Use of a Geographic Information System to Represent Landscape and Population States During Population Simulations.

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Slide 1.

ABSTRACT

This report describes the use of a geographic information system for dynamic, run-time representation of landscape and population states in computer simulations of animal populations. Simulations are built with CRITTRZ, an open-source simulation library written in Python, an object-oriented scripting language. CRITTRZ includes an interface to the Idrisi geographic information system. This interface permits use of Idrisi-format rasters to represent spatially structured data and calls to Idrisi functions. CRITTRZ includes a Python module that permits direct reading, writing and content manipulation of Idrisi raster files, so that simulations can manipulate rasters in ways not provided by Idrisi functions. Examples of simulations of demographic, genetic and disease processes in spatially and socially subdivided populations are presented. In these models, rasters store information on resource distributions, changing population densities, movement costs and subpopulation locations.   Applicability of models to conservation biology, wildlife disease studies and basic biological research are discussed.

INTRODUCTION

Mammalian populations may be organized by age, sex, kinship links and social groupings and subdivided by geographic space. These structural features can lead to complex interplays between demographic, population genetic, disease transmission and social behavioral processes. The interplay of these processes and population organization is of interest to biologists engaged in both basic and applied research. Computer simulations can model complex population processes. However, simulations developed to model particular complex processes in one population may have little use in modeling another.

GOALS

My goal in developing the simulation system I will report on today, CRITTRZ, has been to create a software library that will provide a generalized foundation for construction of simulations of mammalian populations variously structured by age, sex, kinship links, social groupings and geographic space.

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IMPLEMENTATION

Here are some main points regarding CRITTRZ implementation.

CRITTRZ Implementation

Written in Python, object-oriented scripting language.

Objects represent simulations, populations, subpopulations, collections of individual data, biological events.

Basic distribution runs under Windows, Linux operating systems

Windows version with interface to IDRISI GIS for run time representation of landscape states.

CRITTRZ Python module allows reading, modification, writing of Idrisi rasters layers independent of GIS.
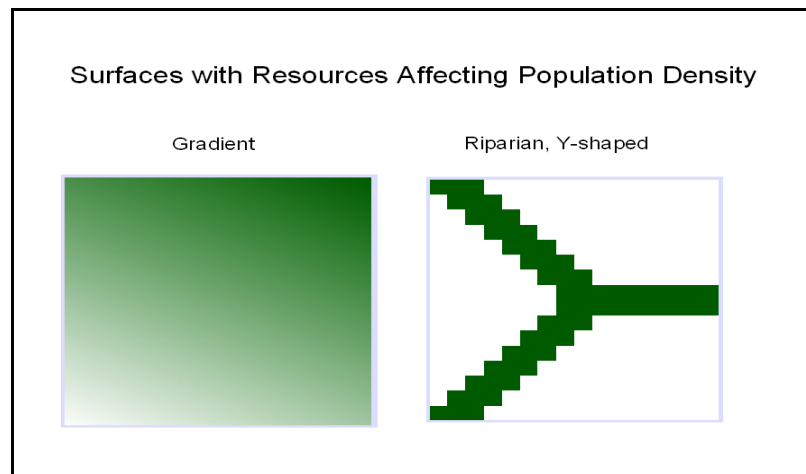
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In an object-oriented language such as Python, programs usually define classes of objects that combine data and functions (or methods). An object could represent, for example, a population. A modeler can easily create multiple instances of objects, simplifying, for example, simulations with multiple species populations. New classes with different data or methods can be derived from more basic classes. Derivation permits well-defined enhancements or specializations of model classes. CRITTRZ contains dozens of different Python modules that are combined to build simulations. Population framework objects maintain widely used population data (e.g., individual data fields, kinship links). Biological event modeling objects are attached to population frameworks to create population model objects.

The base version of CRITTRZ runs under both Windows and Linux operating systems. The base version does not include a GIS interface. A spatially-enabled version uses the Idrisi GIS (Clark Labs, 2006) and runs only under the Windows operating system. Idrisi is oriented toward raster representations of geographic data. The Idrisi raster format is simple. The GIS includes many analytical tools of use useful to conservation biologists.

Python programs can call Idrisi functions via Microsoft's COM interface. Idrisi functions accessible via the COM interface often provide high-level operations, similar to those users could access via menu selections.   A CRITTRZ module supports reading, writing and modification of Idrisi rasters in Python code, without use of GIS calls. This permits fine-grained manipulation of raster data not accomplished readily by calls to Idrisi functions.

CRITTRZ USE OF RASTER LAYERS

The following examples illustrate use of raster layers by the GIS-enabled version of CRITTRZ to represent landscape and population states.

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The numbers of population members present and resources available (such as food) can influence the rates at which some population events occur. The image on the left of slide four illustrates a surface with resources used by a model population. This modeled population potentially exists throughout the raster area. A gradient in resources available locally increases from lower left to upper right of the raster. A darker hue indicates more resources in the underlying pixel. In contrast, the image on the right of the slide illustrates a Y-shaped, possibly riparian, area occupied by another modeled population. Resource levels within the utilized area are constant. In this second image, occupied areas form a network. In a simulation of two populations occupying the same landscape, the area in the raster on the right might overlay the area on the left. For models of real populations, resource layers might be based on vegetation or land cover layers for areas occupied by the actual populations.

