

GENETIC DIFFERENTIATION IN SIMULATED MONKEY POPULATIONS WITH SPATIAL SUBSTRUCTURE AND VARYING GROUP FUSION AND FISSION SIZE THRESHOLDS.

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Abstract

This study examines genetic differentiation levels in simulated, monkey populations containing social groups of different sizes, subjected to density-dependent population regulation and existing on landscapes with some spatial subdivision. Models are built using the CRITTRZ simulation system. The models simulate individual life histories and maintain age, sex, genotype and pedigree information on simulated individuals. Groups in the simulated populations resemble cercopithecine multi-male groups. They contain immigrant adult males and natal animal segments composed of matriline. Groups may fission, partly along matriline, and they may fuse. Group sizes are influenced by group size fusion and fission threshold parameters. Four simulation series with varying fusion and fission threshold size pairs were conducted. The fusion/fission parameter pair values were a) 16/32 b) 20/40 c) 24/48 d) 28/56. Terminal, mean Fst measures of genetic differentiation in the same simulation series were a) .062 b) .043 c) .032 d) .028, indicating strong decline in genetic differentiation among simulated monkey groups with increasing group fusion and fission threshold values. These results are compared with those of previous simulations that employed similar fusion/fission size parameter pairs, but fixed, age-specific birth and survival rates and no spatial substructure.

Key words: monkey, simulation, CRITTRZ, genetic

Introduction

CRITTRZ is an open source population simulation system developed by the author using the Python computer language. It is intended for modeling demographic, genetic and infectious diseases processes in mammalian populations divided by various forms of social groupings and optionally by geographic space. CRITTRZ uses syntactically organized character strings, or equivalent graphs or indented text blocks, to represent social group structures (Olivier, 1985, 2003).

Figure 1 illustrates the structure of one simulated group using the indented text block form of keyed structure. In this figure, "G,82", "H,82" and "N,82" are unique identifiers in the system for a simulated group and its adult male and natal segments, respectively. Letter and number pairs beginning with "A" identify individuals belonging to group elements.

Figure 1. Example simulated group structure

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G, 82
H, 82
  A, 29743 A, 29816 A, 29855 A, 30022 A, 30178 A, 30095
N, 82
  A, 29663 A, 30320 A, 29665 A, 30082 A, 30321 A, 30323 A, 30322
  A, 30085 A, 30089 A, 30326 A, 30325 A, 30324 A, 30090 A, 30327
  A, 30086
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A programming interface to the Idrisi GIS and code for manipulation of GIS data is included with one CRITTRZ distribution. With this version, GIS raster files can be used during simulations to represent group home ranges, resource distributions, costs of movement and other spatially distributed features of model populations or the simulated landscape they occupy (Olivier, 2007).

The next two figures present examples of rasters used in simulations discussed in this paper. Figure 2 illustrates the home range of one simulated monkey group at one point in time. Home range is represented by orange pixels. White pixels represent landscape areas not occupied by this group.

Figure 2. Home range of group represented by a raster.



Figure 3 illustrates simulated monkey population density variations over space at one point in time.

Figure 3. Population density represented by a raster



In CRITTRZ models, simulations step through discrete time periods. In simulated populations, animals and social groups are identified uniquely. Kinship links between animals are stored. In each time period, individuals are born, age, reproduce and die. Age and sex specific survival and reproduction probabilities are employed. Depending on assumptions of particular models, social groups may fission or fuse. Home ranges of groups may change size or location. The system provides facilities for logging and summarizing simulated biological events.

Curious about CRITTRZ?

Downloads, documentation and reports on applications are available at:

www.greencreekparadigms.com/CRITTRZ.htm

CRITTRZ distributions include a series of applications built to resemble cercopithecine multi-male groups. In these "cercomm" family models, simulated populations are subdivided into social groups that contain a segment composed of immigrant adult males and a natal segment. The natal segment is composed of matriline, that in turn are composed of adult females and their immature offspring. Natal males emigrate on reaching adulthood. Adult males may migrate between social groups. Groups may fission (partly along matriline) and may fuse. In models utilizing the GIS interface, groups possess overlapping home ranges that change with time and events.

One application of cercomm models without spatial substructuring (Olivier, 2004) investigated gene frequency differentiation levels among social groups in populations that were growing, stable and declining in size, with different group fission and fusion size thresholds. Another (Olivier, 2005) examined matrilineal genetics in cercomm populations. Olivier (2007) reported on preliminary applications of GIS-enabled cercomm models to the study of gene frequency distributions in a single population and infectious disease transmission within and between populations.

Purpose

This study examines genetic differentiation in simulated monkey populations. The populations are distributed over rectangular landscapes. Populations are divided into social groups resembling cercopithecine multi-male groups. Group fusion and fission size parameters influence group sizes. Effects of different group fusion and fission parameter pair sizes on group genetic differentiation are examined.

