**Supplementary Material File S.2**

**S2.1 Parameters received from jModelTest based on selection of GTR+I+G substitution model as best suitable according to AIC (Akaike Information Criterion).**



**S2.2 Prior distributions for tree calculation based on GTR+I+G substitution model in BEAUTi.**



|  |  |  |  |
| --- | --- | --- | --- |
| **Parameter** | **Prior** | **Bound** | **Description** |
| gtr.rates | Dirichlet [1,1] | [0, ∞] | GTR transition rates parameter |
| Frequencies | \* Dirichlet [1,1] | [0, ∞] | base frequencies |
| alpha | Uniform [0.1, 1], initial =0.579 | [0.1, 1] | gamma shape parameter |
| pInv | Fixed value, value=0.427 | [0, 1] | proportion of invariant sites parameter |
| clock.rate | \* Fixed value, value=1 | [0, ∞] | substitution rate |
| treeModel.rootHeight | \* Using Tree Prior in [0, ∞]  | [0, ∞] | root height of the tree |
| Yule.birthRate | Uniform [0, 1E100]. Initial = 1 | [0, 1E100] | Yule speciation process birth rate |

**Operator parameters:**



**S2.3 Arguments and list of commands for GMYC single threshold applied with SPLITS package in R (according to Fujisawa and Barraclough 2013 and Manual of SPLITS package)**

**Arguments:**

|  |  |
| --- | --- |
| tr | An ultrametric, dichotomous tree object in ape format. |
| method | Method of analysis, either "single" for single-threshold version or "multiple" for multiple-threshold version. |
| interval | Upper and lower limit of estimation of scaling parameters, e.g. c(0,10) |
| quiet | By default shows progress on console. Use quiet = FALSE to disable. |

**Commands:**

library(splits)

tr <- read.tree(file = "C:/PATH/TO/THE/TREE/mcc\_tree.newick", text = NULL, tree.names = NULL, skip = 0)

result <- gmyc(tr, method = "single”, interval = c(0, 10))

summary(result)

plot(result)

**Fujisawa T and** **Barraclough TG** (2013) Delimiting species using single-locus data and the Generalized Mixed Yule Coalescent approach: a revised method and evaluation on simulated data sets. *Systematic Biology* **62**, 707–724.