

Erratum

doi:10.1093/molbev/mss127

An Improved Likelihood Ratio Test for Detecting Site-Specific Functional Divergence among Clades of Protein-Coding Genes

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Mol. Biol. Evol. 29(5):1297–1300. 2012 doi:10.1093/molbev/msr311

There was an error in the layout of Table 2. The table below shows the proper alignment of the columns. The publisher regrets the error.

Table 2. LRT Results for Biological Data Sets.

| Data Set | Model: Divergent Clade | Ln Likelihood | n.p. | LRT P Values | |
|----------------------|------------------------|---------------|------|-----------------------|----------------------|
| | | | | CmC versus M1a | CmC versus M2a_rel |
| Primate RNases | CmC: ECP | −2049.506 | 36 | 2.5×10^{-6} | 0.0786 |
| | M2a_rel | −2051.053 | 35 | — | — |
| | M1a | −2063.958 | 33 | — | — |
| Mammalian Rhodopsins | CmC: Mole rats | −9528.166 | 117 | 3.9×10^{-77} | 0.3433 |
| | CmC: Bats | −9518.779 | 117 | 3.3×10^{-81} | 9.2×10^{-6} |
| | CmC: Cetaceans | −9512.950 | 117 | 9.9×10^{-84} | 2.2×10^{-8} |
| | CmC: Pinnipeds | −9510.250 | 117 | 6.7×10^{-85} | 1.4×10^{-9} |
| | M2a_rel | −9528.615 | 116 | — | — |
| | M1a | −9706.830 | 114 | — | — |
| Bat Rhodopsins | CmC: Fruit bats | −2828.207 | 33 | 0.0010 | 0.0697 |
| | CmC: Yangochiroptera | −2828.858 | 33 | 0.0019 | 0.1585 |
| | CmC: Rhinolophidae | −2828.921 | 33 | 0.0020 | 0.1723 |
| | M2a_rel | −2829.853 | 32 | — | — |
| | M1a | −2836.319 | 30 | — | — |

NOTE.—n.p., number of parameters.