The cost of movement over a landscape can vary with place and species. So, the effective distances between subpopulations may vary considerably from the Euclidean distances separating them. Effective distances can influence patterns of movement of animals between subpopulations. Idrisi functions can help estimate effective distances between subpopulations by estimating costs of movements on surfaces where movement costs vary with locations.
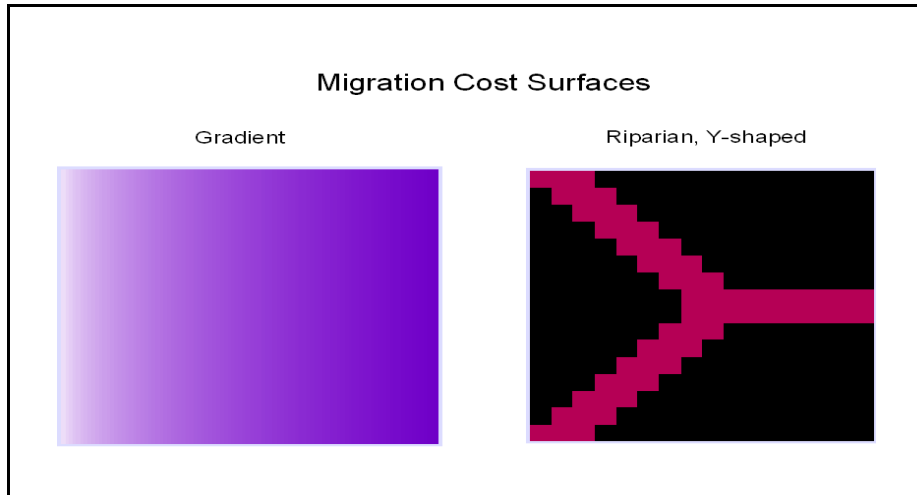
Slide 5.

The raster on the left represents a rectangular area of occupation, where movement costs increase from left to right (darker is costlier).   Such a cost surface might exist for terrestrial species living in an area that was flat and easily traversed on the left that gradually changed to rough, difficult-to-traverse topography on the right. Populations in the two left-hand corners are effectively closer than the two on the right corners. The raster on the right again portrays a Y-shaped, perhaps riparian, occupied area. Here the cost of movement within the movement network is homogeneous. Black areas represent impenetrable barriers to movement for the associated population.

In Idrisi-using CRITTRZ models, each subpopulation occupies a location raster.
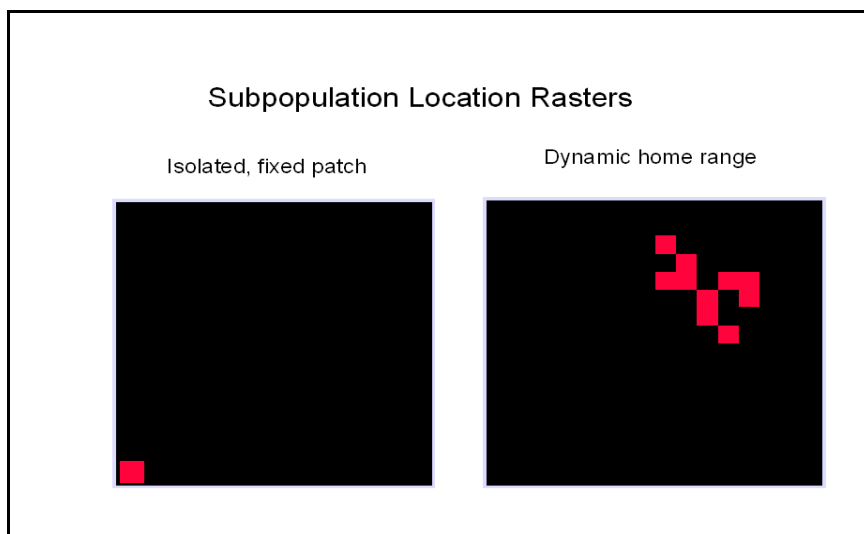
Slide 6.

In slide six, the left raster displays the location of a subpopulation in the lower left corner (an orange rectangle). This raster will represent the location of an isolated patch subpopulation in a later simple, idealized model. The raster on the right represents the home range (also shown in orange) of a monkey group in a more complex later model. The home ranges in the monkey model can change shape and location over time.   In CRITTRZ, these home ranges tend toward areas with favorable resource/demand ratios. Also, in this monkey model, home ranges may overlap.

