

# Design Goals and Application of a Simulation System for Conservation Biology

Thomas Olivier, Green Creek Paradigms, LLC, 4632 Green Creek Road, Schuyler, VA 22969, USA, [tolivier@cstone.net](mailto:tolivier@cstone.net)

## ABSTRACT

This paper presents a population simulation system that models processes in animal populations subdivided by space or social groupings. The system is designed to allow modeling of varied population processes in particular population structure and landscape settings. The simulation system presented here uses syntactically organized character strings and equivalent data structures to represent local population structures. It is implemented in Python and uses object-oriented methods to portray population features at varied levels of specialization. The system also contains a run-time link to a geographic information system. A model of a socially subdivided mammalian population has been built. Model assumptions are similar to the organization seen in some species of Old World monkeys. Applicability of the system is shown in simulations illustrating interactions between demographic rates, infectious diseases, genetic structures and social structural events.

## INTRODUCTION

This report presents a population simulation system developed to model a range of processes in animal populations subdivided by space or social behavior. The system is designed to permit examination of the interplay of demographic, genetic, social and other processes in populations, and the interactions between landscape states and population processes. Results of such modeling are potentially of use to conservation planners and managers, as well as basic researchers in population biology. The author plans to release a test version of this system under an open source license in late 2003.

## DESIGN

Good conservation models must reflect important features of populations and their habitats. However, models framed too particularly may have prohibitively limited applicability. Much of the design of the system is aimed at effectively resolving these sometimes-conflicting requirements. Simulations that exploit methods and data structures indigenous to digital computers appear particularly well suited to meeting such heterogeneous requirements. In this vein, the simulation system presented here uses syntactically organized character strings and other equivalent data structures to represent local population structures. It is implemented in Python and uses object-oriented methods to portray population features at varied levels of biological specificity. The system includes a run-time link to a geographic information system (GIS). Strategically, this system is designed to provide a library of programming tools that can be extended with modest programming effort to effectively model processes in many real populations.

In this system, a single simulation steps a population through a series of discrete time periods, with births, deaths and other biological events potentially taking place in each time period. Each population contains subpopulations, representing occupants of different spatial neighborhoods or social groups. The system is designed to eventually permit simultaneous simulation of populations of different species, so that competition, predator-prey relationships and disease transmission between species can be modeled.

Members of modeled populations are identified individually and their life histories are simulated in detail. Attributes of each simulated individual are stored in a Python dictionary. Coupled with Python's dynamic typing, named attributes of different types can easily be added to individuals in a simulation. Age, sex, genotypes and infectious disease states are used in models described in this report. A separate dictionary maintains records of kinship links among individuals.

In nature, local populations may be relatively unstructured (i.e. random mating aggregates of individuals, joined mainly by spatial proximity) or highly complex (i.e. multi-layered social groups with complex internal structures and dynamics, such as those known to occur in some species of primates). Keyed character strings are able to represent a wide range of such population structures (Olivier, 1985). Keyed character strings and equivalent graphs or indented text blocks are used in this system to store memberships of individuals in subpopulations and, if applicable, social structures. A template provided by the modeler at run time specifies many features of permissible subpopulation structures. Olivier (2003) presents details on use of keyed structures to represent subpopulation structures in this system along with other details of the implementation.

Python is designed for use with object-oriented programming methods. In this approach, functions (or methods) and the data (or attributes) they operate on are bound together into objects. More specialized or complex classes can be derived from simpler or more general classes defined within the same program. Object-oriented methods are naturally well suited to representing dynamic, hierarchically structured systems common in biology.

A hierarchy of class objects embedded within other objects provides a basic framework in the modeling system. In each application, a simulation class object contains a range of other objects, including a population class object. In turn, each population contains various attributes, including a set of subpopulation objects. Information on composition of each subpopulation is stored in a keyed structure embedded in each subpopulation.

