

Appendix

list of all transition/transversion split models

model number	r_{ac}	r_{ag}	r_{at}	r_{cg}	r_{ct}	r_{gt}	name
0	1	1	1	1	1	1	JC69/F81
1	1	2	1	1	2	1	K80/HKY
2	1	2	1	1	2	3	
3	1	2	1	1	3	1	TN93
4	1	2	1	1	3	4	
5	1	2	1	3	2	1	
6	1	2	1	3	2	3	
7	1	2	1	3	2	4	
8	1	2	1	3	4	1	
9	1	2	1	3	4	3	
10	1	2	1	3	4	5	
11	1	2	3	1	2	1	
12	1	2	3	1	2	3	
13	1	2	3	1	2	4	
14	1	2	3	1	4	1	
15	1	2	3	1	4	3	
16	1	2	3	1	4	5	
17	1	2	3	3	2	1	K81
18	1	2	3	3	2	3	
19	1	2	3	3	2	4	
20	1	2	3	3	4	1	TIM
21	1	2	3	3	4	3	
22	1	2	3	3	4	5	
23	1	2	3	4	2	1	
24	1	2	3	4	2	3	
25	1	2	3	4	2	4	
26	1	2	3	4	2	5	TVM
27	1	2	3	4	5	1	
28	1	2	3	4	5	3	
29	1	2	3	4	5	4	
30	1	2	3	4	5	6	GTR

List of all named models, and potential models to split into

JC69/F81 111111 : 121121

K80/HKY 121121 : 121131, 123321

TN93 121131 : 123341

K81 123321 : 123341,123324

TIM 123341 : 123345

123324 : 123345,123425

123345 : 123456

TVM 123425 : 123456

123345 : 123456

GTR 123456 :

List of all transition/tranversionsplit models, and potential models to split into

111111 : 121121
121121 : 121123, 121131, 121321, 121323, 123121, 123123, 123321, 123323
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123454 : 123456
123456 :

List of all reversible models, and potential models to split into

111111 : 111112, 111121, 111122, 111211, 111212, 111221, 111222, 112111, 112112, 112121, 112122, 112211, 112212, 112221, 112222, 121111, 121112, 121121, 121122, 121211, 121212, 121221, 121222, 122111, 122112, 122121, 122122, 122211, 122212, 122221, 122222
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123456 :

List of parameters reported by the model

- BMT_ModelIndicator is the index of the substitution model as listed in the Appendix.
- substmodel is the model represented as a 6-digit number, where the position of the digit refers to rates ac, ag, at, cg, ct and gt respectively, and equal digits indicates that rates are shared, so 111111 is Jukes Cantor (if frequencies are kept equal), 121121 is HKY, 123456 is GTR etc.
- rateAC, . . . , rateGT are the rates according to the model. ESSs should be good for these rates, but if you plot joint-marginals of pairs you may find high correlation between some of these rates.
- BMT_Rates.1 to 6 are the rates used to build up the rate matrix. If only low parameter models are samples, the higher rates will be sampled very infrequently, and you should expect low ESSs for them. Correlation between pairs of rates should be low.
- BM_gammaShape is the gamma shape parameter as it is being sampled. For parts of the chain that gamma rate heterogeneity is switched off, the parameter will not be sampled, and the trace will show periods where the parameter is stuck.
- hasGammaRates indicates whether gamma rate heterogeneity it used (1) or not used (0). The mean can be interpreted as the proportion of time that gamma rate heterogeneity is switched on.
- ActiveGammaShape is the gamma shape parameter when it is sampled, but it is zero when it is not sampled. To get the estimate of the mean of the shape parameter, divide the mean ActiveGammaShape by the mean of hasGammaRates.
- BMT_ProportionInvariable, hasInvariableSites and ActivePropInvariable are the value for proportion invariable similar to BMG_gammaShape, hasGammaRates and ActiveGammaShape respectively.

- hasEqualFreqs indicates whether equal frequencies are used and the mean can be interpreted as the proportion of time that equal frequencies is used. When empirical frequencies are used, this parameter is not reported.

