jModelTest 2: more models, new heuristics and parallel computing

To the Editor: The statistical selection of best-fit models of nucleotide substitution is routine in the phylogenetic analysis of DNA sequence alignments. With the advent of next-generation sequencing technologies, most researchers are moving from phylogenetics to phylogenomics, in which large sequence alignments typically include hundreds or thousands of loci. Phylogenetic resources therefore need to be adapted to a high-performance computing paradigm so as to allow demanding analyses at the genomic level. Here we introduce jModelTest 2, a program for nucleotide-substitution model selection that incorporates more models, new heuristics, efficient technical optimizations and parallel computing.

jModelTest 2 includes important features not present in the previous versions (Supplementary Table 1). We expanded the set of candidate models from 88 to 1,624, and we implemented two heuristics for model selection: a greedy, hill-climbing hierarchical clustering approach (Supplementary Note 1) and a filtering algorithm based on similarity among parameter estimates (Supplementary Note 2).

Supplementary Note 1

Heuristic accuracy

Computational savings (%)

0 25 50 75 100

0 0.01 0.05 0.1 0.5 1.0

Threshold

Supplementary Note 2

Figure 1 | Benchmarking of the filtering heuristic in jModelTest 2. The threshold of the filtering heuristic (Supplementary Note 2) is directly correlated with the probability of finding the true best-fit model (heuristic accuracy) and inversely related to the number of models for which we avoided the likelihood calculation (computational savings). AIC, Akaike information criterion; BIC, Bayesian information criterion.

CircadiOomics: integrating circadian genomics, transcriptomics, proteomics and metabolomics

To the Editor: Circadian rhythms govern a large array of physiological and metabolic functions. It is critical to decode circadian oscillations by integrating multiple ‘omic’ approaches. Circadian genomic and