Division of the number of individuals in a subpopulation by the number of pixels in its home range produces a per-pixel measure of demand for resources by that subpopulation. A population demand layer can be created by adding for each pixel in the population demand raster the demand values from each subpopulation that includes that pixel in its home range. The resource and demand raster layers are used in modeling density-dependent processes.
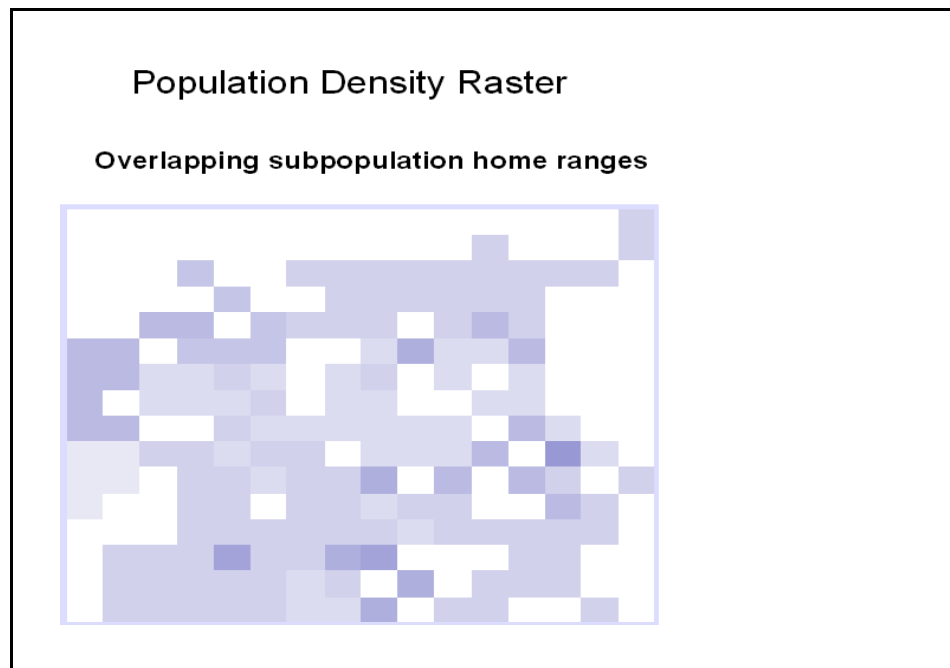
Slide 7.

In this slide, the darkness of each pixel increases with the demand placed upon it by members of one or more subpopulations. As you can see, demand levels vary, with a white, unoccupied area present next to most of the top margin. One of the simulations I will discuss later produced the raster in this slide.

SIMULATION EXAMPLES

CRITTRZ supports construction of simple and more complex population models. I will begin with a simple, idealized model (agesex) and follow this with more complex (cercomm) examples.

Agesex Model

Simple CRITTRZ population model.

Individuals vary by age, sex.

Live in subpopulations in fixed patches.

Migration between subpopulations using cost surfaces.

Density dependent survival, birth rates.

Developed as simple example application, testing tool.

Might be suited for modeling of simply organized populations.

Slide 8.

I created the agesex model, described in slide eight, to provide an example application and a test platform. It might serve as a useful model of some real populations.

In this agesex application three subpopulations occupying rectangular locations are present. The areas of their location are identical. The starting sizes of subpopulations are almost the same. The subpopulations are distributed along a diagonal beginning in the lower left of the area modeled to the upper right. The location raster for the subpopulation in the lower left of the raster was presented earlier in slide six. Resources affecting population growth varied along a diagonal, matching the diagonal distribution of subpopulations. The resource raster was presented previously in slide four.
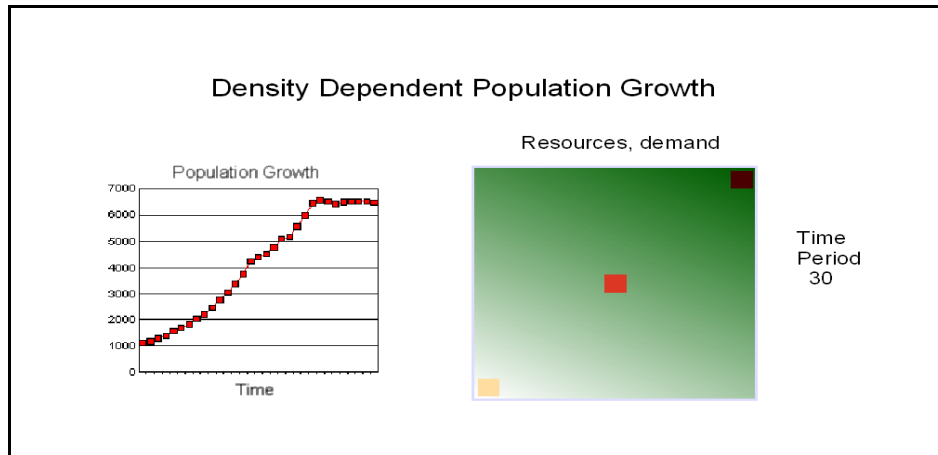
Slide 9.

