Console | Data | **Settings** | Results

① Data type: ◉ DNA ○ Protein

② Templates: ◉ ModelTest ○ MrBAYES ○ RAxML ○ PhyML ○ PAUP*

Models

③ ○ 3 ○ 5 ○ 7 ◉ 11 ○ 203 ○ User defined

Ascertainment bias correction

④ ◉ None ○ Lewis ○ Felsenstein ○ Stamatakis

Rate variation

⑤ ☑ uniform ☑ gamma (+G) ☑ pinv (+I) ☑ +I+G

⑥ ▬○──────── 4 categories

⑦ *Frequencies* ☑ Equal frequencies ☑ ML frequencies

Number of models: 0

⑧
☑ 000000 JC / F81
☑ 010010 K80 / HKY85
☑ 010020 TrNef / TrN
☑ 012210 TPM1 / TPM1uf
☑ 010212 TPM2 / TPM2uf
☑ 012012 TPM3 / TPM3uf
☑ 012230 TIM1ef / TIM1
☑ 010232 TIM2ef / TIM2
☑ 012032 TIM3ef / TIM3
☑ 012314 TVMef / TVM
☑ 012345 SYM / GTR

Advanced options

⑨ Parameter epsilon: [0.001]

⑩ Optimization epsilon: [0.01]

MSA: [Load MSA] -

Tree: [Maximum Parsimony]

[Load Tree] -

Partitions: [Load Partitions] -

Threads: ▬▬▬▬○▬▬▬▬ 2

Memory: -

[Run]

[Save Report]

[Reset]