



Using the Tools of the Species Conservation Toolkit Initiative

Participants

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Background

The Species Conservation Toolkit Initiative (SCTI) is a partnership to ensure that the new innovations and tools needed for species risk assessment, evaluating conservation actions, and managing populations are developed, globally available, and *used effectively*. The tools in the toolkit include Vortex (extinction risk assessment) and Vortex Adaptive Manager (model dynamic management strategies), Outbreak (stochastic simulation of disease dynamics), Spatial (modeling animal movements on landscapes), PMx (genetic/demographic management of pedigreed populations), MetaModel Manager (linking multiple models for simulation of interacting systems) and more. It is not always apparent how to use the many features of the various software packages, which can be quite complex. In this working group, we provided a short training session on focused components of a few of these tools. The specific tool(s) to be the focus of the training session were identified by a survey of the meeting participants prior to the meeting.

Working Group Objectives

1. Provide a description of the uses and methods for using the Vortex PVA software to model genetic management of captive or wild populations.
2. Provide a description of the uses and methods for using the MetaModel Manager software to model multi-species PVAs, in which the species interact or are inter-dependent.
3. During #1 and #2, above, elicit suggestions for further applications and features that would be valuable in our species conservation toolkit.
4. Discuss what kinds of training approaches would be most helpful to users of SCTI software.

Summary of Working Group process and discussions

(Suggestions made for enhancements to SCTI tools and their uses are italicized below.)

Vortex

Kathy Traylor-Holzer presented training focusing on modeling genetic management using Vortex. Participants shared why they wanted to use Vortex to model genetic management (or potential applications), and these included:

- Modeling integration of captive and wild population management to support One Plan Approach to conservation
- Testing different management strategies for breeding or exploring lifetime reproductive planning, especially for species like big cats where their biology requires careful planning to protect fertility and reproductive health of the females
- To model insurance populations or translocated populations in conjunction with populations that have studbook data

Kathy described the two systems Vortex uses to model genetic information: a gene drop simulation of genetic diversity and a kinship matrix. The gene drop simulation assigns two unique alleles to each founder of the population and is used in the model to calculate population heterozygosity, mean inbreeding, kinships among populations, and for modeling lethal recessive alleles, whereas the kinship matrix depends on the user specifying an initial matrix of relationships between animals that is used in the model to calculate individual inbreeding coefficients, kinships among individuals, and general inbreeding depression. It is important for users to know which aspects of the model are affected by each system for modeling genetics, because various special options in the genetic management parts of Vortex can change which calculations use the user-specified kinship matrix vs. the gene drop simulation. Users should carefully decide what is appropriate for their situation and then determine what options to use to create their model. A suggestion was made that *it would be useful for Vortex to include a pop-up box informing users of the genetic model implications of selecting the various check boxes.*

Kathy provided an example from Eastern Barred Bandicoots for how to specify initial allele frequencies that Vortex would use to model population-level gene diversity and inbreeding. A question was raised on whether Vortex models linked loci; currently all loci in Vortex are considered to be unlinked and independent, but *it might be useful in the future to add an option for linked loci.*

There was some discussion on what approach should be used for wild populations where you don't have kinship data; suggestions were made to use the information available to parameterize the model for the simulation to be as close as possible to the real situation.

A studbook file can be used to specify the initial population in Vortex (or can be added to an initial population created by Vortex). There was discussion about how to get this studbook file from PMx, by creating a PMx project, changing the extension from '.pmxproj' to '.zip', and then using the lineage.txt file from that zipped directory. When importing a studbook, it's important to include all animals, not just the living animals, because that information is used to determine the ancestry of the current population. Within the studbook discussion, there was also some conversation about dealing with groups or multiple possible parents ("Mults"). Vortex does not handle Mults the same way as PMx does, so

studbooks with Mults will need to be manually edited so that each different Mult is included as a unique 'individual' for the input file for Vortex. Exchange files from SPARKS won't work with Vortex because of the Mult issue. A question was raised about species that are hermaphrodites or other special cases (e.g. partula snails); Vortex should be able to handle these cases.

If users include a studbook file, or a kinship file, or an allele frequency file (or any other extra file) in their Vortex model, they'll need to make sure they include those files with the Vortex project file any time they share or save the project.

