Bayesian Inference of Species Networks from Multilocus Sequence Data

Supplemental Material

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Table 1: Posterior estimates (medians and 95% HPD intervals) of inheritance probability (γ), node heights (τ's), and population sizes (θ's) for the truncated dataset 1, when the species network topology was fixed to the one in Figure 8. Three different priors were used for the population sizes: inverse-gamma(3,0.0003) with mean 0.00015 (small), inverse-gamma(3,0.003) with mean 0.0015 (medium), and inverse-gamma(3,0.03) with mean 0.015 (large). The population sizes were either inferred using MCMC or integrated out analytically.

	Posterior (median & 95% HPD)		
	inverse-gamma(3, 0.0003)	inverse-gamma(3, 0.003)	inverse-gamma(3, 0.03)
Population sizes inferred			
γ	0.408 (0.199, 0.623)	0.317 (0.152, 0.506)	0.309 (0.102, 0.579)
τ_R	0.0013 (0.00098, 0.0016)	0.0014 (0.0010, 0.0017)	0.0013 (0.0010, 0.0016)
τ_D	0.00031 (0.00024, 0.00039)	0.00017 (0.00009, 0.00029)	0.00039 (0.00019, 0.00054)
τ_E	0.00034 (0.00026, 0.00042)	0.00039 (0.00018, 0.00057)	0.00057 (0.00041, 0.00074)
τ_H	0.00030 (0.00023, 0.00038)	0.00007 (0.00000, 0.00019)	0.00027 (0.00003, 0.00047)
θ_W	0.0010 (0.00070, 0.0015)	0.0012 (0.00061, 0.0018)	0.0020 (0.0014, 0.0027)
θ_P	0.0057 (0.0031, 0.0099)	0.0033 (0.00035, 0.0083)	0.0056 (0.0027, 0.016)
θ_L	0.00080 (0.00051, 0.0012)	0.00064 (0.00035, 0.0011)	0.0017 (0.0012, 0.0026)
θ_R	0.0012 (0.00073, 0.0018)	0.0012 (0.00075, 0.0018)	0.0020 (0.0014, 0.0026)
θ_D	0.0026 (0.00099, 0.0054)	0.0027 (0.0013, 0.0057)	0.0028 (0.0015, 0.0052)
θ_E	0.0042 (0.0016, 0.0079)	0.0045 (0.0021, 0.0085)	0.0052 (0.0025, 0.0099)
θ_{DH_1}	0.00015 (0.00003, 0.00060)	0.0014 (0.00029, 0.0050)	0.010 (0.0024, 0.035)
θ_{EH_1}	0.00019 (0.00004, 0.00065)	0.0022 (0.00036, 0.0050)	0.0056 (0.0023, 0.021)
Population sizes integrated out			
γ	0.362 (0.152, 0.595)	0.331 (0.175, 0.516)	0.319 (0.158, 0.551)
τ_R	0.0012 (0.00091, 0.0015)	0.0014 (0.00098, 0.0018)	0.0013 (0.0010, 0.0017)
τ_D	0.00032 (0.00025, 0.00041)	0.00020 (0.00010, 0.00030)	0.00038 (0.00025, 0.00053)
τ_E	0.00033 (0.00026, 0.00043)	0.00039 (0.00017, 0.00065)	0.00055 (0.00038, 0.00072)
τ_H	0.00031 (0.00024, 0.00040)	0.00010 (0.00000, 0.00024)	0.00027 (0.00003, 0.00047)

Table 2: Posterior estimates (medians and 95% HPD intervals) of inheritance probability (γ), node heights (τ's), and population sizes (θ's) for the truncated dataset 2. See legend to Table S1.

	Posterior (median & 95% HPD)		
	inverse-gamma(3, 0.0003)	inverse-gamma(3, 0.003)	inverse-gamma(3, 0.03)
Population sizes inferred			
γ	0.477 (0.264, 0.710)	0.340 (0.154, 0.569)	0.344 (0.129, 0.694)
τ_R	0.0011 (0.00080, 0.0014)	0.0013 (0.00094, 0.0015)	0.0012 (0.0009, 0.0015)
τ_D	0.00027 (0.00019, 0.00036)	0.00014 (0.00004, 0.00025)	0.00036 (0.00023, 0.00052)
τ_E	0.00030 (0.00021, 0.00039)	0.00039 (0.00023, 0.00056)	0.00056 (0.00035, 0.00073)
τ_H	0.00027 (0.00019, 0.00035)	0.00008 (0.00000, 0.00021)	0.00024 (0.00001, 0.00041)
θ_W	0.0011 (0.00071, 0.0017)	0.0015 (0.00092, 0.0022)	0.0022 (0.0015, 0.0029)
θ_P	0.0061 (0.0030, 0.011)	0.0031 (0.00038, 0.0073)	0.0060 (0.0029, 0.014)
θ_L	0.00080 (0.00046, 0.0012)	0.00064 (0.00028, 0.0011)	0.0017 (0.0012, 0.0023)
θ_R	0.0013 (0.00074, 0.0020)	0.0012 (0.00068, 0.0021)	0.0020 (0.0014, 0.0026)
θ_D	0.0039 (0.0016, 0.0071)	0.0035 (0.0021, 0.0057)	0.0036 (0.0019, 0.0062)
θ_E	0.0040 (0.0014, 0.0081)	0.0044 (0.0016, 0.0083)	0.0052 (0.0026, 0.0099)
θ_{DH_1}	0.00015 (0.00003, 0.00061)	0.0014 (0.00030, 0.0045)	0.011 (0.0027, 0.036)
θ_{EH_1}	0.00016 (0.00003, 0.00061)	0.0022 (0.00045, 0.0049)	0.0061 (0.0021, 0.023)
Population sizes integrated out			
γ	0.460 (0.252, 0.703)	0.366 (0.167, 0.571)	0.364 (0.137, 0.678)
τ_R	0.0011 (0.00086, 0.0014)	0.0013 (0.00095, 0.0015)	0.0012 (0.00089, 0.0015)
τ_D	0.00029 (0.00021, 0.00037)	0.00015 (0.00009, 0.00026)	0.00037 (0.00026, 0.00052)
τ_E	0.00031 (0.00021, 0.00041)	0.00037 (0.00023, 0.00054)	0.00050 (0.00035, 0.00066)
τ_H	0.00028 (0.00020, 0.00037)	0.00007 (0.00000, 0.00021)	0.00025 (0.00002, 0.00042)