**Table S1.** The effect of character sampling (bp) for estimating divergence times when there is no among-branch-variation in *r*, diversification parameters are constant and *µ* = 0

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Taxon Sampling** | **Character Sampling** | **% error** | **95% HPD width** | **% with correct value in 95% HPD** |
| low | low | 33.110 | 92.197 | 94.667 |
| low | medium | 7.060 | 33.604 | 94.000 |
| low | high | 2.415 | 11.181 | 90.667 |
| low | no seq data | 1868.263 | 198.255 | 100.000 |

**Table S2.** The effect of taxon sampling for estimating divergence times when there is no among-branch-variation in *r*, and no variation in diversification parameters

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Branching process** | **Taxon Sampling** | **Character Sampling** | **% error** | **95% HPD width** | **% with correct value in 95% HPD** |
| Yule | low | low | 33.110 | 92.197 | 94.667 |
| Yule | medium | low | 31.094 | 82.543 | 95.000 |
| Yule | high | low | 24.795 | 74.525 | 93.333 |
| Yule | low | no seq data | 1868.263 | 198.255 | 100.000 |
| Yule | medium | no seq data | 540.924 | 219.129 | 100.000 |
| Yule | high | no seq data | 134.149 | 191.518 | 96.333 |
| birth-death | high | low | 114.685 | 142.852 | 92.000 |
| birth-death | high | no seq data | 312.212 | 238.145 | 97.000 |

**Table S3.** The effect of character sampling (bp) for estimating divergence times when there is among-branch-variation in *r*, but diversification parameters are constant and *µ = 0*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Taxon Sampling** | **Character Sampling** | **Method** | **% error** | **95% HPD width** | **% with correct value in 95% HPD** |
| low | low | strict clock | 59.614 | 97.975 | 71.000 |
| low | medium | strict clock | 31.252 | 37.457 | 34.333 |
| low | high | strict clock | 28.867 | 12.687 | 12.000 |
| low | high | relaxed clock | 54.429 | 147.213 | 97.667 |
| low | no seq data | -- | 3198.324 | 198.449 | 100.000 |
| low | high | relaxed clock with node calibrations | 27.460 | 65.690 | 72.667 |
| low | no seq data | node calibrations | 2654.803 | 50.234 | 48.667 |

**Table S4.** The effect of taxon sampling for estimating divergence times when there is variation in diversification parameters, *µ = 0*, and no among-branch-variation in *r*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Taxon Sampling** | **Character Sampling** | **Method** | **% error** | **95% HPD width** | **% with correct value in 95% HPD** |
| low | low | strict clock | 124.036 | 187.914 | 92.308 |
| medium | low | strict clock | 99.157 | 164.760 | 93.289 |
| high | low | strict clock | 64.228 | 144.313 | 92.333 |
| low | no seq data | -- | 3261.898 | 174.035 | 90.970 |
| medium | no seq data | -- | 783.678 | 189.911 | 85.906 |
| high | no seq data | -- | 238.290 | 190.245 | 84.333 |
| high | low | node calibrations | 54.112 | 110.971 | 54.333 |
| high | no seq data | node calibrations | 102.577 | 116.112 | 50.333 |

**Table S5.** Divergence time estimates for the radiation node in *Ipomoea*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Taxon Sampling** | **Character Sampling** | **Method** | **Mean posterior estimate** | **95% HPD width** |
| low | low | strict | 13.494 | 42.249 |
| low | low | relaxed | 12.161 | 73.503 |
| medium | low | strict | 15.632 | 11.176 |
| medium | low | relaxed | 15.607 | 11.659 |
| high | low | strict | 16.057 | 3.535 |
| high | low | relaxed | 15.987 | 4.707 |
| low | high | strict | 16.115 | 1.426 |
| low | high | relaxed | 13.074 | 57.907 |
| medium | high | strict | 16.185 | 1.054 |
| medium | high | relaxed | 15.720 | 9.417 |
| high | high | strict | 16.172 | 1.371 |
| high | high | relaxed | 16.035 | 3.851 |
| low | no seq data | -- | 8.924 | 170.226 |
| medium | no seq data | -- | 15.360 | 16.710 |
| high | no seq data | -- | 15.832 | 8.284 |

**Table S6.** The effect of taxon sampling for estimating diversification parameters when diversification parameters are constant

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Branching Process** | **Parameter** | **Taxon Sampling** | **% error** | **95% HPD width** | **% with correct value in 95% HPD** |
| Yule | *λ* | low | 28.628 | 142.145 | 98.667 |
| Yule | *λ* | medium | 16.377 | 35.104 | 100.000 |
| Yule | *λ* | high | 1.833 | 22.033 | 100.000 |
| Yule | *λ* | low (no input) | 23.070 | 123.189 | 99.333 |
| Yule | *λ* | medium (no input) | 17.904 | 32.778 | 0.200 |
| Yule | *λ* | high (no input) | 55.977 | 22.172 | 0.000 |
| birth-death | *λ* | high | 2.805 | 39.953 | 100.000 |
| birth-death | *µ* | high | 3.406 | 61.010 | 100.000 |
| birth-death | *λ*-*µ* | high | 40.100 | 87.283 | 100.000 |
| birth-death | *λ* | high (no input) | 57.752 | 28.498 | 0.000 |
| birth-death | *µ* | high (no input) | 92.744 | 207.136 | 0.000 |
| birth-death | *λ*-*µ* | high (no input) | 152.200 | 32.111 | 0.000 |

