Marginal likelihood estimates for different molecular clock models of each PPV1- PPV7 dataset using path sampling

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| **Dataset** | **Molecular clock model** |
| ***UCED*** | ***UCLD*** | ***RLC*** | ***Strict*** |
| PPV1 | -11843.2 | -11839.5 | -11682.6 | -11823.5 |
| PPV2 | -16010 | -16011.7 | -15956.7 | -16060.2 |
| PPV3 | -11313.2 | -11317.1 | -11237.4 | -11340.7 |
| PPV4 | -9463.15 | -9465.41 | -9401.27 | -9473.83 |
| PPV5 | -9450.87 | -9447.16 | -9384.3 | -9463.28 |
| PPV6 | -12364.6 | -12370.4 | -12264.5 | -12434.5 |
| PPV7 | -13015.5 | -12985 | -12915.2 | -13211.8 |

*Notes:*

* *To selecte the data best-fit molecular clock model, it was kept constant for models of* ***(i)*** *nucleotide substutition model (BEAST Model Test, implemented in BEAST 2) and* ***(ii)*** *the coalescent Bayesian skyline plot*
* *UCED: Uncorrelated exponential relaxed- clock, UCLD: Uncorrelated lognormal relaxed- clock, RLC: Random local clock, Strict: Strict molecular clock*
* *Molecular clock model resulted in the lowest marginal likelihood value (highlighted in yellow) is considered the most suitable for the corresponding data*