There was a question on how to model dead animals whose gametes have been preserved in a gamete resource bank (GRB). Discussion ensued on how to do this in Vortex without having the GRB 'animals' treated as individuals in the model. There wasn't time to fully explore this in the working group, but it would probably need to be done with a modifier model using MetaModel Manager.

After discussing how Vortex uses and models genetic data, Kathy talked about specific model considerations when modeling genetic management strategies. There are Special Options in the Project Settings tab and other options throughout the project specifications tabs that are useful for genetic management. 'Breed to maintain K' is the scariest checkbox because if it's not checked and your modeled population ends up above carrying capacity, Vortex will randomly cull animals, effectively nullifying your genetic management strategy! It could be useful to include functions in genetic management options in Vortex to help the model be more realistic- it assumes all recommended pairings occur 100% of the time and are successful, but there are ways you can adjust the model to bring it closer to reality.

The Zoological Information Management System (ZIMS), a global animal information system governed by Species360 to cover records for husbandry, medical, and population management processes for over 1015 Species360-member zoos worldwide, will contain information on demographic rates, pairing success, and other population management parameters. It *could be useful to have integration of some Vortex routines in ZIMS* to help managers easily see that they might need to take some management actions (i.e., respond to predictions in the model). This could also help guide managers to see that they might need to use more thorough modeling processes in a given situation to avoid a predicted problem with their population. There was discussion about how it would be *useful to incorporate some Vortex mini-modeling into day-to-day ZIMS* so it would be automatically available to managers and help flag areas needing more attention.

A general closing comment to the Vortex section was that it's tricky and complex, and you should not do it alone! *Get help to make sure your model is doing what you expect.*

MetaModel Manager

Bob Lacy gave a demonstration on how to use MetaModel Manager to interactively and simultaneously run multiple models (of species, or landscapes, or epidemiological, or climate... really anything). There was discussion in the group about how PVA models traditionally consider other species to be more or less static, but that we'd like to move towards modeling ecosystems as a whole. Bob used an example

model of a big cat predator and its deer prey to demonstrate how results were dramatically different when the species were modeled separately vs. together using a metamodel process.

When looking at the results of a metamodel, Bob mentioned that it's useful to run the first few iterations one at a time, so you can look at the paired/grouped results for the species that you're modeling together. This helps you understand how they are interacting and what might be driving the trends in each system. At the end of all your iterations, what you see in MetaModel Manager is all the results from all species for all the runs, in effect letting you see the average for each species. However, in some cases, there are patterns in the data so in reality there might be a few paired patterns that are the dominant scenarios. The presence of multiple dominant patterns can be obscured when viewing all the results at once. *A suggestion was made to have the program automatically detect patterns for you.* There are classical predator-prey models that exist to describe common equilibrium patterns and these are helpful in interpreting the MetaModel Manager output. However, the group felt that it was important to look at the results to see if systems being modeled actually fell into patterns that are already known. When displaying the results of a metamodel for more than one species, you should plot population density so the population numbers will be on a comparable scale.

There was a suggestion about MetaModel Manager to *include the ability to model animal locations on X, Y, and Z axes.* Is it possible to model plants in Vortex and MMM? It is possible to model plants if they have similar life history to animals, with relatively low fecundity, etc. Otherwise, you can find and link a plant model using MMM. *A suggestion was made to create and make available a database of models that have been/could be used with MMM.* Currently there are several databases that include information about life tables and vital rates that could be used to help parameterize models.

Action Steps:

1. Further discussion on training possibilities for SCTI tools will be done by email and include the types of training people would like to have or feel would be useful. (To be done within a month.)
2. The results from the email discussion will be used to help guide the work of a new Coordinator of Training who will have the task of developing an overall training strategy and program for SCTI. (Coordinator to be hired as soon as the ideal candidate is identified, but most likely not until January 2017.)
3. SCTI will provide examples on how to link non-SCTI models using MMM and will work to compile a list of models that people have used with MMM. (To be worked on throughout the year.)
4. Each enhancement of the tools that was suggested in the working group will be added to the "wish-list" to be considered as resources allow.