95% HPD of models for Primates data

empirical freqs			estimated freqs		
posterior support	cumulative support	model	posterior support	cumulative support	model
21.12 %	21.12 %	121323	16.19%	16.19%	121121
17.48 %	38.60 %	123424	14.09%	30.27%	121123
13.71 %	52.31 %	123324	10.25%	40.53%	121323
10.13 %	62.44 %	123323	9.71%	50.24%	121131
7.82 %	70.26 %	121324	5.31%	55.55%	121134
7.74 %	78.00 %	121123	4.63%	60.18%	123323
5.48 %	83.48 %	123425	4.28%	64.46%	121321
2.87 %	86.35 %	123423	3.94%	68.40%	121324
2.69 %	89.03 %	121343	2.98%	71.38%	121343
2.24 %	91.28 %	123454	2.79%	74.17%	123324
1.50 %	92.78 %	123345	2.43%	76.60%	121341
1.38 %	94.16 %	123343	2.37%	78.97%	123123
1.27 %	95.42 %	123124	2.24%	81.21%	123343
			2.09%	83.30%	123424
			1.96%	85.26%	123321
			1.96%	87.21%	123124
			1.94%	89.16%	123121
			1.52%	90.68%	123143
			1.36%	92.03%	123341
			1.32%	93.36%	123423
			1.17%	94.52%	123141
			1.14%	95.67%	121345

Freqs	Site Model	rate coverage						mean rate	Subst. Model coverage
		AC	AG	AT	CG	CT	GT		
equal	plain	94	94	98	93	97	96	95.3	97
equal	+G	96	94	91	97	96	98	95.3	95
equal	+I	95	95	94	92	94	93	93.8	96
equal	+G+I	95	95	96	95	94	97	95.3	95
unequal	plain	96	95	93	95	99	97	95.8	95
unequal	+G	93	97	90	92	95	96	93.8	97
unequal	+I	94	97	96	96	97	96	96.0	95
unequal	+G+I	93	92	97	91	93	96	93.7	96
Mean		94.5	94.9	94.4	93.9	95.6	96.1	94.9	95.8

Freqs	Site Model	Site Model coverage	α	p_{inv}	frequency coverage	frequency coverage			
						A	C	G	T
equal	plain	100			100	100	100	100	100
equal	+G	98	90		100	100	100	100	100
equal	+I	94		92	100	100	100	100	100
equal	+G+I	98	92	90	100	100	100	100	100
unequal	plain	100			100	94	95	92	96
unequal	+G	95	94		100	95	95	93	94
unequal	+I	94		89	100	96	90	92	94
unequal	+G+I	97	95	95	100	96	95	97	96
Mean		97.0	92.8	91.5	100.0	97.6	96.9	96.8	97.5

Table S1: Results as in Table 1, but for 5 taxa, relaxed clock, sequence length of 10K

Freqs	Site Model	rate coverage						mean rate	Subst. Model coverage
		AC	AG	AT	CG	CT	GT		
equal	plain	9	54	10	8	56	11	24.7	4
equal	+G	9	54	11	11	55	11	25.2	4
equal	+I	11	50	13	10	50	14	24.7	4
equal	+G+I	10	54	13	10	55	14	26.0	4
unequal	plain	7	32	10	9	30	9	16.2	4
unequal	+G	11	35	16	11	33	13	19.8	4
unequal	+I	12	37	14	12	35	15	20.8	4
unequal	+G+I	13	36	15	12	36	13	20.8	4
Mean		10.2	44.0	12.8	10.4	43.8	12.5	22.3	4.0

Freqs	Site Model	Site Model coverage	α	p_{inv}	frequency coverage	frequency coverage			
						A	C	G	T
equal	plain	88			34	49	46	44	51
equal	+G	94	79		43	53	55	54	59
equal	+I	93		71	35	49	53	51	51
equal	+G+I	96	89	87	42	55	57	56	59
unequal	plain	84			100	31	36	33	44
unequal	+G	92	83		100	43	46	33	46
unequal	+I	91		69	100	37	40	38	46
unequal	+G+I	95	86	89	100	43	44	40	46
Mean		91.6	84.2	79.0	69.2	45.0	47.1	43.6	50.2