Class inheritance is used to derive more specialized classes from basic classes. Derived classes provide features important in models of particular real populations. For example, classes `base_popframe` and `base_subpopframe` provide some basic input, output and other informational handling capabilities. Classes `mammal_popframe` (derived from `base_popframe`) and `mammal_subpopframe` (derived from `base_subpopframe`) add functionality to assist in modeling age-specific fertility and survival commonly employed in studies of mammals. In turn, the mammal population and subpopulation classes serve in one existing application as basis for a model of mammals living in patches with little internal organization. In another application, these same mammal classes are foundations for a model with subpopulations resembling the complex structures seen in some groups of Old World monkeys.

Interactions between landscape states and population processes must be considered in most conservation efforts. One would like to represent subpopulation locations in space along with local landscape variations in altitude, vegetation, water resources and other features known to influence organisms. Ideally, interactions between populations and landscape features should be possible during the course of a simulation.

GIS software provides many of the desired landscape portrayal and analysis capabilities. To exploit GIS capabilities, the simulation system includes a Python run-time interface to the Idrisi GIS (Clark Labs, 2001). At present, the interface permits calling Idrisi functions while simulations are in process. A goal of this project is extension of the GIS interface to include Python methods tailored to the needs of population simulations. Problems that might be addressed with simulations incorporating the GIS link include analyses of gene flow patterns over landscapes, analyses of infectious disease levels in varying habitats and studies of interactions between population source and sink areas.

The simulation system has been developed to date on a Microsoft Windows 2000 platform. An effort has been made to use portable programming methods so that the system will be portable to Linux. However, GIS packages tend to be bound to particular operating systems and complete portability of GIS interfaces across operating systems seems unrealistic.

## APPLICATIONS

Models of populations with structures similar to those observed in some Old World monkeys demonstrate capabilities of this system. Rhesus monkeys ordinarily are divided into social groups that exhibit complex structures and dynamics (Sade 1965, Sade et al. 1977). Males usually leave the groups in which they are born when they become adult. Immigrant males in a group commonly form a dominance hierarchy and mate with the different adult females residing there. Males may migrate through a series of groups during their lifetimes. Females ordinarily remain in the group in which they are born. These natal females are organized into matrilineal groups of adult females related by descent through females, along with their immature offspring of both sexes. Many of the behaviors of females are influenced by matrilineal memberships. Large groups may divide, with some adult males and some matrilineal groups joining each fission product group. Small groups may fuse. Savanna baboon groups have shown some similar features.

The monkey simulation proceeds through a series of simulated time periods. Simulated monkeys live to a maximum age of five periods; each simulated time period corresponds to perhaps four years in the life of a monkey. In each simulated time period, the population and its groups undergo birth, survival, ageing and migration processes. In addition, matrilineal groups that become large may subdivide along female sublineal lines. Groups that grow large may subdivide and groups that become small may fuse with another group in the simulation. Initial populations in the various simulations described here consisted of five social groups containing a total of 193 individuals.

Figure 1. Example Monkey Group in Simulation

```
G, 3
H, 3
A, 589 A, 647 A, 713 A, 719 A, 601 A, 652 A, 653 A, 630
A, 635 A, 723 A, 661 A, 752 A, 766
N, 3
M, 31
A, 617 A, 733 A, 663 A, 803 A, 802 A, 801 A, 800 A, 666
A, 805 A, 804 A, 728 A, 807 A, 806
M, 32
A, 598 A, 620 A, 808 A, 737 A, 810 A, 809 A, 621 A, 811
A, 736 A, 813 A, 812 A, 753 A, 815 A, 814
```

Figure 1 presents an example of a simulated monkey group structure. The group has a hierarchical internal structure and contains elements of different types. Line indentations are used to represent structural nesting relations. The string "G,3" indicates that this example represents group instance number three. "H,3" refers to the segment of the group containing immigrant adult males. "N,3" identifies the natal segment of this group, with "M,31" and "M,32" identifying two matrilineal groups present within the group's natal segment. Strings of the form "A,<n>" identify simulated individual animals. As can be seen, matriline "M,32" contains 14 members.

