

About the evolution of the genomic diversity in a population reproducing through partial asexuality

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Abstract

Reproductive systems define how the genetic diversity is transmitted through generations and thus highly constraint the genetic evolution of species. Many species of relevant interests for human activities and ecosystems can reproduce both through sexual or asexual events during their life. Despite their widespread interests, we have few tools to predict the evolution of the genetic diversity within those partially asexual species. Moreover, the scarce previous models propose contradictory or unclear results. We thus formalized the exact probabilities of evolving genotypic states through generations using transition probabilities as function of the rate of asexuality and embedded them within a Markov chain. The model takes into account for mutation and drift forces, giving the opportunity to assess the distributions of any expected genetic index at a locus that did not experiment selection. Such model computation relies on fat matrices because of the number of genotypic states. We used massive parallelized algorithm to compute them. It provided unseen results, enabled precise predictions and clarified some controversial biological points.

Keywords

Markov chain, Rate of clonality, Mutation, Genetic drift, Matrix calculus, Maximum likelihood.

References

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