The simulation was run for thirty time periods. The image on the left of slide nine represents the size of the population at the end of each period. Conspicuously, the size of the population rises rapidly for a while after the start of modeling and eventually levels off, possibly after a small overshoot. In the image on the right of this slide, one can see the three rasters representing subpopulation demand densities overlain on the resource raster. In the subpopulation location rasters, darker reddish-brown represents greater subpopulation demand. As you can see, at the end of the simulation, subpopulation demand densities increase consistently in direction with the gradient in population-sustaining resources.

I now want to present some examples of applications of the CRITTRZ cercomm model. Its assumptions resemble properties of some Old World monkey populations, such as rhesus monkeys and savanna baboons.
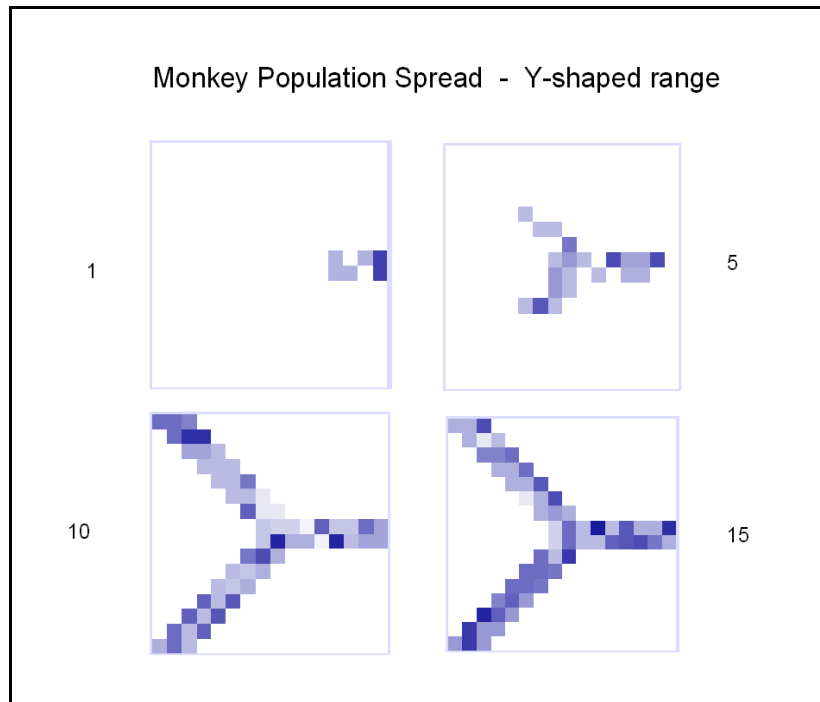

Slide 10.

Groups (subpopulations) in the cercomm model occupy home ranges that change over time. The cercomm model shares some code with the agesex model. Modules to model group fissions and fusions have been added. These events do not occur in agesex models. Group fissions occur partly along matrilines. Growing populations should undergo frequent fissions, with group home ranges expanding into unoccupied areas with unutilized resources.
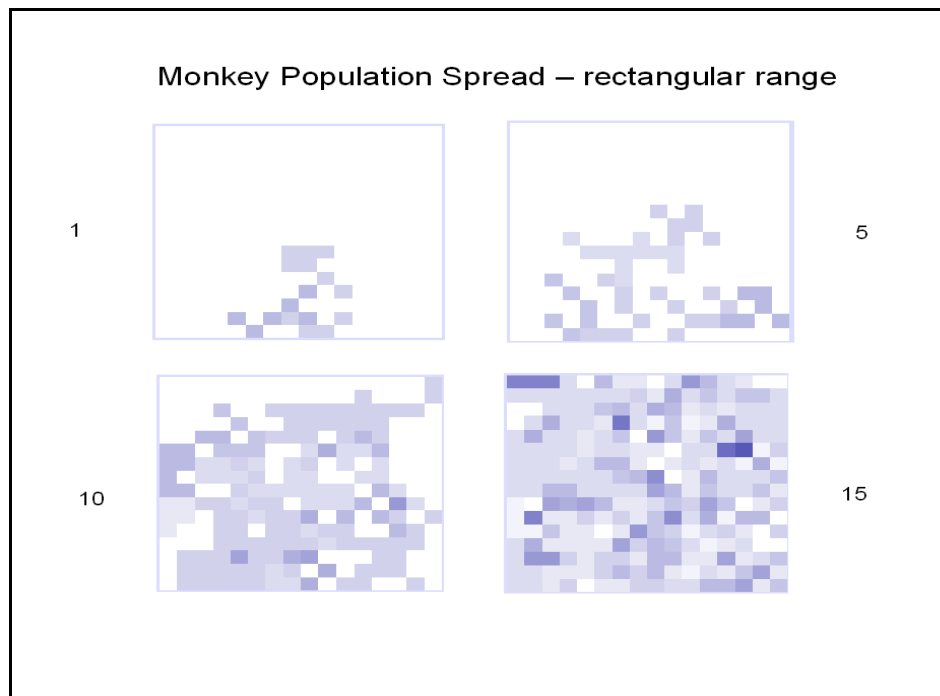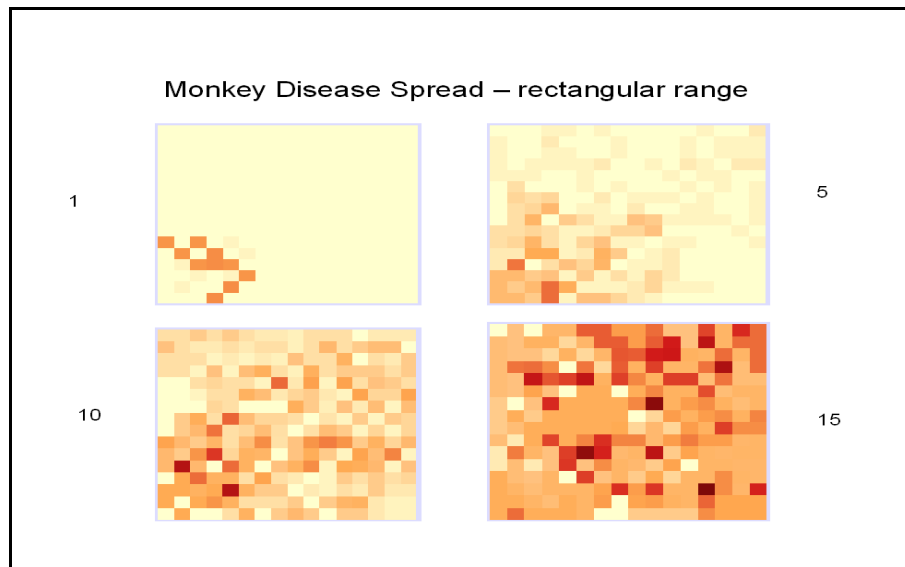

