A Cauchy process to model trait evolution on a phylogeny

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Abstract

Phylogenetic comparative methods correct for the shared evolutionary history among a set of non-independent organisms by modeling the sampled continuous trait as arising from a diffusion process along the branches of a phylogenetic tree. Beyond the Brownian motion, several processes have been proposed in the literature, either Gaussian, in which case efficient algorithms relying on the Kalman filter are available, or based on more general Lévy processes, that can model a realistic evolution with jumps, but that are computationally intensive. Here, we propose to use a Cauchy process, for which we derive a recursive algorithm to compute the likelihood in a polynomial time. The Cauchy process is a pure jump process, that can also be seen as a Brownian motion with an inverse gamma relaxed variance parameter. It is already widely used to model virus spatial diffusion in phylodynamics approaches, as it can capture both small scale and large scale diffusion events, that are common in an epidemics. It can also be used in ecology to account for the heterogeneous evolution of functional traits of related organisms on long time scales.