

Supplementary Tables for: Quantifying Age-dependent Extinction from Species Phylogenies

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Parameter set		λ				k				θ			
True η	True k	true	estimate		norm. CI	true	estimate		norm. CI	true	estimate		norm. CI
0.25	0.5	1.36	1.49	[0.984, 2.30]	0.964	0.500	0.455	[0.161, 0.890]	1.46	2.00	2.00	[0.997, 3.42]	1.21
	1	1.25	1.33	[1.04, 1.92]	0.703	1.00	0.903	[0.257, 1.68]	1.42	1.00	1.06	[0.531, 2.18]	1.65
	5	1.15	1.19	[1.06, 1.31]	0.215	5.00	4.59	[1.70, 25.9]	4.83	0.200	0.212	[4.21e-3, 0.511]	2.53
	100	1.13	1.14	[1.07, 1.26]	0.162	100.	116	[4.18, 1.61e3]	16.0	0.0100	8.67e-3	[4.23e-4, 0.127]	12.6
0.5	0.5	1.71	1.77	[1.30, 4.84]	2.08	0.500	0.467	[4.66e-3, 0.926]	1.84	2.00	1.90	[0.764, 6.16]	2.70
	1	1.50	1.55	[1.18, 1.96]	0.517	1.00	1.03	[0.246, 2.36]	2.12	1.00	0.981	[0.390, 2.08]	1.69
	5	1.32	1.34	[1.21, 1.50]	0.221	5.00	5.41	[1.04, 39.1]	7.60	0.200	0.178	[3.92e-4, 0.538]	2.69
	100	1.27	1.29	[1.18, 1.41]	0.180	100.	78.8	[1.66, 3.24e3]	32.4	0.0100	0.0130	[1.88e-4, 0.276]	27.6
1	0.5	2.37	2.56	[1.68, 13.4]	4.93	0.500	0.417	[3.77e-3, 1.36]	2.71	2.00	2.35	[0.0840, 15.0]	7.46
	1	2.00	2.06	[1.62, 2.92]	0.650	1.00	0.955	[0.117, 2.88]	2.77	1.00	1.01	[0.0897, 4.79]	4.70
	5	1.67	1.69	[1.59, 1.91]	0.189	5.00	4.10	[0.521, 139]	27.6	0.200	0.224	[1.83e-4, 1.26]	6.31
	100	1.59	1.61	[1.47, 1.75]	0.177	100.	116	[1.30, 6.42e3]	64.2	0.0100	8.47e-3	[1.11e-4, 0.485]	48.5
1.5	0.5	3.00	3.26	[2.21, 43.4]	13.7	0.500	0.368	[2.74e-3, 1.39]	2.78	2.00	2.73	[0.318, 20.9]	10.3
	1	2.50	2.57	[2.09, 31.9]	11.9	1.00	0.892	[2.66e-3, 3.74]	3.74	1.00	1.03	[1.43e-4, 46.5]	46.5
	5	2.05	2.07	[1.90, 2.74]	0.405	5.00	5.82	[7.44e-4, 8.11e3]	1.62e3	0.200	0.170	[8.40e-5, 35.1]	175
	100	1.94	1.98	[1.80, 2.97]	0.603	100.	27.1	[6.77e-4, 9.57e4]	95.7	0.0100	0.0419	[8.67e-5, 5.38e5]	5.38e5

Table S1: **Simulation study: 1000-tip trees, complete sampling – inference results under gamma model.** We report results of inference under the gamma model on simulated trees with sampling fraction $p = 1$ and $n = 1000$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the model parameters λ (speciation rate), k (lifetime shape parameter), and θ (lifetime scale parameter). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”).