Methods

Simulations employed CRITTRZ cercomm models with the GIS interface. Four simulation series were conducted. The four series differed in group fusion and fission size threshold pairs employed: a) 16,32 b) 20, 40 c) 24, 48 d) 28, 56. Maximum group home range size parameters were increased with increases with fusion/fission parameter values. In all run series, other conditions were identical. Each series consisted of 15 simulations run for 30 time periods.

In all runs, the starting population contained 625 individuals divided into 31 social groups. Simulated individuals possessed two independent autosomal genetic loci that were polymorphic in the population. Genotypes in the initial population were assigned randomly. Birth and survival probabilities were density-dependent, with resources affecting these probabilities distributed homogeneously in the environment.

Each social group possessed a home range that varied in space over time. Home ranges of neighboring groups sometimes overlapped. Emigrant adult males tended to move into groups 1) with low ratios of adult males to adult females and 2) relatively close geographically. In these simulations, greater weight was given to geographic distance in selecting groups that emigrant adult males would join. Costs of movement in all directions were identical.

CRITTRZ log files were used to record temporal variations in population sizes, group numbers, group Fst gene frequency differentiation levels and group fusion and fission events.

The hard drive containing simulation files was defragmented between some simulation runs.

Results

Mean group sizes at ends of simulations for different fusion/fission series are presented in Table 1. Mean sizes lie between fusion and fission size thresholds for each series.

Table 1. Mean group sizes at ends of simulations.

Series	16/32	20/40	24/48	28/56
Group Size Means	21.1	27.0	32.1	36.3

Figure 4 is a gene frequency surface for one allele from the last time period of one simulation in the 20/40 fusion/fission series. Black pixels are not occupied by the simulated population. Frequencies for the mapped allele increase from dark brown to white. On this raster, local allele frequencies vary from approximately 0.39 to 0.94.

Figure 4. Simulation gene frequency surface.



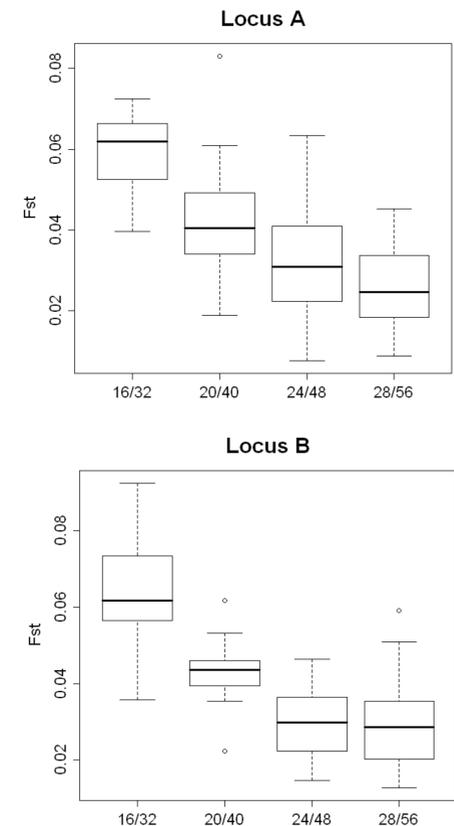
Table 2 presents mean Fst values among groups at simulation ends for the four simulation series and for both loci. Fst values in the table decline as one proceeds from smaller fusion/fission value pairs on the left to larger values on the right. The decline from the 24/48 series to the 28/56 series in the locus B series is less than that seen in the locus A series.

Table 2. Mean Fst values among groups.

Fusion/Fission	16/32	20/40	24/48	28/56
Locus A	.0588	.0426	.0324	.0262
Locus B	.0645	.0430	.0309	.0301
Both Loci	.0617	.0428	.0317	.0281

Figures 5a and 5b present box plots of Fst values at ends of simulations for all fusion/fission series and for both loci. Median values are represented by dark horizontal lines in each box. Medians decline with increasing fusion/fission values, much like the declines seen for Fst means. These boxplots also demonstrate much variability in end-of-simulation Fst values within each simulation series.

Figures 5a, 5b. Boxplots of locus Fst distributions



Discussion

Olivier (2004) examined genetic differentiation in simulations of cercopithecine multi-male groups with fixed survival and reproduction rates set to produce growing, stable and declining populations. In simulations for that study, variations in growth circumstances were coupled with variations in fusion/fission parameter pairs similar to this study.

That earlier study also found increases in mean group sizes with increasing fusion/fission parameter values. Declines in mean Fst values with increasing fusion/fission parameter values also were found. Fst values for declining populations were lower than those found in the current study for comparable fusion/fission value pairs. Fst values for stable and growing populations in the earlier study were near to those reported here.

Further investigations using CRITTRZ are planned.

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