Appendix 3 - Supporting Information

Digging their own macroevolutionary grave: Fossoriality as an evolutionary dead-end in snakes

Running head: Macroevolutionary Consequences of Fossoriality in Snakes

**Table S1:** Number of fossorial and non-fossorial species included in each dataset and sampling fraction used for the two states in the BiSSE and HiSSE analysis for the seven datasets.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Dataset** | **Fossorial species** | | | **Non-fossorial species** | | | **Total Sampling Fraction** |
| **This study** | **Total number** | **Sampling fraction** | **This study** | **Total number** | **Sampling fraction** |
| ***squamate*** | 317 | 1658 | 0.19919 | 1761 | 8238 | 0.2137 | 0.2099 |
| ***lizard*** | 88 | 679 | 0.1296 | 734 | 5586 | 0.1314 | 0.1312 |
| **Fossorial weighted *snake*** | 239 | 979 | 0.2441 | 1017 | 2652 | 0.3834 | 0.3459 |
| **Non-fossorial weighted *snake*** | 196 | 979 | 0.2002 | 1060 | 2622 | 0.3996 | 0.3459 |
| ***BC-squamate*** | 435 | 1658 | 0.2623 | 2162 | 8238 | 0.2624 | 0.2624 |
| ***BC-lizard*** | 270 | 679 | 0.3976 | 1590 | 5586 | 0.2846 | 0.2968 |
| ***BC-snake*** | 147 | 979 | 0.1501 | 572 | 6257 | 0.2156 | 0.1980 |

**Table S2:** BiSSE model comparisons between state dependent and state independent models for the squamate and lizard datasets. Lambda and mu are the speciation and extinction rates respectively for the fossorial (0) and non-fossorial (1) states. Transition rates between states are represented by q. The best fit model is highlighted in bold. \* indicates where the analysis encountered convergence problems.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Constraint** | **parameters** | **lnLik** | **AIC** | **deltaAIC** | **p value** |
| ***Squamate* dataset** | | | | | |
| Full model | 6 | -9135.86 | 18283.71 | 0.29 |  |
| lambda0 = lambda1 | 5 | -9140.58 | 18291.17 | 7.75 | 0.002109 |
| mu0 = mu1 | 5 | -9138.08 | 18286.15 | 2.73 | 0.03516 |
| lambda0 = lambda1, mu0 = mu1 | 4 | -9148.2 | 18304.4 | 20.98 | 0.00000436 |
| q01=q10 | 5 | -9137.73 | 18285.46 | 2.04 | 0.05299 |
| lambda0 = lambda1, q01=q10 | 4 | -9142.74 | 18293.49 | 10.07 | 0.001021 |
| mu0 = mu1, q01=q10 | 4 | -9140.38 | 18288.76 | 5.34 | 0.01086 |
| lambda0 = lambda1, mu0 = mu1, q01=q10 | 3 | -9149.05 | 18304.1 | 20.68 | 0.0000079 |
| **q01 = 0** | **5** | **-9136.71** | **18283.42** | **0** | **0.1914** |
| q10 = 0 | 5 | -9329.98 | 18669.97 | 386.55 | < 2.2e-16 |
| ***Lizard* dataset** | | | | | |
| Full model | 6 | -3886.331 | 7784.662 | 2.187 |  |
| lambda0 = lambda1 | 5 | -3886.997 | 7783.993 | 1.518 | 0.2486 |
| mu0 = mu1 | 5 | -3886.73 | 7783.459 | 0.984 | 0.372 |
| lambda0 = lambda1, mu0 = mu1 | 4 | -3887.624 | 7783.249 | 0.774 | 0.2743 |
| q01=q10 | 5 | -3886.877 | 7783.755 | 1.28 | 0.2959 |
| lambda0 = lambda1, q01=q10 | 4 | -3887.888 | 7783.775 | 1.3 | 0.2108 |
| mu0 = mu1, q01=q10 | 4 | -3887.581 | 7783.161 | 0.686 | 0.2866 |
| **lambda0 = lambda1, mu0 = mu1, q01=q10** | **3** | **-3888.238** | **7782.475** | **0** | **0.2824** |
| q01 = 0 | 5 | -3886.325 | 7782.65 | 0.175 | \* |
| q10 = 0 | 5 | -3921.179 | 7852.358 | 69.883 | < 2.2e-16 |