Parameter set		ℓ				η				ϵ			
True η	True k	true	estimate		norm. CI	true	estimate		norm. CI	true	estimate		norm. CI
0.25	0.5	1.00	0.901,	[0.614, 1.27]	0.656	0.250	0.238,	[0.200, 0.308]	0.431	0.816	0.841,	[0.787, 0.917]	0.160
	1	1.00	0.936,	[0.697, 1.16]	0.463	0.250	0.247,	[0.193, 0.316]	0.494	0.800	0.821,	[0.774, 0.875]	0.127
	5	1.00	0.975,	[0.878, 1.10]	0.225	0.250	0.251,	[0.180, 0.317]	0.549	0.784	0.792,	[0.725, 0.850]	0.160
	100	1.00	0.998,	[0.884, 1.08]	0.200	0.250	0.259,	[0.187, 0.358]	0.685	0.779	0.775,	[0.692, 0.838]	0.187
0.5	0.5	1.00	0.900,	[0.354, 1.40]	1.05	0.500	0.500,	[0.425, 0.625]	0.399	0.707	0.728,	[0.599, 0.913]	0.444
	1	1.00	0.962,	[0.724, 1.19]	0.462	0.500	0.490,	[0.427, 0.613]	0.371	0.667	0.678,	[0.587, 0.765]	0.267
	5	1.00	0.980,	[0.837, 1.14]	0.300	0.500	0.486,	[0.356, 0.589]	0.465	0.621	0.635,	[0.538, 0.709]	0.275
	100	1.00	0.987,	[0.838, 1.13]	0.294	0.500	0.498,	[0.384, 0.599]	0.429	0.607	0.613,	[0.531, 0.729]	0.326
1	0.5	1.00	0.870,	[0.0892, 1.42]	1.33	1.00	1.00,	[0.808, 1.17]	0.365	0.577	0.618,	[0.446, 0.919]	0.819
	1	1.00	0.921,	[0.708, 1.38]	0.673	1.00	0.980,	[0.791, 1.15]	0.356	0.500	0.532,	[0.410, 0.654]	0.487
	5	1.00	0.988,	[0.797, 1.37]	0.573	1.00	0.989,	[0.765, 1.17]	0.401	0.402	0.418,	[0.276, 0.540]	0.657
	100	1.00	1.01,	[0.833, 1.27]	0.434	1.00	1.01,	[0.864, 1.20]	0.339	0.370	0.375,	[0.251, 0.461]	0.568
1.5	0.5	1.00	0.929,	[0.0381, 1.76]	1.72	1.50	1.51,	[1.31, 1.74]	0.284	0.500	0.549,	[0.377, 0.991]	1.23
	1	1.00	0.964,	[0.215, 1.80]	1.58	1.50	1.50,	[1.29, 1.75]	0.307	0.400	0.439,	[0.308, 0.981]	1.68
	5	1.00	1.00,	[0.711, 5.40]	4.69	1.50	1.52,	[1.26, 1.84]	0.387	0.269	0.277,	[0.074, 0.447]	1.38
	100	1.00	1.05,	[0.712, 658]	658	1.50	1.51,	[1.26, 1.88]	0.413	0.226	0.247,	[0.000, 0.437]	1.94

Table S2: **Simulation study: 1000-tip trees, complete sampling – inference results under gamma model, continued.** We report results of inference under the gamma model on simulated trees with sampling fraction $p = 1$ and $n = 1000$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the composite parameters ℓ (mean lifetime), η (net diversification rate), and ϵ (turnover). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”).

