.2 \pm 0.6	6.6 \pm 0.6	5.8 \pm 0.7
0.2	7.5 \pm 0.5	5.3 \pm 0.5	5.3 \pm 0.5	7.4 \pm 0.5	5.5 \pm 0.5	5.3 \pm 0.5	5.6 \pm 0.6	4.9 \pm 0.6	5.7 \pm 0.6
0.3	6.0 \pm 0.5	5.6 \pm 0.6	6.4 \pm 0.5	6.4 \pm 0.6	5.6 \pm 0.6	7.0 \pm 0.6	3.8 \pm 0.7	2.5 \pm 0.6	4.4 \pm 0.7
1.0	4.3 \pm 0.5	3.1 \pm 0.5	3.3 \pm 0.6	4.0 \pm 0.5	3.0 \pm 0.5	2.9 \pm 0.6	2.4 \pm 0.6	1.5 \pm 0.6	1.5 \pm 0.6

Notes: JC - Jukes-Cantor, HKY - Hishino-Kasegawa-Yano, SA - stepwise-addition, NNI - nearest neighbor interchange, TBR - tree bisection-reconnection

Table B.

Average topological distances from the true tree (d_T) (\pm SE) of trees inferred according to JC, Kimura and HKY+ Γ models under the ML criteria (24 taxa data sets generated according to HKY+ Γ model with $\kappa=20$ and based on CR topology).

Gamma parameter	JC			Kimura			HKY+ Γ		
	SA	SA+NNI	SA+TBR	SA	SA+NNI	SA+TBR	SA	SA+NNI	SA+TBR
300 nucleotides									
0.1	22.2 \pm 0.5	21.6 \pm 0.5	18.8 \pm 0.6	21.1 \pm 0.6	20.0 \pm 0.6	18.9 \pm 0.7	20.5 \pm 0.6	20.2 \pm 0.6	18.9 \pm 0.6
0.2	16.8 \pm 0.5	14.9 \pm 0.5	13.6 \pm 0.6	14.8 \pm 0.6	13.8 \pm 0.6	12.9 \pm 0.6	15.3 \pm 0.6	14.3 \pm 0.7	12.2 \pm 0.8
0.3	15.0 \pm 0.5	11.9 \pm 0.5	10.7 \pm 0.6	13.4 \pm 0.6	11.3 \pm 0.6	10.4 \pm 0.6	12.5 \pm 0.6	10.9 \pm 0.6	8.6 \pm 0.7
1.0	15.7 \pm 0.4	13.1 \pm 0.5	12.1 \pm 0.5	9.1 \pm 0.6	7.5 \pm 0.7	7.6 \pm 0.7	8.9 \pm 0.7	6.8 \pm 0.7	6.9 \pm 0.7
1000 nucleotides									
0.1	11.0 \pm 0.6	9.8 \pm 0.7	9.6 \pm 0.7	10.4 \pm 0.8	9.0 \pm 0.8	8.2 \pm 0.9	9.3 \pm 0.9	9.1 \pm 0.9	7.8 \pm 0.9
0.2	6.7 \pm 0.6	6.7 \pm 0.6	6.7 \pm 0.8	6.3 \pm 0.8	7.7 \pm 0.9	7.0 \pm 1.0	5.7 \pm 0.9	6.9 \pm 0.9	4.6 \pm 0.9
0.3	12.7 \pm 0.7	9.3 \pm 0.8	9.3 \pm 0.8	12.7 \pm 0.7	9.3 \pm 0.8	6.0 \pm 0.9	6.0 \pm 0.8	2.5 \pm 0.9	2.5 \pm 0.9
1.0	7.3 \pm 0.7	6.9 \pm 0.8	7.0 \pm 0.9	5.1 \pm 0.8	4.9 \pm 0.8	4.9 \pm 0.9	3.1 \pm 0.9	2.4 \pm 0.8	2.4 \pm 0.9

Notes: JC - Jukes-Cantor, HKY - Hishino-Kasegawa-Yano, SA - stepwise-addition, NNI - nearest neighbor interchange, TBR - tree bisection-reconnection

Table C.

Average topological distances from the true tree (d_T) of trees inferred according to JC, JC+ Γ , Kimura, Kimura+ Γ and HKY+ Γ models under the ML criteria (24 taxa data sets generated according to JC+ Γ model and based on VR topology).