**Table S3:** BiSSE model comparisons between state dependent and state independent models for the snake dataset and the two coding schemes. Lambda and mu are the speciation and extinction rates respectively for the fossorial (0) and non-fossorial (1) states. Transition rates between states are represented by q. The best fit model is highlighted in bold.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Constraint** | **parameters** | **lnLik** | **AIC** | **deltaAIC** | **p value** |
| **fossorial weighted *snake* dataset** | | | | | |
| **Full model** | **6** | **-4931.98** | **9875.966** | **0** |  |
| lambda0 = lambda1 | 5 | -4934.37 | 9878.743 | 2.777 | 0.02883 |
| mu0 = mu1 | 5 | -4933.51 | 9877.017 | 1.051 | 0.08068 |
| lambda0 = lambda1, mu0 = mu1 | 4 | -4979.27 | 9966.533 | 90.567 | < 2.2e-16 |
| q01=q10 | 5 | -4938.95 | 9887.9 | 11.934 | 0.000189 |
| lambda0 = lambda1, q01=q10 | 4 | -4945.77 | 9899.5 | 23.534 | 1.02E-06 |
| mu0 = mu1, q01=q10 | 4 | -4938.96 | 9885.9 | 9.934 | 0.000935 |
| lambda0 = lambda1, mu0 = mu1, q01=q10 | 3 | -4985.36 | 9976.718 | 100.752 | < 2.2e-16 |
| q01 = 0 | 5 | -4934.35 | 9878.694 | 2.728 | 0.02967 |
| q10 = 0 | 5 | -5127.69 | 10265.37 | 389.404 | < 2.2e-16 |
| **non-fossorial weighted *snake* dataset** | | | | | |
| Full model | 6 | -4858.66 | 9729.323 | 1.093 | - |
| **lambda0 = lambda1** | **5** | **-4859.12** | **9728.23** | **0** | **0.3408** |
| mu0 = mu1 | 5 | -4860.85 | 9731.7 | 3.47 | 0.03638 |
| lambda0 = lambda1, mu0 = mu1 | 4 | -4895.42 | 9798.8 | 70.57 | < 2.2e-16 |
| q01=q10 | 5 | -4870.83 | 9751.7 | 23.47 | 8.09E-07 |
| lambda0 = lambda1, q01=q10 | 4 | -4874.00 | 9756 | 27.77 | 2.19E-07 |
| mu0 = mu1, q01=q10 | 4 | -4870.95 | 9749.9 | 21.67 | 4.58E-06 |
| lambda0 = lambda1, mu0 = mu1, q01=q10 | 3 | -4904.52 | 9815.041 | 86.811 | < 2.2e-16 |
| q01 = 0 | 5 | -4860.58 | 9731.2 | 2.97 | 0.04989 |
| q10 = 0 | 5 | -5059.99 | 10129.99 | 401.76 | < 2.2e-16 |