Parameter set		λ			ℓ			η			ϵ		
True η	True k	true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI
0.25	0.5	1.36	1.10, [0.978, 1.22]	0.175	1.00	1.13, [0.945, 1.30]	0.351	0.250	0.218, [0.179, 0.270]	0.364	0.816	0.806, [0.746, 0.843]	0.119
	1	1.25	1.29, [1.17, 1.42]	0.201	1.00	0.964, [0.820, 1.12]	0.299	0.250	0.246, [0.201, 0.302]	0.402	0.800	0.810, [0.741, 0.848]	0.133
	5	1.15	1.46, [1.32, 1.60]	0.243	1.00	0.858, [0.724, 1.02]	0.292	0.250	0.302, [0.231, 0.388]	0.626	0.784	0.794, [0.720, 0.846]	0.161
	100	1.13	1.49, [1.36, 1.62]	0.227	1.00	0.872, [0.750, 1.04]	0.286	0.250	0.348, [0.241, 0.467]	0.904	0.779	0.771, [0.666, 0.831]	0.212
0.5	0.5	1.71	1.42, [1.27, 1.57]	0.175	1.00	1.03, [0.815, 1.27]	0.455	0.500	0.463, [0.391, 0.553]	0.323	0.707	0.673, [0.589, 0.747]	0.224
	1	1.50	1.52, [1.37, 1.70]	0.217	1.00	0.983, [0.800, 1.21]	0.409	0.500	0.496, [0.428, 0.588]	0.322	0.667	0.673, [0.591, 0.739]	0.221
	5	1.32	1.59, [1.35, 1.70]	0.264	1.00	1.01, [0.757, 1.21]	0.454	0.500	0.584, [0.475, 0.714]	0.477	0.621	0.631, [0.554, 0.723]	0.272
	100	1.27	1.56, [1.40, 1.68]	0.224	1.00	1.09, [0.765, 1.45]	0.687	0.500	0.639, [0.507, 0.765]	0.516	0.607	0.589, [0.453, 0.695]	0.398
1	0.5	2.37	2.01, [1.83, 2.24]	0.173	1.00	0.921, [0.715, 1.25]	0.537	1.00	0.936, [0.821, 1.08]	0.261	0.577	0.539, [0.434, 0.631]	0.341
	1	2.00	2.02, [1.81, 2.26]	0.223	1.00	0.964, [0.730, 1.27]	0.544	1.00	0.981, [0.830, 1.12]	0.291	0.500	0.516, [0.421, 0.614]	0.385
	5	1.67	1.87, [1.69, 2.06]	0.221	1.00	1.36, [0.798, 2.20]	1.40	1.00	1.13, [0.956, 1.36]	0.405	0.402	0.396, [0.251, 0.549]	0.740
	100	1.59	1.75, [1.60, 1.94]	0.220	1.00	1.92, [1.03, 3.16]	2.13	1.00	1.22, [1.02, 1.36]	0.338	0.370	0.303, [0.181, 0.466]	0.773
1.5	0.5	3.00	2.61, [2.37, 2.91]	0.182	1.00	0.852, [0.597, 1.18]	0.585	1.50	1.43, [1.22, 1.62]	0.271	0.500	0.449, [0.348, 0.584]	0.472
	1	2.50	2.50, [2.25, 2.75]	0.198	1.00	1.00, [0.658, 1.51]	0.850	1.50	1.50, [1.30, 1.70]	0.264	0.400	0.406, [0.281, 0.509]	0.571
	5	2.05	2.16, [1.98, 2.49]	0.247	1.00	2.01, [0.883, 6.89]	6.00	1.50	1.68, [1.44, 1.92]	0.323	0.269	0.226, [0.0430, 0.398]	1.32
	100	1.94	2.04, [1.87, 2.31]	0.224	1.00	3.00, [1.16, 1.96e4]	1.96e4	1.50	1.72, [1.48, 1.96]	0.317	0.226	0.162, [3.81e-10, 0.323]	1.43

Table S3: **Simulation study: 1000-tip trees, complete sampling – inference results under exponential model.** We report results of inference under the exponential model on simulated trees with sampling fraction $p = 1$ and $n = 1000$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the parameters λ (speciation rate), ℓ (mean lifetime), η (net diversification rate), and ϵ (turnover). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”).

