

USE OF THE CRITTRZ SIMULATION SYSTEM TO MODEL GENETIC AND DISEASE PROCESSES IN POPULATIONS WITH DYNAMIC SPATIAL AND SOCIAL STRUCTURES.

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CRITTRZ is an open-source population simulation library developed by the author to model varied processes in socially and spatially subdivided mammalian populations. In models built with this system, life histories of individuals are simulated over a series of discrete time periods. CRITTRZ is written in the Python computer language and includes an interface to the Idrisi geographic information system. The home page for CRITTRZ is www.greencreekparadigms.com/CRITTRZ.htm.

CRITTRZ has been used to model populations subdivided into local multi-male social groups resembling those seen in savanna baboons, rhesus monkeys and some other Cercopithecine monkey species. In these populations, males emigrate from their natal groups at adulthood. Short term mating relations exist between adult males and females in a group. Females remain in their groups of birth, with matrilineal relations structuring much behavior. Groups may fission (largely on matrilineal lines) and fuse. Groups occupy home ranges that may change with time. This family of CRITTRZ models based on these populations is known as the 'cercomm' type.

Previous studies with cercomm models examined microevolutionary genetics of populations subdivided solely by social groupings. Olivier (2004) showed that F_{st} differentiation levels among groups declined with increasing group sizes. In addition, with fixed age-specific birth and survival rates, F_{st} levels were highest in growing populations, lowest in declining populations and intermediate in approximately stable populations. Olivier (2005) examined genetic lineal effects during simulated group fissions.

Olivier(2007) described implementation of and simulations with cercomm models that use the Idrisi GIS interface. These models include dynamic home ranges for social groups, density dependent reproduction and survival and population distributions affected by landscape resource distributions. In these models, migration between groups may be structured by Euclidean distances or distances evaluated over heterogeneous movement cost surfaces. The present report presents some applications of GIS-enabled cercomm models to simulation of gene frequency dynamics and infectious disease transmission.

In CRITTRZ simulations group or subpopulation internal structures are represented by hierarchical data structures. These are interchangeably represented by graphs, syntactically structured character strings or indented text blocks, depending on the phase of modeling. Figure 1 presents the indented block representation of one social group from a cercomm simulation. 'G' is a group label. 'H' labels the group adult male segment. 'N' identifies the natal segment. 'A' is the label for individuals.

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G, 16
H, 16
A, 2341 A, 2228 A, 2202 A, 2555
A, 2440 A, 2494
N, 16
A, 2551 A, 2177 A, 2553 A, 2556
A, 2362 A, 2361 A, 2787 A, 2786
A, 2790 A, 2789 A, 2788 A, 2184
A, 2791 A, 2183 A, 2792 A, 2367
A, 2793 A, 2186 A, 2794 A, 2796
A, 2795
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Figure 1. Group structure.

Each social group occupies a home range represented by a raster file. Figure 2 presents the raster image of the home range of one simulated cercomm social group. Shapes of home ranges may evolve over time, particularly in response to spatial variations in resource availabilities. Home ranges divide or combine during group fissions and fusions. Home ranges of groups may overlap.



Figure 2. Group home range.

Population densities vary with space and time. Figure 3 is a raster illustrating population density in a simulated cercomm population that potentially exists throughout a rectangular habitat. Figure 4 illustrates density in a simulated population whose home ranges are restricted by resource availability to a Y-shaped area. The population in Figure 3 might represent a generalized, semi-terrestrial monkey species. The population in Figure 4 might represent a species restricted to riparian areas.

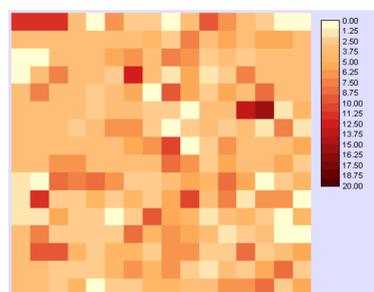


Figure 3. Population density.