**Table S4:** BiSSE model comparisons between state dependent and state independent models for the squamate, lizards and snake dataset of Bars-Closel et al., 2017. The best fit model is highlighted in bold.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Constraint** | **parameters** | **lnLik** | **AIC** | **deltaAIC** | **p value** |
| ***BC-squamate* dataset** | | | | | |
| **Full model** | **6** | **-11139.01** | **22290.02** | **0** | **-** |
| lambda0 = lambda1 | 5 | -11141.5 | 22293 | 2.98 | 0.02574 |
| mu0 = mu1 | 5 | -11143.51 | 22297 | 6.98 | 0.002695 |
| lambda0 = lambda1, mu0 = mu1 | 4 | -11145.34 | 22299 | 8.98 | 0.001772 |
| q01=q10 | 5 | -11143.48 | 22297 | 6.98 | 0.002778 |
| lambda0 = lambda1, q01=q10 | 4 | -11152.67 | 22313 | 22.98 | 1.17E-06 |
| mu0 = mu1, q01=q10 | 4 | -11158.88 | 22326 | 35.98 | 2.34E-09 |
| lambda0 = lambda1, mu0 = mu1, q01=q10 | 3 | -11160.38 | 22327 | 36.98 | 2.79E-09 |
| q01 = 0 | 5 | -11185.75 | 22382 | 91.98 | 2.2E-16 |
| q10 = 0 | 5 | -11185.25 | 22380 | 89.98 | 2.2E-16 |
| ***BC-lizard* dataset** | | | | | |
| Full model | 6 | -8079.73 | 16171.46 | 0.61 | **-** |
| **lambda0 = lambda1** | **5** | **-8080.42** | **16170.85** | **0** | **0.2381** |
| mu0 = mu1 | 5 | -8081.54 | 16173.08 | 2.23 | 0.0569 |
| lambda0 = lambda1, mu0 = mu1 | 4 | -8083.36 | 16174.72 | 3.87 | 0.02652 |
| q01=q10 | 5 | -8100.68 | 16211.35 | 40.5 | 9.64E-11 |
| lambda0 = lambda1, q01=q10 | 4 | -8099.88 | 16207.76 | 36.91 | 1.77E-09 |
| mu0 = mu1, q01=q10 | 4 | -8099.78 | 16207.55 | 36.7 | 1.97E-09 |
| lambda0 = lambda1, mu0 = mu1, q01=q10 | 3 | -8099.94 | 16205.89 | 35.04 | 8.64E-09 |
| q01 = 0 | 5 | -8112.66 | 16235.31 | 64.46 | 4.44E-16 |
| q10 = 0 | 5 | -8092.56 | 16195.11 | 24.26 | 4.08E-07 |
| ***BC-snake* dataset** | | | | | |
| Full model | 6 | -2933.25 | 5878.5 | 1.301 | - |
| **lambda0 = lambda1** | **5** | **-2933.61** | **5877.2** | **0** | **0.3944** |
| mu0 = mu1 | 5 | -2939.54 | 5889.1 | 11.9 | 0.00039 |
| lambda0 = lambda1, mu0 = mu1 | 4 | -2965.51 | 5939 | 61.8 | 9.77E-15 |
| q01=q10 | 5 | -2942.14 | 5894.3 | 17.1 | 2.47E-05 |
| lambda0 = lambda1, q01=q10 | 4 | -2943.64 | 5895.3 | 18.1 | 3.08E-05 |
| mu0 = mu1, q01=q10 | 4 | -2942.52 | 5893 | 15.8 | 9.44E-05 |
| lambda0 = lambda1, mu0 = mu1, q01=q10 | 3 | -2966.3 | 5938.6 | 61.4 | 2.92E-14 |
| q01 = 0 | 5 | -2950.6 | 5911.2 | 34 | 3.93E-09 |
| q10 = 0 | 5 | -3000.1 | 6010.1 | 132.9 | < 2.2e-16 |

**Table S5:** HiSSE model comparisons between character dependent and character independent models for the squamate and lizard datasets. The best fit model is highlighted in bold.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **parameters** | **lnLik** | **AIC** | **AICc** | **deltaAIC** |
| ***Squamate* dataset** | | | | | |
| Bisse.like.hisse\_null | 4 | -9178.2 | 18364.4 | 18364.4 | 1043.78 |
| Bisse.like.hisse\_irrev | 5 | -9159.7 | 18329.3 | 18329.4 | 1008.76 |
| Bisse.like.hisse\_full | 6 | -9163.4 | 18338.8 | 18338.8 | 1018.22 |
| hisse.null2\_8transRate | 12 | -8849.9 | 17723.8 | 17723.9 | 403.19 |
| hisse.null2\_Eq\_Div | 10 | -9105.1 | 18230.1 | 18230.3 | 909.57 |
| hisse.null2\_1transRate | 5 | -8884.9 | 17779.7 | 17779.7 | 459.14 |
| hisse.null4\_Equal | 9 | -8673.9 | 17365.7 | 17365.8 | 45.15 |
| hisse.null4\_3transRate | 11 | -8741.9 | 17505.9 | 17506 | 185.29 |
| **hisse.full2** | **16** | **-8644.3** | **17320.6** | **17320.8** | **0** |
| hisse.full\_3transRate | 11 | -8809 | 17639.9 | 17640.1 | 319.37 |
| hisse.full\_EqTransRate | 9 | -8854.1 | 17726.1 | 17726.2 | 405.55 |
| hisse.full.10irriv | 14 | -8685.8 | 17399.5 | 17399.7 | 78.93 |
| hisse.full.01irriv | 14 | -8680.2 | 17388.3 | 17388.5 | 67.75 |
| ***Lizard* dataset** | | | | | |
| Bisse.like.hisse\_null | 4 | -3887.716 | 7783.432 | 7783.481 | 181.913 |
| Bisse.like.hisse\_irrev | 5 | -3922.063 | 7854.127 | 7854.2 | 252.608 |
| Bisse.like.hisse\_full | 6 | -3907.904 | 7827.808 | 7827.911 | 226.289 |
| hisse.null2\_8transRate | 12 | -3840.244 | 7704.488 | 7704.874 | 102.969 |
| hisse.null2\_Eq\_Div | 10 | -3871.205 | 7762.409 | 7762.681 | 160.89 |
| hisse.null2\_1transRate | 5 | -3831.819 | 7673.637 | 7673.711 | 72.118 |
| **hisse.null4\_Equal** | **9** | **-3791.76** | **7601.519** | **7601.741** | **0** |
| hisse.null4\_3transRate | 11 | -3803.42 | 7628.839 | 7629.165 | 27.32 |
| hisse.full2 | 16 | -3806.751 | 7645.502 | 7646.178 | 43.983 |
| hisse.full\_3transRate | 11 | -3825.913 | 7673.825 | 7674.151 | 72.306 |
| hisse.full\_EqTransRate | 9 | -3821.717 | 7661.433 | 7661.655 | 59.914 |
| hisse.full.10irriv | 14 | -3814.317 | 7656.634 | 7657.155 | 55.115 |
| hisse.full.01irriv | 14 | -3842.073 | 7712.145 | 7712.666 | 110.626 |