Parameter set		λ			k			θ		
True η	True k	true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI
0.25	0.5	1.36	1.38, [0.768, 3.57]	2.05	0.500	0.485, [0.0302, 1.26]	2.45	2.00	1.98, [0.675, 3.79]	1.56
	1	1.25	1.31, [0.980, 1.77]	0.632	1.00	0.957, [0.344, 1.95]	1.61	1.00	0.975, [0.425, 1.66]	1.23
	5	1.15	1.16, [1.04, 1.34]	0.263	5.00	5.02, [1.53, 67.4]	13.2	0.200	0.202, [6.74e-4, 0.418]	2.09
	100	1.13	1.15, [1.04, 1.21]	0.152	100.	84.6, [2.49, 974]	9.72	0.0100	0.0127, [6.41e-4, 0.146]	14.6

Table S4: **Simulation study: 1000-tip trees, incomplete sampling – inference results under gamma model.** We report results of inference under the gamma model on simulated trees with sampling fraction $p = 0.5$ and $n = 1000$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the model parameters λ (speciation rate), k (lifetime shape parameter), and θ (lifetime scale parameter). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”).

Parameter set		ℓ				η				ϵ			
True η	True k	true	estimate		norm. CI	true	estimate		norm. CI	true	estimate		norm. CI
0.25	0.5	1.00	0.974	[0.417, 1.53]	1.11	0.250	0.250	[0.208, 0.293]	0.340	0.816	0.822	[0.747, 0.952]	0.251
	1	1.00	0.967	[0.712, 1.24]	0.529	0.250	0.249	[0.208, 0.292]	0.336	0.800	0.811	[0.748, 0.869]	0.151
	5	1.00	0.978	[0.833, 1.10]	0.263	0.250	0.238	[0.192, 0.291]	0.396	0.784	0.798	[0.747, 0.831]	0.108
	100	1.00	0.991	[0.914, 1.09]	0.181	0.250	0.245	[0.204, 0.307]	0.411	0.779	0.783	[0.738, 0.832]	0.121

Table S5: **Simulation study: 1000-tip trees, incomplete sampling – inference results under gamma model, continued.** We report results of inference under the gamma model on simulated trees with sampling fraction $p = 0.5$ and $n = 1000$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the composite parameters ℓ (mean lifetime), η (net diversification rate), and ϵ (turnover). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”).

Parameter set		λ			ℓ			η			ϵ		
True η	True k	true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI
0.25	0.5	1.36	1.06, [0.944, 1.16]	0.161	1.00	1.22, [1.03, 1.42]	0.392	0.250	0.234, [0.202, 0.273]	0.287	0.816	0.778, [0.730, 0.827]	0.119
	1	1.25	1.25, [1.13, 1.41]	0.222	1.00	0.996, [0.802, 1.13]	0.325	0.250	0.242, [0.203, 0.282]	0.315	0.800	0.806, [0.758, 0.847]	0.112
	5	1.15	1.56, [1.42, 1.71]	0.254	1.00	0.775, [0.696, 0.903]	0.207	0.250	0.276, [0.226, 0.328]	0.408	0.784	0.826, [0.781, 0.866]	0.108
	100	1.13	1.62, [1.47, 1.77]	0.266	1.00	0.759, [0.675, 0.876]	0.201	0.250	0.301, [0.243, 0.366]	0.495	0.779	0.813, [0.759, 0.858]	0.127

Table S6: **Simulation study: 1000-tip trees, incomplete sampling – inference results under exponential model.** We report results of inference under the exponential model on simulated trees with sampling fraction $p = 0.5$ and $n = 1000$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the parameters λ (speciation rate), ℓ (mean lifetime), η (net diversification rate), and ϵ (turnover). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”).