Slide 11

In this simulation, two cercomm groups are present at the start of modeling. They are in the bottom center of a landscape that might become fully occupied by groups of this species. Slide eleven presents population density rasters generated at various times in the simulation. As shown, the population expands steadily over time, growing in size and roughly filling the landscape.
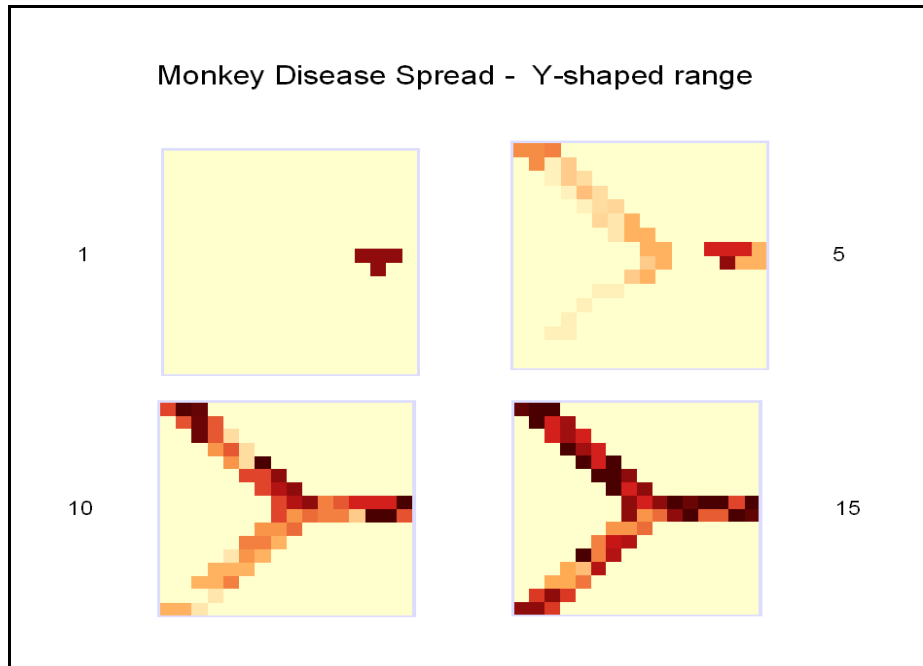
Slide 12.

Here we have a cercomm population restricted to occupancy of the Y-shaped range, discussed previously. At the start of simulations, two groups are present at the base of the Y, in the center right area of the raster. Over time we see spread of the population throughout the Y-shaped range.

Next, I will present some illustrations of raster outputs from cercomm population simulations that include infectious disease transmission. In these simulations, parameters influencing disease propagation are set to foster rapid disease spread.

Slide 13.