	JC			JC+ Γ			Kimura			Kimura+ Γ			HKY+ Γ		
Gamma parameter	SA	SA+N NI	SA+ TBR	SA	SA+N NI	SA+ TBR	SA	SA+N NI	SA+ TBR	SA	SA+N NI	SA+ TBR	SA	SA+N NI	SA+ TBR
300 nucleotides															
0.1	19.7	19.2	18.3	16.0	15.8	19.7	20.1	17.9	18.7	18.0	19.2	11.3	20.4	18.2	17.6
0.2	15.2	13.1	12.4	16.5	23.2	12.5	15.2	13.0	12.4	18.0	23.5	11.3	16.1	13.8	13.4
0.3	12.0	9.7	8.6	11.0	8.8	8.8	11.8	9.2	8.2	10.0	8.8	7.3	11.8	9.5	8.9
1.0	10.8	8.1	8.6	3.3	3.6	3.6	10.9	8.9	7.5	3.3	3.6	4.0	10.3	8.0	7.4
1000 nucleotides															
0.1	8.9	7.3	6.4	4.7	3.3	3.3	8.9	7.3	6.4	4.7	3.0	3.0	7.0	6.2	5.7
0.2	7.5	5.2	4.4	4.0	3.0	3.0	7.5	5.2	4.1	2.0	2.0	2.0	5.2	3.0	3.2
0.3	5.9	2.8	2.8	2.0	2.0	2.0	5.7	2.8	2.9	4.0	2.0	0.0	3.7	1.8	2.0
1.0	3.3	2.0	1.6	0.7	0.0	0.0	3.3	2.0	1.6	0.7	0.0	0.0	0.9	0.6	0.3

Notes: JC - Jukes-Cantor, HKY - Hishino-Kasegawa-Yano, SA - stepwise-addition, NNI - nearest neighbor interchange, TBR - tree bisection-reconnection

Table D.

Average topological distances from the true tree (d_T) of trees inferred according to JC, JC+ Γ , Kimura, Kimura+ Γ and HKY+ Γ models under the ML criteria (24 taxa data sets generated according to Kimura+ Γ model and based on VR topology).

Gamma parameter	JC			JC+ Γ			Kimura			Kimura+ Γ			HKY+ Γ		
	SA	SA+N	SA+	SA	SA+N	SA+	SA	SA+N	SA+	SA	SA+N	SA+	SA	SA+N	SA+
		NI	TBR		NI	TBR		NI	TBR		NI	TBR		NI	TBR
300 nucleotides															
0.1	23.3	22.5	19.7	17.7	21.1	16.0	22.1	20.4	19.2	18.4	22.7	13.7	20.5	18.9	14.9
0.2	16.9	14.4	12.7	16.4	13.0	10.2	14.7	12.9	10.8	13.6	9.2	9.5	13.6	11.4	9.4
0.3	15.2	12.1	10.7	11.2	12.2	9.9	11.9	8.4	8.8	12.8	10.6	9.4	10.9	8.1	7.6
1.0	9.1	7.3	5.9	9.2	6.4	4.5	8.0	5.9	5.4	9.2	4.3	4.3	8.4	5.5	4.9
1000 nucleotides															
0.1	9.2	6.0	6.0	22.7	17.6	17.0	8.4	6.4	6.0	20.7	14.9	13.6	4.8	5.0	3.0
0.2	9.2	7.6	6.4	10.7	6.8	6.8	9.2	7.2	6.8	8.0	5.6	8.3	6.0	3.0	3.0
0.3	4.0	4.0	4.0	16.7	17.2	9.3	6.8	2.8	3.5	14.7	8.0	8.0	5.5	2.0	3.0
1.0	4.8	2.4	2.4	9.3	10.0	8.8	3.6	2.8	2.8	8.7	6.0	5.5	3.2	2.0	2.0

Notes: JC - Jukes-Cantor, HKY - Hishino-Kasegawa-Yano, SA - stepwise-addition, NNI - nearest neighbor interchange, TBR - tree bisection-reconnection

Table E.

The negative log likelihood values (-LnL) of trees inferred according to JC, JC+ Γ , Kimura, Kimura+ Γ and HKY+ Γ models under the ML criteria (24 taxa data sets generated according to HKY+ Γ model with $\kappa=5$, $a=0.2$ and based on VR topology).

Heuristic search	JC	JC+ Γ	Kimura	Kimura+ Γ	HKY+ Γ
300 nucleotides					
SA	2928.72	2559.45	2910.70	2537.80	2410.09
SA+NNI	2918.92	2557.53	2901.78	2535.59	2406.66
SA+TBR	2912.98	2557.23	2896.70	2489.36	2405.80
1000 nucleotides					
SA	10326.60	9272.26	10273.31	9200.05	9052.11
SA+NNI	10316.60	9270.28	10260.56	9199.27	8597.38
SA+TBR	10311.61	9270.28	10260.56	9146.36	8565.23

Notes: JC - Jukes-Cantor, HKY - Hishino-Kasegawa-Yano, SA - stepwise-addition, NNI - nearest neighbor interchange, TBR - tree bisection-reconnection