Parameter set		Method	λ			k			θ		
True η	True k		true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI
0.5	0.5	gsa=F	1.71	3.86, [0.969, 130.]	75.7	0.500	0.163, [1.73e-3, 58.4]	117	2.00	2.18, [2.96e-4, 18.1]	9.03
		gsa=T	1.71	1.68, [0.750, 83.1]	48.2	0.500	0.565, [2.34e-3, 2.21e3]	4.42e3	2.00	1.61, [2.16e-4, 18.0]	9.01
0.5	1	gsa=F	1.50	1.95, [1.03, 89.3]	58.8	1.00	0.664, [2.26e-3, 1.63e3]	1.63e3	1.00	1.03, [3.03e-4, 11.6]	11.6
		gsa=T	1.50	1.46, [0.958, 58.2]	38.1	1.00	1.08, [3.54e-3, 1.51e3]	1.51e3	1.00	0.898, [1.91e-4, 6.76]	6.76
0.5	5	gsa=F	1.32	1.54, [0.999, 39.7]	29.3	5.00	3.83, [2.84e-3, 2.20e3]	439	0.200	0.208, [1.25e-4, 26.9]	135
		gsa=T	1.32	1.43, [0.899, 5.73]	3.66	5.00	5.97, [5.19e-3, 5.54e3]	1.11e3	0.200	0.149, [9.64e-5, 5.62]	28.1
0.5	100	gsa=F	1.27	1.38, [1.01, 11.5]	8.27	100.	29.2, [2.48e-3, 4.84e3]	48.4	0.0100	0.0342, [1.26e-4, 7.80]	780
		gsa=T	1.27	1.35, [0.951, 2.28]	1.05	100.	46.4, [6.21e-3, 5.35e3]	53.5	0.0100	0.0175, [1.60e-4, 2.02]	202

Table S7: **Simulation study: 100-tip trees, complete sampling – inference results under gamma model.** We report results of inference under the gamma model on simulated trees with sampling fraction $p = 1$ and $n = 100$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the model parameters λ (speciation rate), k (lifetime shape parameter), and θ (lifetime scale parameter). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”). Two sets of simulated trees were generated under two alternative simulation methods (using the option ‘gsa=F’ versus ‘gsa=T’ in TreeSimGM; see main text Methods and Supplementary Text for details).

Parameter set		Method	ℓ			η			ϵ		
True η	True k		true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI
0.5	0.5	gsa=F	1.00	0.461, [8.69e-3, 1.40]	1.39	0.500	0.445, [0.218, 0.710]	0.984	0.707	0.878, [0.570, 0.998]	0.606
		gsa=T	1.00	0.852, [0.0125, 1.83]	1.81	0.500	0.446, [0.219, 0.744]	1.05	0.707	0.780, [0.490, 0.997]	0.717
0.5	1	gsa=F	1.00	0.650, [0.0157, 1.24]	1.22	0.500	0.468, [0.173, 0.781]	1.22	0.667	0.815, [0.566, 0.996]	0.646
		gsa=T	1.00	0.928, [0.0156, 1.67]	1.65	0.500	0.438, [0.144, 0.732]	1.18	0.667	0.721, [0.486, 0.996]	0.765
0.5	5	gsa=F	1.00	0.799, [0.0485, 1.45]	1.41	0.500	0.436, [0.137, 1.03]	1.78	0.621	0.757, [0.464, 0.989]	0.846
		gsa=T	1.00	0.940, [0.0292, 1.48]	1.45	0.500	0.502, [0.133, 0.811]	1.36	0.621	0.695, [0.394, 0.959]	0.910
0.5	100	gsa=F	1.00	0.934, [0.120, 1.70]	1.58	0.500	0.501, [0.140, 0.968]	1.66	0.607	0.677, [0.360, 0.986]	1.03
		gsa=T	1.00	0.946, [0.547, 1.59]	1.05	0.500	0.491, [0.148, 0.832]	1.37	0.607	0.659, [0.375, 0.886]	0.843

Table S8: **Simulation study: 100-tip trees, complete sampling – inference results under gamma model, continued.** We report results of inference under the gamma model on simulated trees with sampling fraction $p = 1$ and $n = 100$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the composite parameters ℓ (mean lifetime), η (net diversification rate), and ϵ (turnover). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”). Two sets of simulated trees were generated under two alternative simulation methods (using the option ‘gsa=F’ versus ‘gsa=T’ in TreeSimGM; see main text Methods and Supplementary Text for details).