The first of these simulations models disease spread in a cercomm population already distributed throughout a rectangular area. At the start of the simulation, infected individuals are found only in one group in the lower left corner.   The raster images in slide thirteen represent the number of infected individuals at different pixel locations at four different time periods. The method of calculation is similar to that described for population density calculations. As the number of infected individuals using a cell increases, the pixel color darkens. Visible in the slide, within fifteen simulated periods, the infection spreads from the lower left corner to all others and becomes more common.
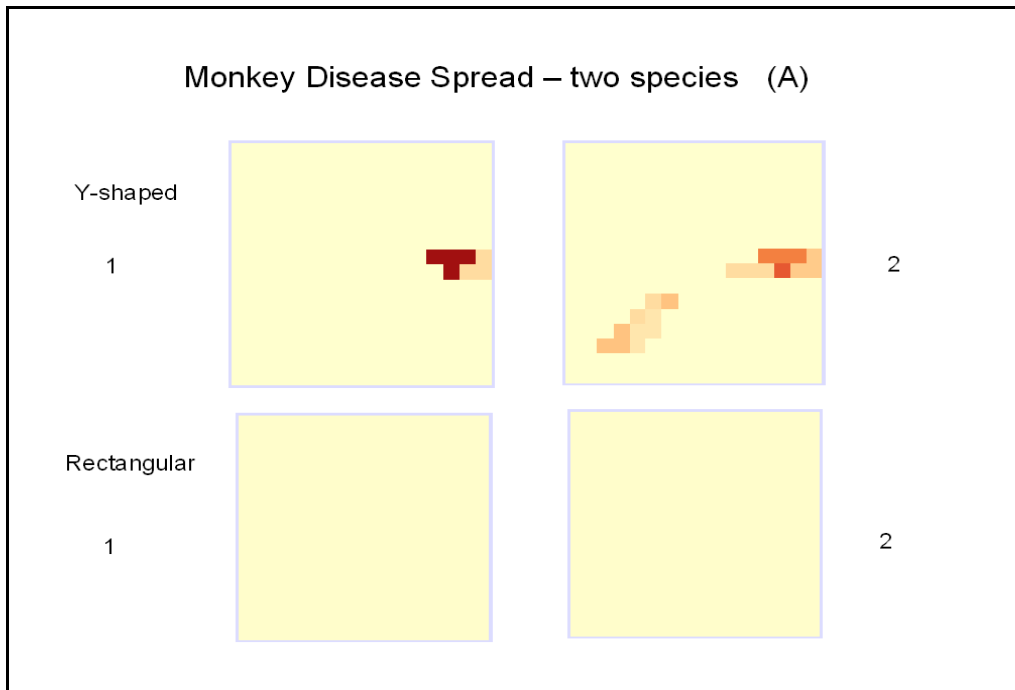
Slide 14.

Slide fourteen illustrates modeled spread of a disease in a cercomm population occupying a Y-shaped area. At the start of simulation, infected individuals are present in a single group located near the base of theY, at the center of the right edge of the raster. Again we see spread of the disease throughout the population within fifteen periods.

CRITTRZ simulations can include multiple population objects that represent different, possibly interacting, species. Model populations may be of the same type or different. Many conservation biologists are concerned about transmission of diseases between species populations living on the same landscape.

This next simulation models disease transmission in two cercomm monkey populations occupying the same landscape. One population occurs throughout the rectangular modeled area. The second occupies the Y-shaped area seen in earlier simulations. The second population spatially overlays the first. At the start of the simulation, both monkey populations have fully occupied their habitats. One group in the population restricted to the Y-shaped habitat, located at the base of the Y near the center of the right margin, contains infected individuals. No infected individuals are present in the second wider-ranging cercomm population. Parameters for the infectious disease module are set to permit easy transmission within populations but less easy transmission between the two populations.

Slide 15.

Slide fifteen shows disease distributions during the first two time periods of the simulation. In the raster from period one, infected individuals are found near the point of origin in the population occupying the Y-shaped habitat. No infected individuals are present in the second population. By period two, the infection spreads into one arm of the Y in the originally infected population. Still, the other population remains uninfected.
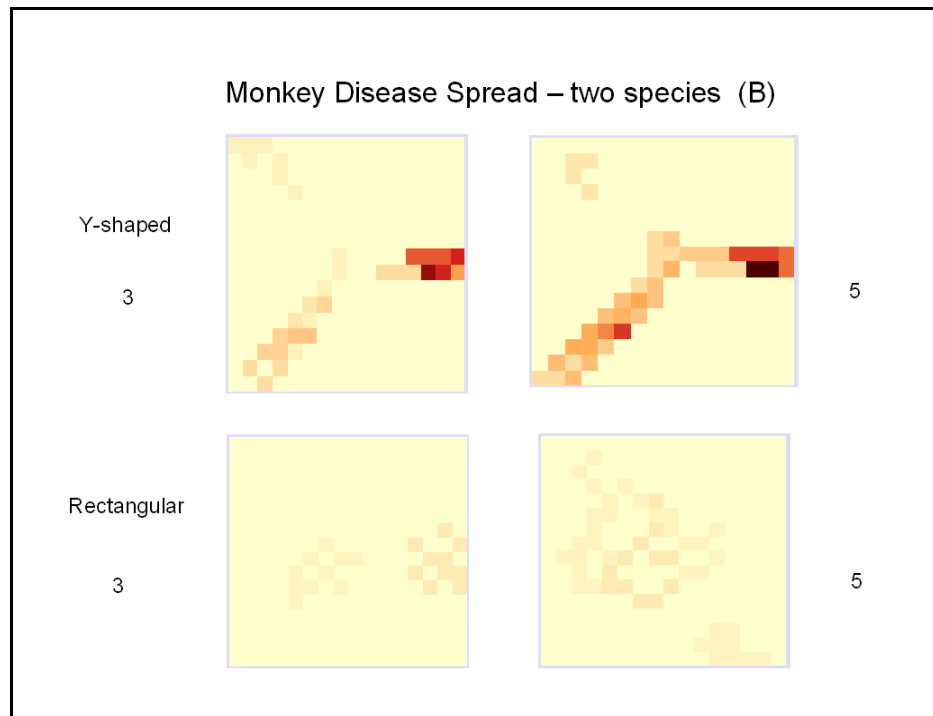
Slide 16.

