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Estimating evolutionary rates of discrete characters, and its application on genome evolution

The study of non-DNA discrete characters is crucial for the understanding of evolutionary processes. Discrete characters often have different transition rate matrices, variable rates among sites and sometimes contain unobservable states. To obtain accurate estimation, we implement sophisticated maximum likelihood methodologies and flexible transition rate matrices capable of analyzing a variety of discrete characters. We then show application examples on gene family data and on intron presence/absence data.