**Table S6:** HiSSE model comparisons between character dependent and character independent models for the snake dataset under the two coding schemes. The best fit model is highlighted in bold

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **parameters** | **lnLik** | **AIC** | **AICc** | **deltaAIC** |
| **fossorial weighted *snake* dataset** | | | | | |
| Bisse.like.hisse\_null | 4 | -4979.18 | 9966.366 | 9966.398 | 360.247 |
| Bisse.like.hisse\_irrev | 5 | -4997.44 | 10004.88 | 10004.93 | 398.761 |
| Bisse.like.hisse\_full | 6 | -4995.57 | 10003.14 | 10003.21 | 397.021 |
| hisse.null2\_8transRate | 12 | -4804.46 | 9632.921 | 9633.172 | 26.802 |
| hisse.null2\_Eq\_Div | 10 | -5022.58 | 10065.16 | 10065.34 | 459.041 |
| hisse.null2\_1transRate | 5 | -4932.16 | 9874.327 | 9874.375 | 268.208 |
| hisse.null4\_Equal | 9 | -4887.78 | 9793.561 | 9793.705 | 187.442 |
| hisse.null4\_3transRate | 11 | -4833.3 | 9688.59 | 9688.802 | 82.471 |
| **hisse.full2** | **16** | **-4787.06** | **9606.119** | **9606.558** | **0** |
| hisse.full\_3transRate | 11 | -4885.09 | 9792.173 | 9792.385 | 186.054 |
| hisse.full\_EqTransRate | 9 | -4897.57 | 9813.138 | 9813.282 | 207.019 |
| hisse.full.10irriv | 14 | -4792.5 | 9613.005 | 9613.343 | 6.886 |
| hisse.full.01irriv | 14 | -4806.51 | 9641.024 | 9641.363 | 34.905 |
| **non-fossorial weighted *snake* dataset** | | | | | |
| Bisse.like.hisse\_null | 4 | -5003.42 | 10014.84 | 10014.87 | 408.66 |
| Bisse.like.hisse\_irrev | 5 | -4991.71 | 9993.418 | 9993.466 | 387.24 |
| Bisse.like.hisse\_full | 6 | -4935.14 | 9882.279 | 9882.346 | 276.1 |
| hisse.null2\_8transRate | 12 | -4871.09 | 9766.182 | 9766.433 | 160 |
| hisse.null2\_Eq\_Div | 10 | -4999.21 | 10018.42 | 10018.6 | 412.24 |
| hisse.null2\_1transRate | 5 | -4917.18 | 9844.358 | 9844.406 | 238.18 |
| hisse.null4\_Equal | 9 | -4824.26 | 9666.519 | 9666.663 | 60.339 |
| hisse.null4\_3transRate | 11 | -4836.86 | 9695.715 | 9695.927 | 89.535 |
| **hisse.full2** | **16** | **-4787.09** | **9606.18** | **9606.62** | **0** |
| hisse.full\_3transRate | 11 | -4892.17 | 9806.34 | 9806.552 | 200.16 |
| hisse.full\_EqTransRate | 9 | -4891.16 | 9800.323 | 9800.468 | 194.14 |
| hisse.full.10irriv | 14 | -4813.87 | 9655.748 | 9656.087 | 49.568 |
| hisse.full.01irriv | 14 | -4812.99 | 9653.971 | 9654.309 | 47.791 |