In slide sixteen we see that by time period three the disease has spread more in the originally infected population and has jumped into what may be two groups in the second population. In period five, we see further spread of the infection in both populations.

CRITTRZ also supports modeling gene transmission in simulated populations. To date, most applications of CRITTRZ have examined population genetic processes in cercomm populations with social subdivisions but no explicit spatial structure. Slide seventten illustrates a result from a previous CRITTRZ analysis of cercomm population genetics (Olivier, 2004).
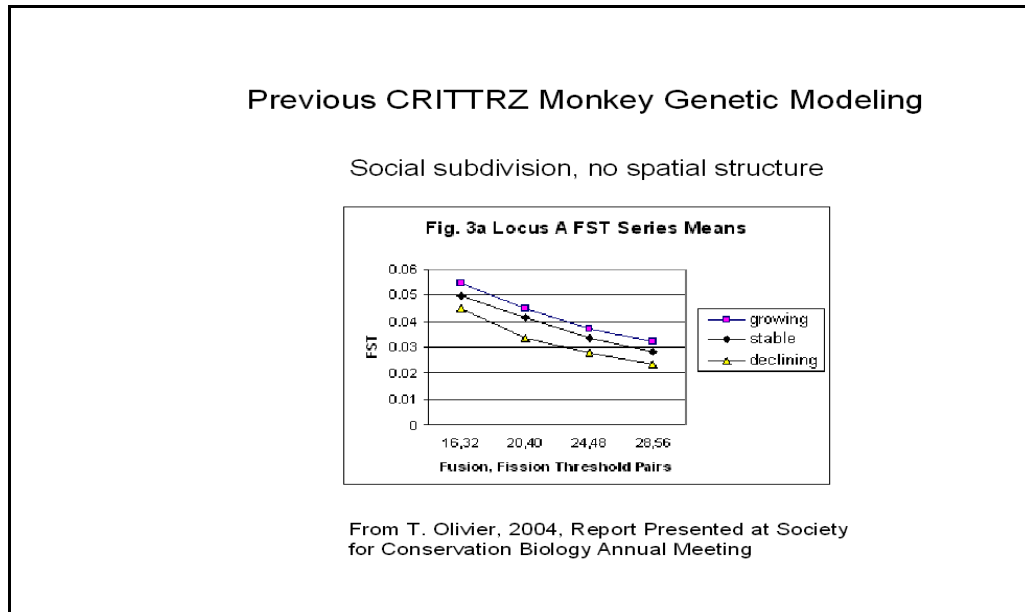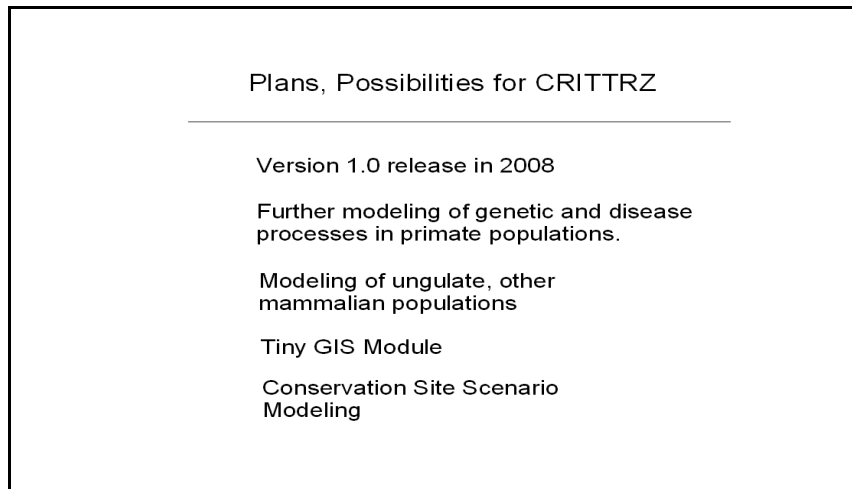

Slide 17

The vertical axis of the graph in this slide represents the FST measure of genetic differentiation between groups in various simulation series. As FST values increase, the mean degree of gene frequency differentiation between groups in the simulation series increases. The horizontal axis represents fission and fusion threshold value combinations used for four different simulation series. As these thresholds increase, the mean sizes of groups in the simulated populations increase.

