

APPENDIX S1: Characteristics of the Bayesian Inference run on a concatenated matrix of four chloroplast sequences on 281 samples across Lamiids.

Average standard deviation of split frequencies: 0.009996

Analysis stopped because convergence diagnostic hit stop value.

Analysis completed in 44 hours 33 mins 33 seconds

Analysis used 159760.82 seconds of CPU time on processor 0

Likelihood of best state for "cold" chain of run 1 was -187518.52

Likelihood of best state for "cold" chain of run 2 was -187540.02

Acceptance rates for the moves in the "cold" chain of run 1:

With prob.	(last 100)	chain accepted proposals by move
14.6 %	(27 %)	Dirichlet(Revmat{all})
24.1 %	(25 %)	Slider(Revmat{all})
19.3 %	(20 %)	Dirichlet(Pi{1})
23.7 %	(28 %)	Slider(Pi{1})
18.7 %	(28 %)	Dirichlet(Pi{2})
23.7 %	(26 %)	Slider(Pi{2})
21.6 %	(16 %)	Dirichlet(Pi{3})
24.7 %	(17 %)	Slider(Pi{3})
20.9 %	(15 %)	Dirichlet(Pi{4})
24.6 %	(20 %)	Slider(Pi{4})
24.4 %	(32 %)	Multiplier(Alpha{all})
25.1 %	(18 %)	Slider(Pinvar{all})
4.3 %	(4 %)	ExtSPR(Tau{all},V{all})
2.9 %	(4 %)	ExtTBR(Tau{all},V{all})
7.0 %	(5 %)	NNI(Tau{all},V{all})
2.4 %	(3 %)	ParsSPR(Tau{all},V{all})
25.8 %	(30 %)	Multiplier(V{all})
21.5 %	(21 %)	Nodeslider(V{all})
24.7 %	(30 %)	TLMultiplier(V{all})

Acceptance rates for the moves in the "cold" chain of run 2:

With prob.	(last 100)	chain accepted proposals by move
14.6 %	(28 %)	Dirichlet(Revmat{all})
23.9 %	(21 %)	Slider(Revmat{all})
19.2 %	(24 %)	Dirichlet(Pi{1})
23.9 %	(18 %)	Slider(Pi{1})
18.8 %	(28 %)	Dirichlet(Pi{2})
23.8 %	(29 %)	Slider(Pi{2})
21.8 %	(26 %)	Dirichlet(Pi{3})
24.8 %	(30 %)	Slider(Pi{3})
20.9 %	(33 %)	Dirichlet(Pi{4})
24.5 %	(36 %)	Slider(Pi{4})
24.3 %	(23 %)	Multiplier(Alpha{all})
24.8 %	(26 %)	Slider(Pinvar{all})
4.3 %	(5 %)	ExtSPR(Tau{all},V{all})
2.9 %	(0 %)	ExtTBR(Tau{all},V{all})
7.1 %	(7 %)	NNI(Tau{all},V{all})
2.4 %	(2 %)	ParsSPR(Tau{all},V{all})
25.8 %	(26 %)	Multiplier(V{all})
21.5 %	(21 %)	Nodeslider(V{all})
24.7 %	(26 %)	TLMultiplier(V{all})

Chain swap information for run 1:

	1	2	3	4
1		0.19	0.01	0.00
2	1199571		0.20	0.02
3	1199213	1198793		0.25
4	1199406	1199278	1198739	

Chain swap information for run 2:

	1	2	3	4
1		0.17	0.01	0.00
2	1196336		0.20	0.01
3	1199739	1200051		0.23
4	1200857	1198597	1199420	

Upper diagonal: Proportion of successful state exchanges between chains

Lower diagonal: Number of attempted state exchanges between chains

Chain information:

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ID -- Heat
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1 -- 1.00 (cold chain)
2 -- 0.91
3 -- 0.83
4 -- 0.77

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Heat = 1 / (1 + T * (ID - 1))

(where T = 0.10 is the temperature and ID is the chain number)