Table S2: Results as in Table 1, but for 5 taxa, relaxed clock, sequence length of 10K, substitution model fixed to HKY

Freqs	Site Model	rate coverage						mean rate	Subst. Model coverage
		AC	AG	AT	CG	CT	GT		
equal	plain	96	96	95	91	96	92	94.3	2
equal	+G	97	96	91	95	96	97	95.3	2
equal	+I	96	98	94	97	95	96	96.0	2
equal	+G+I	92	91	96	97	93	94	93.8	2
unequal	plain	97	92	96	91	97	98	95.2	2
unequal	+G	95	97	92	90	94	93	93.5	2
unequal	+I	95	96	97	94	93	95	95.0	2
unequal	+G+I	92	94	95	92	96	95	94.0	2
Mean		95.0	95.0	94.5	93.4	95.0	95.0	94.6	2.0

Freqs	Site Model	Site Model coverage	α	p_{inv}	frequency coverage	frequency coverage			
						A	C	G	T
equal	plain	100			99	100	100	100	100
equal	+G	92	88		100	100	100	100	100
equal	+I	96		97	100	100	100	100	100
equal	+G+I	98	92	89	98	100	100	100	100
unequal	plain	100			100	95	96	95	95
unequal	+G	95	95		100	95	97	93	92
unequal	+I	94		90	100	95	89	96	92
unequal	+G+I	97	89	90	100	93	94	97	96
Mean		96.5	91.0	91.5	99.6	97.2	97.0	97.6	96.9

Table S3: Results as in Table 1, but for 5 taxa, relaxed clock, sequence length of 10K, substitution model fixed to GTR

Freqs	Site Model	rate coverage						mean rate	Subst. Model coverage
		AC	AG	AT	CG	CT	GT		
equal	plain	95	97	95	92	95	93	94.5	97
equal	+G	92	94	94	96	92	94	93.7	96
equal	+I	92	94	89	91	93	94	92.2	99
equal	+G+I	94	98	91	96	93	92	94.0	96
unequal	plain	94	94	94	93	92	95	93.7	96
unequal	+G	95	96	92	94	98	93	94.7	98
unequal	+I	93	94	93	94	94	92	93.3	96
unequal	+G+I	96	94	94	96	94	92	94.3	98
Mean		93.9	95.1	92.8	94.0	93.9	93.1	93.8	97.0

Freqs	Site Model	Site Model coverage	α	p_{inv}	frequency coverage	frequency coverage			
						A	C	G	T
equal	plain	100			100	100	100	100	100
equal	+G	95	93		100	100	100	100	100
equal	+I	98		94	100	100	100	100	100
equal	+G+I	94	88	88	99	100	100	100	100
unequal	plain	99			100	92	94	95	96
unequal	+G	88	87		100	92	90	95	94
unequal	+I	98		94	100	95	95	99	96
unequal	+G+I	94	86	87	100	96	95	88	92
Mean		95.8	88.5	90.8	99.9	96.9	96.8	97.1	97.2

Table S4: Results as in Table 1, but for 16 taxa, relaxed clock, sequence length of 5K

Freqs	Site Model	rate coverage						mean rate	Subst. Model coverage
		AC	AG	AT	CG	CT	GT		
equal	plain	96	95	93	94	95	91	94.0	96
equal	+G	91	94	92	95	93	93	93.0	96
equal	+I	98	91	94	95	96	96	95.0	93
equal	+G+I	97	99	96	97	96	98	97.2	97
unequal	plain	95	97	96	95	93	92	94.7	96
unequal	+G	95	95	97	95	94	95	95.2	96
unequal	+I	93	94	94	100	95	92	94.7	98
unequal	+G+I	94	93	97	98	93	96	95.2	97
Mean		94.9	94.8	94.9	96.1	94.4	94.1	94.9	96.1

Freqs	Site Model	Site Model coverage	α	p_{inv}	frequency coverage	frequency coverage			
						A	C	G	T
equal	plain	100			97	100	100	100	100
equal	+G	92	86		96	100	100	100	100
equal	+I	95		93	94	100	99	99	100
equal	+G+I	94	93	88	94	100	100	100	100
unequal	plain	100			99	96	93	90	92
unequal	+G	92	89		98	93	96	97	97
unequal	+I	99		91	100	97	93	93	94
unequal	+G+I	95	87	84	100	94	95	95	95
Mean		95.9	88.8	89.0	97.2	97.5	97.0	96.8	97.2

