A novel method to estimate substitution rate variation among sites in large dataset of homologous DNA sequences

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We present here a novel method to estimate the site specific relative variability in large sets of homologous sequences. It is based on the simple idea that the more closely related are the compared sequences, the higher the probability to observe nucleotide changes at rapidly evolving sites.
A simulation study has been carried out to support the reliability of the method, which has been applied also to analyze the site variability of all available human sequences corresponding to the two hypervariable regions of the mitochondrial D-loop.