This analysis showed that intergroup genetic differentiation levels decreased as group sizes increased. This study also systematically varied demograhic circumstances in which simulation series. In some series fixed birth and survival rates were set to produce populations that on average were 1) stable in size 2) growing 3) declining. The line plots in this slide show gene frequency differences in growing populations were highest, declining populations were lowest and stable populations were intermediate.

Mathematical population genetic models suggest that an isolation by distance effect should occur in spatially distributed populations. That is, genetic similarity of subpopulations should decline with increasing geographic separation. A cercomm model with gene transmission and GIS-based treatment of spatial structure in population and landscape states now exists. In coming months I plan to examine how spatial structure introduces new effects, possibly including isolation by distance, into cercomm population genetic processes. I also aim to examine how spatial structuring modifies characteristics of population genetic processes found in earlier cercomm simulations.
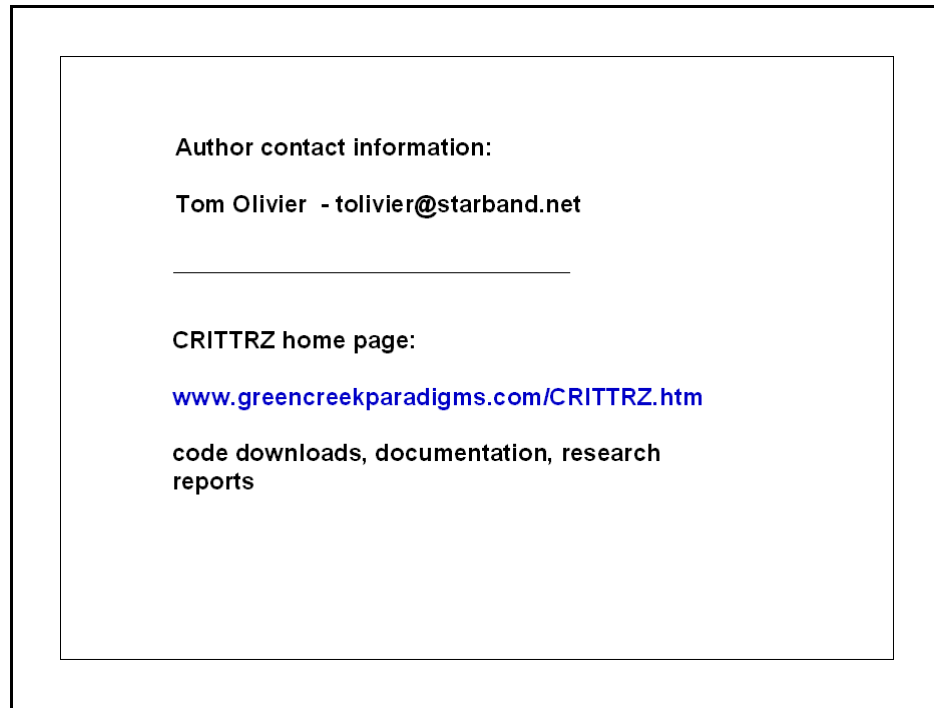
LOOKING AHEAD

I have a mix of firm plans and thoughts about possibilities for CRITTRZ in the future.

Plans, Possibilities for CRITTRZ

Version 1.0 release in 2008

Further modeling of genetic and disease processes in primate populations.

Modeling of ungulate, other mammalian populations

Tiny GIS Module

Conservation Site Scenario Modeling

Slide 18.

I aim to release version 1.0 of CRITTRZ in 2008. The library is released under an open source license and is freely available. So far I have publicly released seven test versions. More integration testing and better documentation are needed to reach the version 1.0 milestone. In coming months I will be modeling disease transmission and genetic dynamics in spatially-structured cercomm simulations. I would like to see CRITTRZ applied to modeling taxa other than primates. Ungulates display many forms of population organization. Conservationists are concerned about disease transmission between domestic and wild ungulates. So, modeling ungulates with CRITTRZ seems an interesting possibility. Another possibility is eventual addition to CRITTRZ of a tiny GIS module that could provide all the GIS raster processing required during simulations. That would allow spatially-enabled versions to run under both Linux and Windows. The most challenging element in construction of such a tiny GIS might be implementation of cost surface analysis tools used to assess distances between subpopulations during migration modeling. Finally, CRITTRZ might be used to model scenarios at conservation sites for primates or other mammalian taxa.

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CRITTRZ home page:

www.greencreekparadigms.com/CRITTRZ.htm

code downloads, documentation, research reports

Slide 19.

Slide ninteen presents my email address, should you wish to contact me. At the CRITTRZ home page you can download CRITTRZ code, documentation and research reports based on CRITTRZ.

REFERENCES

Clark Labs. 2006. Idrisi Ver. 15.0 Andes. Worcester

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

ACKNOWLEDGEMENT

I thank my wife, Wren, for encouraging me to develop CRITTRZ.