Table S5: Results as in Table 1, but for 16 taxa, relaxed clock, sequence length of 1K

Freqs	Site Model	rate coverage						mean rate	Subst. Model coverage
		AC	AG	AT	CG	CT	GT		
equal	plain	93	96	94	93	97	98	95.2	94
equal	+G	92	94	98	96	95	97	95.3	94
equal	+I	97	94	94	93	95	91	94.0	96
equal	+G+I	99	95	96	97	93	99	96.5	95
unequal	plain	90	97	90	98	93	97	94.2	96
unequal	+G	95	95	98	96	94	96	95.7	97
unequal	+I	96	95	96	95	97	93	95.3	98
unequal	+G+I	95	93	94	93	93	95	93.8	98
Mean		94.6	94.9	95.0	95.1	94.6	95.8	95.0	96.0

Freqs	Site Model	Site Model coverage	α	p_{inv}	frequency coverage	frequency coverage			
						A	C	G	T
equal	plain	100			89	99	100	100	99
equal	+G	93	88		85	100	100	100	100
equal	+I	98		96	85	93	100	100	100
equal	+G+I	93	87	85	81	94	99	100	100
unequal	plain	98			99	95	92	90	87
unequal	+G	93	94		98	92	97	98	94
unequal	+I	99		90	99	91	93	95	93
unequal	+G+I	94	87	85	98	95	94	95	94
Mean		96.0	89.0	89.0	91.8	94.9	96.9	97.2	95.9

Table S6: Results as in Table 1, but for 16 taxa, relaxed clock, sequence length of 0.5K

5 taxa 10K sequences					
	jModelTest			bModelTest	
	AIC	AIC	BIC	BIC	
	95% coverage best fit		95% coverage best fit		coverage
Equal Freq	92	53	90	82	97
Equal Freq + G	85	47	84	72	96
Equal Freq + G + I	93	46	86	70	97
Equal Freq + I	93	44	87	78	96
Unequal Freq	93	42	89	75	97
Unequal Freq + G	84	47	79	69	95
Unequal Freq + G + I	87	45	77	68	93
Unequal Freq + I	88	52	81	77	97
mean:	89.4	47.0	84.1	73.9	96

16 taxa 1K sequences					
	jModelTest			bModelTest	
	AIC	AIC	BIC	BIC	
	95% coverage best fit		95% coverage best fit		coverage
Equal Freq	73	34	71	48	96
Equal Freq + G	76	34	74	40	96
Equal Freq + G + I	73	32	68	42	97
Equal Freq + I	72	38	74	48	93
Unequal Freq	73	43	73	45	96
Unequal Freq + G	69	37	65	38	96
Unequal Freq + G + I	62	30	59	35	97
Unequal Freq + I	70	37	72	39	98
mean:	71.0	35.6	69.5	41.9	96.1

16 taxa 0.5K sequences					
	jModelTest			bModelTest	
	AIC	AIC	BIC	BIC	
	95% coverage best fit		95% coverage best fit		coverage
Equal Freq	66	31	66	32	94
Equal Freq + G	73	41	69	38	94
Equal Freq + G + I	64	32	56	31	95
Equal Freq + I	64	31	63	38	96
Unequal Freq	72	37	67	34	96
Unequal Freq + G	58	28	56	29	97
Unequal Freq + G + I	58	21	55	21	98
Unequal Freq + I	59	25	57	27	98
mean:	64.3	30.8	61.1	31.3	96

Table S7: Model coverage by jModelTest and bModelTest. **jModelTest 95% coverage** columns show the number of times the true substitution model was included in the smallest set of substitution models covering 95% of the weight according to the AIC and BIC criterion in jModelTest. **jModelTest best fit** columns show the number of times the best scoring model according to the BIC criterion is the true model. **bModelTest coverage** columns show the number of times the 95% credible set of substitution models contains the true model.