Introduction to the Mini-track on Population Modeling

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Where population and evolutionary biology are called upon to help manage biological diversity and other natural resources, it must usually respond with models that are more realistic and precise than is the case for more purely scientific questions. Such precise and realistic models are usually computer simulations. This conference track has emphasized such models and in this summary we review some of the issues raised by these models.

1 Biological Issues

The models presented in this track are simulations of populations of individual organisms. This is a common research activity where an account of the behavior of individuals is developed in relation to their environment and other individuals. Such behavior may be cast in what may be called *ecological behavioral* categories such as eating or moving. Less commonly the model of behavior may be more *ethological* and consist of categories such as threat display or simple descriptions such as "double head bob."

A central challenge is to understand the relationship between these two approaches to the categorization of behavior. An animal may want to eat a particular food item, but may be prevented by the dominance behavior of another individual. An ecological accounting which might be based on caloric content of food does not easily accommodate this situation. On the other hand, modeling ethological behavior is much less clear and vastly more complicated.

Another challenge is related to grid generation in the representation of the environment. Square grids are common and easy to generate, but they lead to problems when the model must account for interactions along diagonals. Interactions between cells on the diagonals require weighting by arbitrary amounts which cannot be answered by appeal to the biology. A hexagonal grid system which is spatially isotropic has equally weighted interactions in each direction and may prove to be a more accurate mesh.

2 Computer Issues

The main challenges in the implementation of the models on computers are related to scalability. The models presented here have the potential for becoming much larger and much more complicated. What are the performance limitations in scaling up these models, either in size (to model larger populations or larger spatial areas) or complexity (e.g. adding new species to the models, or adding more complexity to the model of each individual)? Are the models parallelizable, and if so, do the parallel approaches scale well with the number of processors? "Time warp" and other technologies developed for distributed discrete event simulation will surely play a role here.

Another set of challenges is in the programming environments provided to modelers. What sorts of tools can computer science research provide to biologists to allow them to develop and evaluate computational models? C++ and other object-oriented languages are very good candidates for implementing simulations, but to date they do not run well on traditional vector-oriented supercomputers and are still in their infancy on newer shared-memory multiprocessors. A very useful tool would be a system that would allow developers to code in C++ on a workstation and then generate code automatically for a wide variety of supercomputers.

3 Papers in this Session

The two papers published in this volume, and other research presented in the mini-track, touch upon several of the issues presented above.

In "Parallel Discrete Event Simulation of Lyme Disease," Ewa Deelman, Thomas Caraco, and Boleslaw Szymanski discuss problems with distributed simulation of organisms that are responsible for the spread of Lyme disease. In their approach, a region to be simulated is divided into discrete subregions and distributed to different processors of an IBM SP-2. The paper describes techniques used to synchronize the events on separate processors, e.g. how to handle the situation when a mouse migrates from the region simulated by processor A to the region simulated by processor B, yet B has moved ahead in time by several generations.

"An Object-Oriented Migration Model Driven by Biological Field Data" by Keith Downing examines the benefits of object-oriented programming techniques in population modeling. The use of multiple inheritance allows the definition of a class hierarchy that greatly simplifies the generation of code for modeling actions, such as migration, that generalize across species.