### simuPOP Cookbook

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#### **Abstract**

simuPOP is a forward-time population genetics simulation environment. Unlike coalescent-based programs, simuPOP evolves populations forward in time, subject to arbitrary number of genetic and environmental forces such as mutation, recombination, migration and population/subpopulation size changes. Statistics of populations can be calculated and visualized dynamically which makes simuPOP an ideal tool to demonstrate population genetics models; generate datasets under various evolutionary settings, and more importantly, study complex evolutionary processes and evaluate gene mapping methods.

simuPOP can be used at two levels. The core of simuPOP is a scripting language (Python) that provides a large number of building blocks (populations, mating schemes, various genetic forces in the form of functions, operators, simulators and gene mapping methods) to construct a simulation. This provides a R/S-Plus or Matlab-like environment where users can interactively create, manipulate and evolve populations; monitor and visualize population statistics and apply gene mapping methods. The full power of simuPOP and Python (even R) can be utilized to simulate arbitrarily complex evolutionary scenarios.

simuPOP also comes with an increasing number of pre-defined simulation scenarios. If one of them happens to fit your need, all you need to do is running the script file with appropriate parameters. No knowledge of Python or simuPOP is required. To make simuPOP readily usable for time-limited users, users of simuPOP are strongly encouraged to submit their simulations to this collection.

This simuPOP cookbook explains in details techniques used in various situations. Detailed information about simuPOP components, functions and operators is available in the *simuPOP Reference Manual*. All resources, including a pdf version of this guide and a mailing list can be found at the simuPOP homepage http://simupop.sourceforge.net.

#### How to cite simuPOP:

Bo Peng and Marek Kimmal (2005) simuPOP: a forward-time population genetics simulation environment. *bioinformatics*, **21**(18): 3686-3687

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# Basic usages

1.1 s

CHAPTER

**TWO** 

### Pedigree tracking

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