**Table S7:** HiSSE model comparisons between character dependent and character independent models for the squamate and lizard dataset of Bars-Closel et al. (2017). The best fit model is highlighted in bold.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **parameters** | **lnLik** | **AIC** | **AICc** | **deltaAIC** |
| ***BC-squamate* dataset** | | | | | |
| Bisse.like.hisse\_null | 4 | -11149 | 22306.03 | 22306.04 | 881.62 |
| Bisse.like.hisse\_irrev | 5 | -11224.6 | 22459.15 | 22459.17 | 1034.74 |
| Bisse.like.hisse\_full | 6 | -11175.7 | 22363.31 | 22363.34 | 938.9 |
| **hisse.null2\_8transRate** | 12 | **-10700.2** | **21424.41** | **21424.53** | **0** |
| hisse.null2\_Eq\_Div | 10 | -11079.2 | 22178.3 | 22178.39 | 753.89 |
| hisse.null2\_1transRate | 5 | -11015.6 | 22041.11 | 22041.14 | 616.7 |
| hisse.null4\_Equal | 9 | -10737.1 | 21492.14 | 21492.21 | 67.73 |
| hisse.null4\_3transRate | 11 | -10751.1 | 21524.25 | 21524.35 | 99.84 |
| hisse.full2 | 16 | -10753.9 | 21539.84 | 21540.05 | 115.43 |
| hisse.full\_3transRate | 11 | -10871.1 | 21764.27 | 21764.38 | 339.86 |
| hisse.full\_EqTransRate | 9 | -10858.6 | 21735.21 | 21735.28 | 310.8 |
| hisse.full.10irriv | 14 | -10726.4 | 21480.74 | 21480.9 | 56.33 |
| hisse.full.01irriv | 14 | -10721.6 | 21471.21 | 21471.37 | 46.8 |
| ***BC-lizard* dataset** | | | | | |
| Bisse.like.hisse\_null | 4 | -8083.36 | 16174.72 | 16174.74 | 607.51 |
| Bisse.like.hisse\_irrev | 5 | -8121.275 | 16252.55 | 16252.58 | 685.34 |
| Bisse.like.hisse\_full | 6 | -8105.233 | 16222.47 | 16222.51 | 655.26 |
| hisse.null2\_8transRate | 12 | -7784.816 | 15593.63 | 15593.8 | 26.42 |
| hisse.null2\_Eq\_Div | 10 | -8066.377 | 16152.75 | 16152.87 | 585.54 |
| hisse.null2\_1transRate | 5 | -7949.835 | 15909.67 | 15909.7 | 342.46 |
| hisse.null4\_Equal | 9 | -7870.622 | 15759.24 | 15759.34 | 192.03 |
| hisse.null4\_3transRate | 11 | -7796.992 | 15615.98 | 15616.13 | 48.77 |
| **hisse.full2** | **16** | **-7767.606** | **15567.21** | **15567.51** | **0** |
| hisse.full\_3transRate | 11 | -7893.85 | 15809.7 | 15809.84 | 242.49 |
| hisse.full\_EqTransRate | 9 | -7964.536 | 15947.07 | 15947.17 | 379.86 |
| hisse.full.10irriv | 14 | -7877.039 | 15782.08 | 15782.31 | 214.87 |
| hisse.full.01irriv | 14 | -7877.039 | 15782.08 | 15782.31 | 214.87 |

