

## Approximate Bayesian Computation: a useful approach for inferring population history and other parameters

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Knowledge of population or species history is of critical importance for both theoretical concepts of evolutionary biology and molecular ecology, and applications in management of animal populations, for example invasive species or those of conservation concern. Although many statistical tools implementing Bayesian concepts has been used in evolutionary and ecological science for several decades, since the beginning of this century (Beaumont et al. 2002) there is a new powerful approach becoming more and more used by biologists: Approximate Bayesian Computation (ABC).

Motivated by the growth in computational power and complexity of data, modelling, ABC is beginning to be intensively used even though it is less accurate than, for example Markov Chain Monte Carlo (MCMC) methods. Nevertheless, ABC allows greater model complexity, especially in the case of more parameters than would be possible with standard likelihood-based algorithms. The ABC approach, based on coalescent theory and comparison of real datasets with those simulated under designed scenarios (consisting of different combinations of parameters) has been recently used for inferring various scenarios of demographic history, as well as estimation of population characteristics, such as effective population size, time of divergence, strength of bottlenecks, etc.

In this contribution, the principle use of ABC will be presented as an example of inferring the colonization history of Senegal using genetic data from the black rat (*Rattus rattus*). In addition, other examples from population genetics, community ecology and epidemiological modelling will be demonstrated.

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