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## The phylogenetic effective sample size and jumps

The phylogenetic effective sample size is a parameter that has as its goal the quantification of the amount of independent signal in a phylogenetically correlated sample. It was studied for Brownian motion and Ornstein–Uhlenbeck models of trait evolution. Here, we study this composite parameter when the trait is allowed to jump at speciation points of the phylogeny. Our numerical study indicates that there is a non-trivial limit as the effect of jumps grows. The limit depends on the value of the drift parameter of the Ornstein–Uhlenbeck process.

### References

- [1] K. Bartoszek, *The phylogenetic effective sample size and jumps*, *Mathematica Applicanda* 46(1) (2018), 25–33, doi=10.14708/ma.v46i1.6368.