**Table S8:** HiSSE model comparisons between character dependent and character independent models for the snake dataset of Bars-Closel et al. (2017). The best fit model is highlighted in bold.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Model** | **parameters** | **lnLik** | **AIC** | **AICc** | **deltaAIC** |
| ***BC-snake* dataset** | | | | | |
| Bisse.like.hisse\_null | 4 | -2965.56 | 5939.11 | 5939.167 | 208.911 |
| Bisse.like.hisse\_irrev | 5 | -2951.2 | 5912.394 | 5912.478 | 182.195 |
| Bisse.like.hisse\_full | 6 | -2972.47 | 5956.932 | 5957.05 | 226.733 |
| hisse.null2\_8transRate | 12 | -2973.24 | 5970.477 | 5970.919 | 240.278 |
| hisse.null2\_Eq\_Div | 10 | -2950.13 | 5920.252 | 5920.562 | 190.053 |
| hisse.null2\_1transRate | 5 | -2907.02 | 5824.039 | 5824.123 | 93.84 |
| hisse.null4\_Equal | 9 | -2867.86 | 5753.725 | 5753.979 | 23.526 |
| hisse.null4\_3transRate | 11 | -2876.07 | 5774.146 | 5774.519 | 43.947 |
| **hisse.full2** | 16 | **-2849.1** | **5730.199** | **5730.974** | **0** |
| hisse.full\_3transRate | 11 | -2904.36 | 5830.712 | 5831.086 | 100.513 |
| hisse.full\_EqTransRate | 9 | -2893.27 | 5804.54 | 5804.794 | 74.341 |
| hisse.full.10irriv | 14 | -2870.48 | 5768.965 | 5769.561 | 38.766 |
| hisse.full.01irriv | 14 | -2851.78 | 5731.556 | 5732.153 | 1.357 |

**Table S9:** Parameter estimates of the best fit HiSSE models for the four datasets and two coding schemes. Models are parameterized on net diversification rate (net.div) and relative extinction rate (ε).

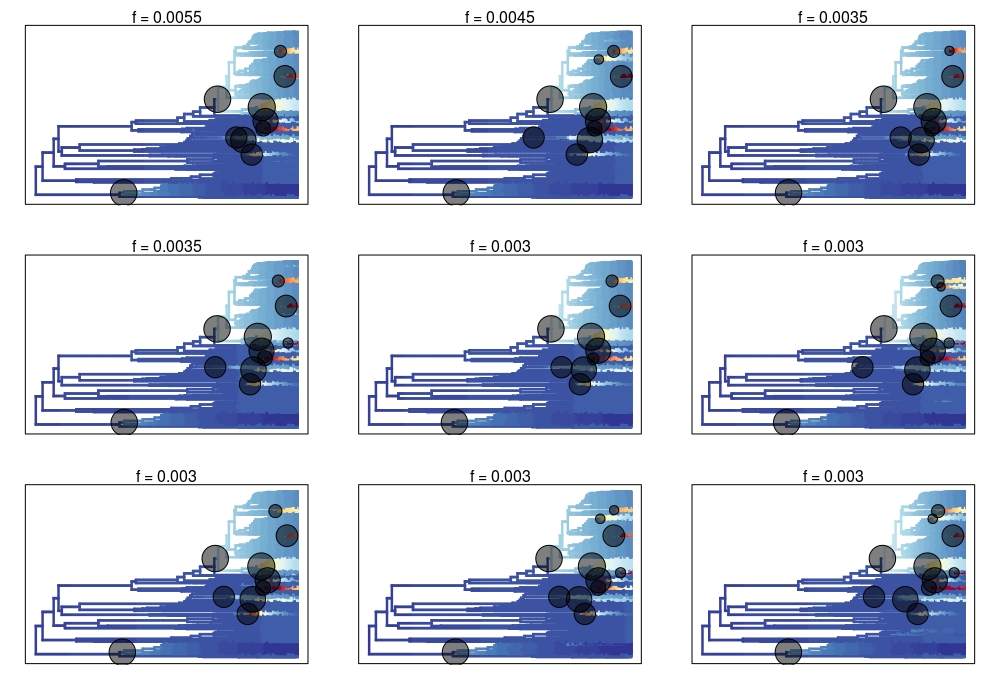
|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Dataset** | **model** | **net.div A0** | **net.div A1** | **net.div B0** | **net.div B1** | **ε A0** | **ε A1** | **ε B0** | **ε B1** |
| ***squamate*** | HiSSE full10irrev | 0.0286 | 0.0364 | 0.0867 | 0.1461 | 0.3902 | 0.3903 | 0.6802 | 0.5476 |
| **Fossorial weighted *snake*** | HiSSE full | 0.0357 | 0.0647 | 0.1859 | 0.3337 | 0.11325 | 2.5e-09 | 0.3090 | 0.3158 |
| **Non-fossorial weighted *snake*** | HiSSE full | -0.004 | 0.0655 | 0.0964 | 0.1733 | 1.2142 | 3.2e-06 | 0.5126 | 0.3215 |
| ***lizard*** | HiSSE null 8 rate | **net.div A** | **net.div B** | **net.div C** | **net.div D** | **ε A** | **ε B** | **ε C** | **ε D** |
| 0.0123 | 0.0838 | 0.2060 | 0.0586 | 2.0e-09 | 0.0628 | 0.2908 | 0.2014 |
| ***BC* Datasets** | **model** | **net.div A0** | **net.div A1** | **net.div B0** | **net.div B1** | **ε A0** | **ε A1** | **ε B0** | **ε B1** |
| ***BC-squamate*** | Hisse null 8 rate | 0.0378 | 0.0378 | 0.1354 | 0.1354 | 0.0305 | 0.0305 | 0.4046 | 0.4046 |
| ***BC-lizard*** | HiSSE full | 0.0283 | 0.0280 | 0.1231 | 0.1378 | 4.5E-07 | 0.2539 | 0.3912 | 0.3049 |
| ***BC-snake*** | HiSSE full | 0.0390 | 0.0806 | 0.1359 | 0.1726 | 0.3822 | 2.0e-09 | 0.5728 | 0.5074 |