Parameter set		Method	λ			ℓ			η			ϵ		
True η	True k		true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI	true	estimate	norm. CI
0.5	0.5	gsa=F	1.71	1.52, [1.05, 2.25]	0.703	1.00	0.901, [0.433, 1.68]	1.25	0.500	0.410, [0.176, 0.670]	0.988	0.707	0.732, [0.484, 0.929]	0.629
		gsa=T	1.71	1.36, [0.938, 2.02]	0.635	1.00	1.05, [0.471, 2.12]	1.65	0.500	0.438, [0.244, 0.691]	0.893	0.707	0.695, [0.396, 0.894]	0.705
0.5	1	gsa=F	1.50	1.66, [1.07, 2.23]	0.773	1.00	0.799, [0.432, 1.53]	1.10	0.500	0.444, [0.195, 0.734]	1.08	0.667	0.729, [0.472, 0.889]	0.626
		gsa=T	1.50	1.53, [1.04, 1.94]	0.599	1.00	1.01, [0.498, 2.00]	1.50	0.500	0.462, [0.233, 0.825]	1.18	0.667	0.681, [0.444, 0.913]	0.704
0.5	5	gsa=F	1.32	1.74, [1.19, 2.22]	0.778	1.00	0.842, [0.451, 2.28]	1.83	0.500	0.548, [0.221, 1.06]	1.67	0.621	0.703, [0.339, 0.889]	0.886
		gsa=T	1.32	1.57, [1.21, 2.14]	0.710	1.00	1.03, [0.538, 3.08]	2.54	0.500	0.578, [0.285, 1.08]	1.59	0.621	0.639, [0.239, 0.890]	1.05
0.5	100	gsa=F	1.27	1.63, [1.17, 2.19]	0.804	1.00	1.03, [0.457, 5.02]	4.56	0.500	0.631, [0.227, 1.11]	1.76	0.607	0.590, [0.149, 0.893]	1.22
		gsa=T	1.27	1.56, [1.07, 2.04]	0.767	1.00	1.11, [0.531, 3.45]	2.92	0.500	0.646, [0.243, 1.00]	1.52	0.607	0.583, [0.250, 0.885]	1.05

Table S9: **Simulation study: 100-tip trees, complete sampling – inference results under exponential model.** We report results of inference under the exponential model on simulated trees with sampling fraction $p = 1$ and $n = 100$ sampled tips, across parameter sets (defined by true η and k) used in the simulation study. Results here are for the parameters λ (speciation rate), ℓ (mean lifetime), η (net diversification rate), and ϵ (turnover). For each parameter we list the “true” value (used for simulation); the median and 95% confidence interval of the maximum likelihood estimates across 100 simulated trees (under “estimate”); and the width of the confidence interval normalized by the true parameter value (under “norm. |CI|”). Two sets of simulated trees were generated under two alternative simulation methods (using the option ‘gsa=F’ versus ‘gsa=T’ in TreeSimGM; see main text Methods and Supplementary Text for details).

Parameter	Median MLE							
	H-full		E-full		H-gen		E-gen	
	Gamma	Exp	Gamma	Exp	Gamma	Exp	Gamma	Exp
speciation rate, λ	0.1267	0.1379	0.1321	0.1451	0.1371	0.1570	0.1343	0.1541
lifetime shape parameter, k	46.46	–	39.33	–	68.08	–	66.89	–
lifetime scale parameter, θ	0.2529	–	0.2888	–	0.1567	–	0.1581	–
mean lifetime, ℓ	12.31	24.11	11.55	21.32	10.61	16.29	10.96	16.28
net diversification rate, η	0.07695	0.09602	0.07846	0.09822	0.07540	0.09465	0.07323	0.09203
turnover, ϵ	0.3923	0.3029	0.4100	0.3244	0.4472	0.3912	0.4544	0.4004

Table S10: **Aves data: inference results for sets of reconstructed phylogenies.** The data consists of sets of 100 trees drawn from the posterior distribution of phylogenies reconstructed by Jetz et al. (*Nature* 491:444-448, 2012) under each of four approaches (see main text Methods): using a Hackett (H-) or Ericson (E-) backbone, and including all species (full) or only those with genetic data (gen). We report the median maximum likelihood parameter estimates across each set of 100 trees, inferred under the gamma and the exponential lifetime distribution models. Time is in units of millions of years.