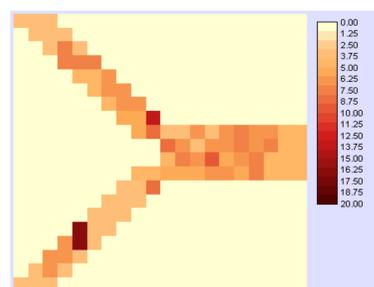


Figure 4. Population density.

Gene frequencies in subdivided populations vary stochastically over space and time. In cercomm populations, reproduction, survival, migration and group fissions and fusions all contribute to chance variations in gene distributions.

Figure 5 presents a surface of frequencies in a simulated cercomm population occupying a rectangular habitat. Frequency values in raster cells ranged from 0.25 to 0.69, with an among social group F_{st} value of 0.068.

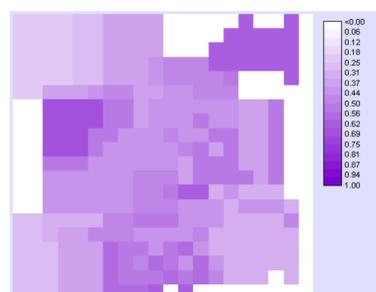


Figure 5. Allele frequency surface.

Figure 6 presents a surface of frequencies of an allele in a simulated population occupying a Y-shaped, possibly riparian habitat. Cell allele frequencies range from 0.47 to 0.78. F_{st} for the allele among social groups is 0.035.

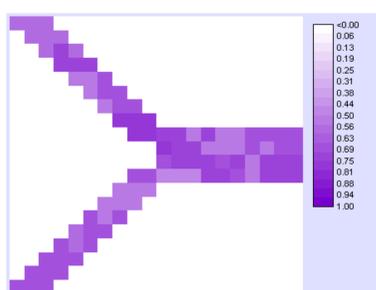


Figure 6. Allele frequency surface.

CRITTRZ supports modeling of infectious disease transmission and multi-species modeling. In the model presented next, one cercomm population with an established infection occupies a Y-shaped habitat. Figure 7 shows the spatial distribution of infected individuals. A second population at the same time occupies a rectangular area that overlaps the Y-shaped habitat of the first. At this time, no members of the second population are infected (Figure 8). Two time periods later, the infection is more widely established in the first population (Figure 9). In addition, it has jumped from the first to the second population, where it now is spreading (Figure 10).

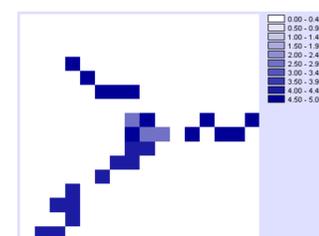


Figure 7. Infections.



Figure 8. Infections.

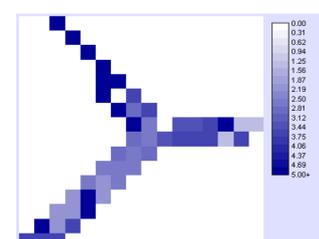


Figure 9. Infections.



Figure 10. Infections.

CRITTRZ is capable of modeling a host of processes of interest to conservation biologists. These include growth, spread and regulation of populations, the evolution of gene distributions in populations, and disease transmission within and between populations. The cercomm family of models allows exploring these processes in populations with dynamic social and spatial structures.

REFERENCES:

Olivier, T.J. 2004. "Interactions between Social, Genetic and Demographic Processes in Simulated Monkey Populations." Poster presentation at the Society for Conservation Biology Meetings, 29 July – 2 August, 2004, New York, NY. . Link to PDF file at www.greencreekparadigms.com/CRITTRZ.htm

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Olivier, T.J. 2007. "Use of a Geographic Information System to Represent Landscape and Population States During Population Simulations." Oral presentation at the Virginia GIS Conference, Virginia Beach, VA, 25 September, 2007. Link to PDF file at www.greencreekparadigms.com/CRITTRZ.htm.

The CRITTRZ home page is www.greencreekparadigms.com/CRITTRZ.htm.

At the home page you can download CRITTRZ code and documentation, as well as previous research reports.

The next public release of CRITTRZ, Version 0.85, will be released later this summer.