One application examines occurrences of fissions and fusions in three simulation series of 20 runs each. In the three simulation series, age-specific birth and survival rates were set to produce expectations of population size stability, growth and decline. In all series, group fission size thresholds of 45 and fusion thresholds of 18 were used. Figure 2 contrasts the mean number of groups present in each simulation over time in stable, growing and declining simulation series.

Figure 2.

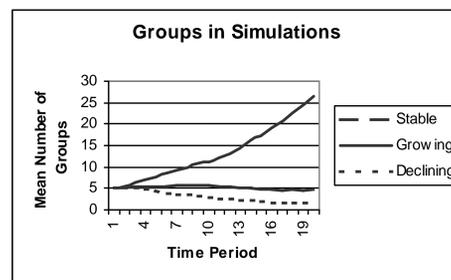


Table 1 presents additional information on this run series. As can be seen, the numbers of fissions and fusions and ratios of fissions to fusions vary greatly between series with different demographic conditions.

Table 1. Group Fissions and Fusions Under Varied Demographic Conditions

	Stable	Growing	Declining
Fissions during series of 20 runs	101	767	22
Fusions during series of 20 runs	103	291	95
Ratio fissions/fusions	.98	2.64	.23
Groups per population (mean at end)	4.90	28.60	1.35
Individuals in population (mean at end)	152.60	928.60	36.90
Group size (mean at end)	31.14	32.47	27.33

Although mean numbers of individuals present in populations at the ends of simulations vary greatly with demographic rate sets, mean group sizes are close. Note that the group numbers in Figure 2 were tallied at the beginning of each simulated time period. Terminal population sizes and group numbers presented in Table 1 were tallied at the end of simulations.

Group fissions affect the distributions of genes in subpopulations. Since modeled groups fission partly along matrilineal lines, genetic lineal effects (Neel and Salzano, 1967) may operate. With lineal effects, genetic differences between fission product groups can be larger than expected under simple random allocation of genes present in the original group. The magnitudes of such lineal effects can vary greatly from one fission to another, as well as from one locus to another.

In another application of the system, transmission of alleles at two genetic loci was simulated in a series of twenty runs with population demographic rates set to produce approximate size stability. Genetic compositions of groups produced by fissions were logged. Levels of genetic differentiation observed between fission product groups varied greatly, as expected, but large differences were seen repeatedly. Table 2 illustrates group gene frequencies produced in one simulated fission.

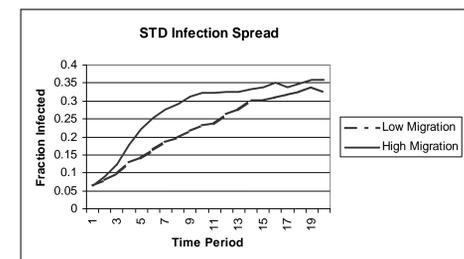
Table 2. Allele Frequencies in a Group Fission

	Original Group	Fission Product Group 1	Fission Product Group 2
Frequency allele A, locus A	.343	.360	.327
Frequency allele B, locus B	.657	.820	.500
Size of group	51	25	26

Allele frequencies at locus A are close in the fission product groups. At locus B, a large difference is present.

A third application examined effects of different rates of adult male migration on spread of a sexually transmitted disease (STD). Two series of twenty runs were conducted. In both series, demographic rates were set to produce approximate population size stability. At the start of all simulations, ten adults in one group were set to be infected. In one run series the probability of a non-natal male moving in a given time period from one group to another was set to 0.1. In the second series, this migration probability was set to 0.6. In matings that produce offspring, there was a probability of 0.8 of transmitting the disease from an infected parent to an uninfected one. As can be seen in Figure 3, the early spread of the infection proceeded more rapidly in simulations with high levels of migration.

Figure 3.



## DISCUSSION

Experiences to date indicate that this system is capable of representing flexibly and in detail a range of processes of interest to conservation and population biologists. Before public release, some redistributions of existing functionality in code modules, some functional extensions and further testing are planned.

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