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INTERSPECIES CORRELATION FOR NEUTRALLY EVOLVING TRAITS

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ABSTRACT

A simple way to model phenotypic evolution is to assume that after splitting, the trait values of the sister species diverge as independent Brownian motions. Relying only on a prior distribution for the underlying species tree (conditioned on the number, n, of extant species) we study the random vector $(X_1, \ldots, X_n)$ of the observed trait values. In this paper we derive compact formulae for the variance of the sample mean and the mean of the sample variance for the vector $(X_1, \ldots, X_n)$. The key ingredient of these formulae is the correlation coefficient between two trait values randomly chosen from $(X_1, \ldots, X_n)$. This interspecies correlation coefficient takes into account not only variation due to the random sampling of two species out of n and the stochastic nature of Brownian motion but also the uncertainty in the phylogenetic tree. The latter is modeled by a (supercritical or critical) conditioned branching process. In the critical case we modify the Aldous–Popovic model by assuming a proper prior for the time of origin.

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REFERENCES

[1] S. Sagitov and K. Bartoszek: *Interspecies correlation for neutrally evolving traits*, J. Theor. Biol. **309** (2012), 11–19.