Parameter	Gamma model			Exponential model	
	MLE	Bootstrap 95% CI	Profile likelihood 95% CI	MLE	Profile likelihood 95% CI
speciation rate, λ	0.1226	[0.1204, 0.1254]	[0.1197, 0.1255]	0.1351	[0.1301, 0.1403]
lifetime shape parameter, k	45.23	[9.289, 269.1]	[14.47, 293.5]	–	–
lifetime scale parameter, θ	0.2796	[0.003121 0.9731]	n.d.	–	–
mean lifetime, ℓ	12.65	[12.02, 13.48]	[11.91, 13.53]	23.03	[19.45, 28.14]
net diversification rate, η	0.07409	[0.06988, 0.07828]	n.d.	0.09170	n.d.
turnover, ϵ	0.3955	[0.3602, 0.4300]	n.d.	0.3214	n.d.

Table S11: **Aves data: inference results for one “typical” reconstructed phylogeny.** Detailed analysis was conducted on one “typical” tree from the posterior distribution of Aves phylogenies, constructed by Jetz et al. (*Nature* 491:444-448, 2012) under the Hackett backbone and including all species (see main text Methods). We report maximum likelihood estimates and 95% confidence intervals of parameters, inferred under the gamma and the exponential lifetime distribution models. Time is in units of millions of years. Bootstrap confidence intervals were determined for all parameters under the gamma model. Profile likelihood confidence intervals were additionally determined for parameters of particular interest (λ and ℓ under both models, as well as k under the gamma model); the rest were not determined (n.d.).

Parameter	Gamma model			Exponential model		
	MLE	Bootstrap 95% CI	Profile likelihood 95% CI	MLE	Profile likelihood 95% CI	
speciation rate, λ	1.946	[1.464, 3.692]	[1.306, 7.450]	2.955	[2.179, 3.992]	
lifetime shape parameter, k	4.528	[0.4375, 98.28]	[0.2331, $> 10^{10}$]	–	–	
lifetime scale parameter, θ	0.1160	[0.003312, 0.4500]	n.d.	–	–	
mean lifetime, ℓ	0.5251	[0.2718, 0.6749]	[0.1379, 0.7935]	0.3470	[0.2540, 0.4797]	
net diversification rate, η	0.06782	[0.03834, 0.1345]	n.d.	0.07305	n.d.	
turnover, ϵ	0.9651	[0.9314, 0.9824]	n.d.	0.9753	n.d.	

Table S12: **Nightshades data: inference results for self-incompatible species.** We report maximum likelihood estimates and 95% confidence intervals (CIs) of parameters inferred under the gamma and exponential lifetime distribution models from the subtree of self-incompatible nightshade species, extracted from the maximum likelihood tree constructed by Goldberg et al. (*Science* 330:493-495, 2010). Time is in units of millions of years. Bootstrap CIs were determined for all parameters under the gamma model. Profile likelihood CIs were additionally determined for parameters of particular interest (λ and ℓ under both models, as well as k under the gamma model); the rest were not determined (n.d.). Under the gamma model, the profile likelihood CI upper bound for k is not precisely determined as increasingly large values of k continued to fall within the likelihood boundary; this outcome is not unreasonable, in light of the convergence to an asymptotic distribution as $k \rightarrow \infty$.