Table S10: STRAPP analysis for association between fossoriality and estimated speciation rates from rate configurations from the BAMM analysis. A Mann Whitney U-test was used on 100000 STRAPP replicates for the rate configurations.

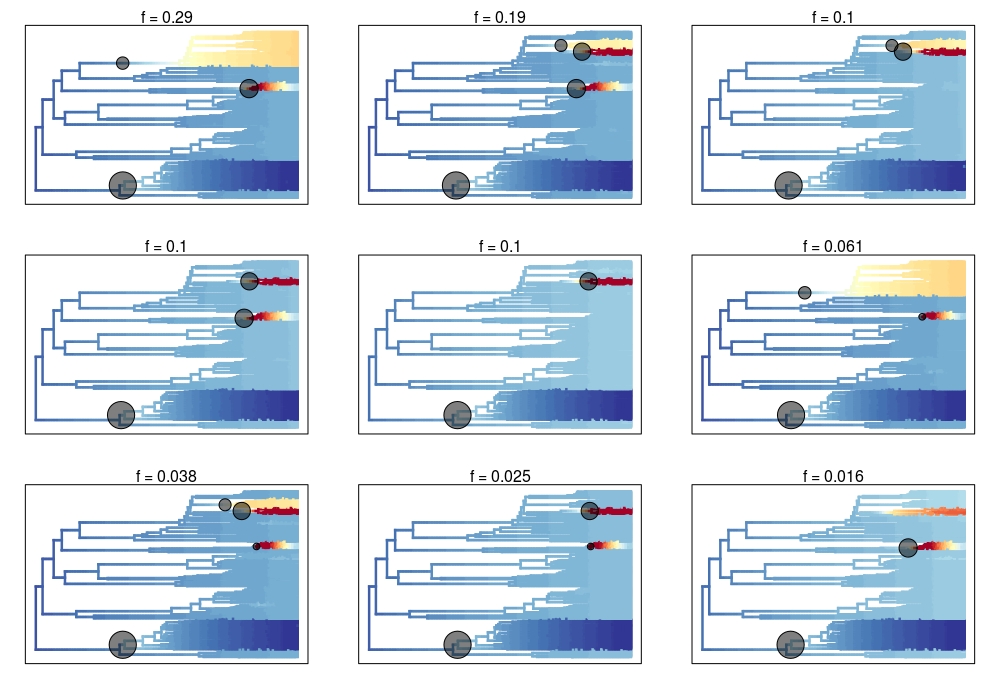
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Dataset** | **Rate Shift Configuration** | **Estimate 0** | **Estimate 1** | **P value** |
| ***Squamates*** | Maximum a posteriori probability (MAP) configuration | 0. 0601458 | 0. 1071338 | 0. 33258 |
| BAMM posterior distribution | 0. 06128423 | 0. 0998389 | 0. 31525 |
| ***Lizards*** | Maximum a posteriori probability (MAP) configuration | 0.08552478 | 0.08552478 | 0. 41263 |
| BAMM posterior distribution | 0. 08773361 | 0. 08776216 | 0. 55176 |
| **Fossorial weighted *snakes*** | Maximum a posteriori probability (MAP) configuration | 0.07342766 | 0.0708742 | 0.56621 |
| BAMM posterior distribution | 0.067654 | 0.07300631 | 0.17554 |
| **Non-fossorial weighted *snakes*** | Maximum a posteriori probability (MAP) configuration | 0.07342766 | 0.0708742 | 0.57092 |
| BAMM posterior distribution | 0.05386598 | 0.07301017 | 0.17539 |

