

# A brief history and popularity of methods and tools used to estimate micro-evolutionary forces

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## Abstract

Enabled by rapid advances in sequencing technologies, population genetics currently experiences a second boom. Established approaches are being adapted to new marker systems, and new methods are developed that allow genome-wide estimates of the four major micro-evolutionary forces – mutation, gene flow, genetic drift and selection. Nevertheless, classic population genetic markers are still commonly used and a plethora of analysis methods and programs are available. With these diverse ranges of datasets and methods, various theoretical and statistical frameworks are employed to varying degrees of success in estimating similar evolutionary parameters making it difficult to get a concise overview across the available approaches. Presently, reviews on this topic generally focus on a particular class of methods to estimate one or two evolutionary parameters. Here, we provide a brief history of methods and a comprehensive list of available programs for estimating micro-evolutionary forces. We furthermore analysed their usage within the research community based on popularity (citation bias) and discuss the implications of this bias on the software community. We found that a few programs received the majority of citations, with program success being independent of both the parameters estimated and the computing platform. The only deviation from a model of exponential growth in the number of citations was found for the presence of a graphical user interface (GUI). Hence, developers should consider implementing GUIs in their programs in order to promote them.

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