Parameter	Gamma model				Exponential model			
	MLE	Stem age Prof. llhd. 95% CI bound	MLE	Crown age Prof. llhd. 95% CI	MLE	Stem age Prof. llhd. 95% CI bound	MLE	Crown age Prof. llhd. 95% CI
speciation rate, λ	≥ 973	≥ 4.32	≥ 801	≥ 4.96	3.87	[2.95, 5.05]	4.24	[3.12, 5.72]
lifetime shape parameter, k	≤ 0.00171	≤ 0.729	≤ 0.00228	≤ 0.655	–	–	–	–
lifetime scale parameter, θ	≈ 0.597	n.d.	≈ 0.537	n.d.	–	–	–	–
mean lifetime, ℓ	≤ 0.00102	≤ 0.229	≤ 0.00122	≤ 0.197	0.256	[0.196, 0.337]	0.231	[0.171, 0.314]
net diversification rate, η	≈ -0.0248	n.d.	≈ -0.0785	n.d.	-0.0399	n.d.	-0.0996	n.d.
turnover, ϵ	≈ 1.00	n.d.	≈ 1.00	n.d.	1.01	n.d.	1.02	n.d.

Table S13: **Nightshades data: inference results for self-compatible species.** We report maximum likelihood estimates and 95% profile likelihood confidence intervals (CIs) of parameters inferred under the gamma and exponential lifetime distribution models from the self-compatible nightshade clades, extracted from the maximum likelihood tree constructed by Goldberg et al. (*Science* 330:493-495, 2010). Inference was conducted twice, with likelihood conditioned on either the stem age of clades (including all clades) or the crown age of clades (including only clades with ≥ 2 species); see main text Methods for details. Time is in units of millions of years. Profile likelihood CIs were only determined for parameters of particular interest (λ , k , and ℓ); the rest were not determined (n.d.). Under the gamma model, a rather flat likelihood surface precluded determination of a precise likelihood peak (see main text Methods) and we can thus give only conservative bounds on the MLEs $\hat{\lambda}$, \hat{k} , and $\hat{\ell}$ and their CIs, and approximate values of the MLEs $\hat{\theta}$, $\hat{\eta}$ and $\hat{\epsilon}$.

Parameter	Reproduction mode	Same- k model		Same- ℓ model		Full model	
		Stem age	Crown age	Stem age	Crown age	Stem age	Crown age
		MLE		MLE		MLE	
speciation rate, λ	SI	7.58	13.6	15.1	32.7	1.95	
	SC	9.53	18.5	14.5	31.1	973	801
lifetime shape parameter, k	SI			0.101	0.0436	4.53	
	SC	0.225	0.112	0.132	0.0626	0.00171	0.00228
lifetime scale parameter, θ	SI	0.604	0.675	0.674	0.723	0.116	
	SC	0.463	0.472	0.516	0.503	0.597	0.537
mean lifetime, ℓ	SI	0.136	0.0756			0.525	
	SC	0.104	0.0529	0.0682	0.0315	0.00102	0.00122

Table S14: **Nightshades data: comparison of self-incompatible and -compatible species under alternative models.** We report maximum likelihood estimates of parameters inferred simultaneously from the subtree of self-incompatible (SI) nightshades and the clades of self-compatible (SC) nightshades, extracted from the maximum likelihood tree constructed by Goldberg et al. (*Science* 330:493-495, 2010). Lifetime is always taken to be gamma distributed, but we consider three alternative models, making different assumptions about the differences between SI and SC species. In the “Same- k ” model, lifetime shape parameter (k) is taken to be the same for both the SI subtree and the SC clades. In the “Same- ℓ ” model, mean lifetime (ℓ) is taken to be the same for both SI and SC. In the “Full” model, all parameters are allowed to differ between SI and SC; thus the estimates, conservative in the SC case, are the same as reported in the preceding Supplementary Tables S12 and S13. “Stem age” and “Crown age” refer to the conditioning on the likelihood formula used for SC clades; likelihood is always conditioned on crown age in the SI subtree.