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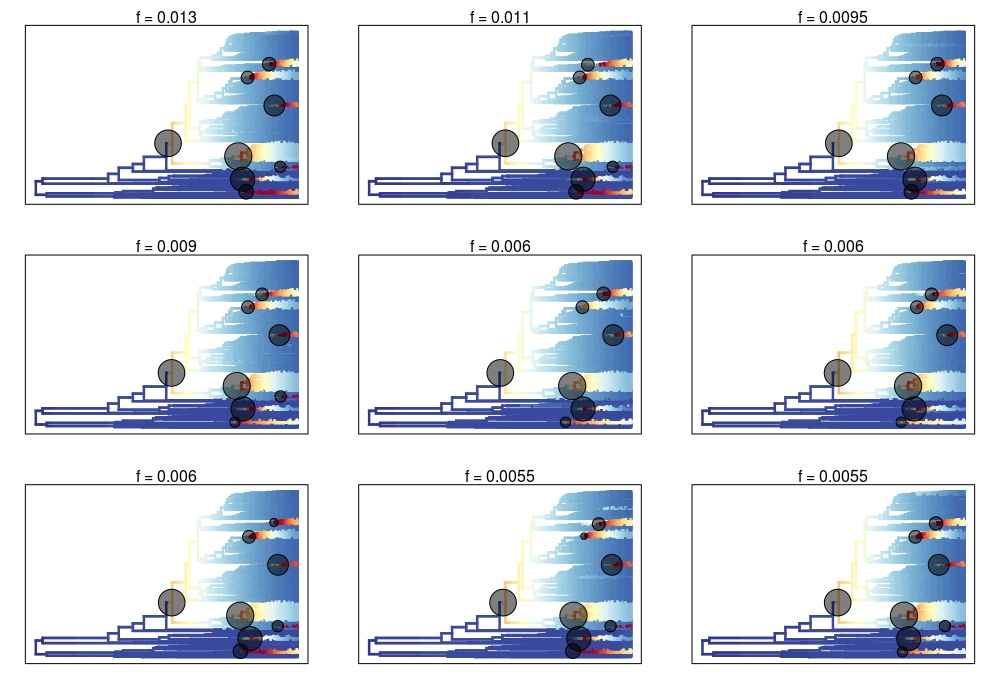
**Figure S1**: Phylorate plot showing the variation in net diversification estimated by BAMM with warm colours indicating high rates and cold colours indicating low rates for lineages in the snake tree under A – Maximum *a posteriori* (MAP) rate configuration, B – Maximum shift credibility (MSC) configuration.

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**Figure S2**: Credible shift set of rate shift configurations obtained from BAMM for the squamate tree using a marginal odds ratio threshold of 5. The frequency (f) of each rate shift configuration from the posterior distribution of BAMM is indicated above each plot.



**Figure S3**: Credible shift set of rate shift configurations obtained from BAMM for the lizard tree using a marginal odds ratio threshold of 5. The frequency (f) of each rate shift configuration from the posterior distribution of BAMM is indicated above each plot.



**Figure S4**: Credible shift set of rate shift configurations obtained from BAMM for the snake tree using a marginal odds ratio threshold of 5. The frequency (f) of each rate shift configuration from the posterior distribution of BAMM is indicated above each plot.

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**Figure S5**: Bayesian parameter estimates and ancestral state reconstruction for the *squamate* dataset. A - Speciation rate, extinction rate and transition rate between the two states, 0 representing fossorial and 1 representing non-fossorial taxa, inferred from the full BiSSE model. B – Ancestral states reconstruction from the HiSSE full model where branches are colour coded as hot and cold colours based on the net diversification rate estimates. The reconstructed states, colour coded as white for fossorial and black for non-fossorial, are embedded within each branch. The snake clade is indicated by a red circle. The inset in B indicates a density plot of the net diversification rates.

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**Figure S6**: Bayesian parameter estimates and ancestral state reconstruction for the *lizard* dataset. A - Speciation rate, extinction rate and transition rate between the two states, 0 representing fossorial and 1 representing non-fossorial taxa, inferred from the full BiSSE model. B – Ancestral states reconstruction from the HiSSE full model where branches are colour coded as hot and cold colours based on the net diversification rate estimates. The reconstructed states, colour coded as white for fossorial and black for non-fossorial, are embedded within each branch. The inset in B indicates a density plot of the net diversification rates.