**Table S7.** The effect of taxon sampling and different inference methods for estimating diversification parameters when diversification parameters vary

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Simulation** | **Parameter** | **Taxon Sampling** | **Method** | **% error** | **95% HPD width** | **% with correct value in 95% HPD** |
| episodic *λ* | *λ* | low | Yule | 71.241 | 140.817 | 17.333 |
| episodic *λ* | *λ* | medium | Yule | 40.143 | 44.250 | 0.000 |
| episodic *λ* | *λ* | high | Yule | 2.634 | 22.441 | 100.000 |
| episodic *λ* | *λ* | low (no input) | Yule | 5.450 | 350.0731 | 100.000 |
| episodic *λ* | *λ* | medium (no input) | Yule | 3.2646 | 345.031 | 100.000 |
| episodic *λ* | *λ* | high (no input) | Yule | 4.216 | 336.786 | 100.000 |
| episodic *λ* | *λ* base | high | episodic *λ* | 5.600 | 69.071 | 100.000 |
| episodic *λ* | *λ* base | high (no input) | episodic *λ* | 282.600 | 409.854 | 0.000 |
| episodic *λ* | *λ* tips | high | episodic *λ* | 3.324 | 22.508 | 100.000 |
| episodic *λ* | *λ* tips | high (no input) | episodic *λ* | 36.352 | 321.534 | 0.000 |
| episodic *λ* | change time | high | episodic *λ* | 2.000 | 10.294 | 100.000 |
| episodic *λ* | change time | high (no input) | episodic *λ* | 478.000 | 183.945 | 0.000 |
| episodic *µ* | *λ* | high | episodic *µ* | 3.685 | 23.155 | 100.000 |
| episodic *µ* | *λ* | high (no input) | episodic *µ* | 15.543 | 327.626 | 100.000 |
| episodic *µ* | *µ* base | high | episodic *µ* | 98.927 | 444.199 | 0.000 |
| episodic *µ* | *µ* base | high (no input) | episodic *µ* | 99.239 | 417.830 | 0.000 |
| episodic *µ* | *µ* tips | high | episodic *µ* | \*0.222 | 475.291 | 0.000 |
| episodic *µ* | *µ* tips | high (no input) | episodic *µ* | \*0.143 | 473.102 | 0.000 |
| episodic *µ* | *λ*-*µ* base | high | episodic *µ* | 567.767 | 24.382 | 0.000 |
| episodic *µ* | *λ*-*µ* base | high (no input) | episodic *µ* | 704.233 | 335.011 | 100.000 |
| episodic *µ* | *λ*-*µ* tips | high | episodic *µ* | 4.742 | 23.360 | 100.000 |
| episodic *µ* | *λ*-*µ* tips | high (no input) | episodic *µ* | 14.892 | 331.216 | 100.000 |
| episodic *µ* | change time | high | episodic *µ* | 187.000 | 186.472 | 100.000 |
| episodic *µ* | change time | high (no input) | episodic *µ* | 191.000 | 182.512 | 100.000 |

\*absolute value, rather than % error. Correct value = 0.

**Table S8.** Diversification parameter estimates for *Ipomoea*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Parameter** | **Taxon Sampling** | **Method** | **Mean posterior estimate** | **95% HPD width** |
| *λ* | low | Yule | 0.188 | 114.644 |
| *λ* | medium | Yule | 0.230 | 27.776 |
| *λ* | high | Yule | 0.160 | 19.401 |
| *λ* | low (no input) | Yule | 0.164 | 78.963 |
| *λ* | medium (no input) | Yule | 0.185 | 25.459 |
| *λ* | high (no input) | Yule | 0.108 | 19.759 |
| *λ* | high | birth-death | 0.165 | 22.727 |
| *λ* | high (no input) | birth-death | 0.1103 | 22.212 |
| *µ* | high | birth-death | 0.00715 | 290.475 |
| *µ* | high (no input) | birth-death | 0.00630 | 282.716 |
| *λ-µ* | high | birth-death | 0.158 | 21.383 |
| *λ-µ* | high (no input) | birth-death | 0.104 | 22.022 |

**Table S9.** The effect of character sampling on phylogenetic inference

|  |  |  |
| --- | --- | --- |
| **Character Sampling** | **Method** | **Posterior Probability of correct clade** |
| 100 | JC | 0.916 |
| 1,000 | JC | 1.000 |
| 10,000 | JC | 1.000 |
| 100,000 | JC | 1.000 |
| 100 | GTR | 0.913 |
| 1,000 | GTR | 0.995 |
| 10,000 | GTR | 1.000 |
| 100,000 | GTR | 1.000 |
| no seq data | -- | 0.196 |

**Table S10.** The effect of character sampling for estimation of *n*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Character Sampling** | **Model** | **% error** | **95% HPD width** | **% with correct value in 95% HPD** |
| 100 | JC | 10.150 | 68.638 | 99.333 |
| 1,000 | JC | 4.582 | 22.923 | 98.000 |
| 10,000 | JC | 1.591 | 7.440 | 95.333 |
| 100,000 | JC | 1.757 | 2.348 | 11.333 |
| 100 | GTR | 10.810 | 71.013 | 100.00 |
| 1,000 | GTR | 5.671 | 23.249 | 95.333 |
| 10,000 | GTR | 1.276 | 7.520 | 97.333 |
| 100,000 | GTR | 0.560 | 2.385 | 89.333 |
| no seq data | -- | 124.345 | 140.189 | 90.667 |