Int. Zoo Yb. (2007) **41:** 38–51
DOI:10.1111/j.1748-1090.2007.00016.x

Tools and techniques for disease risk assessment in threatened wildlife conservation programmes

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Disease plays a significant role as a risk factor in wildlife conservation programmes involving animal movements, such as translocation, transportation among zoos or reintroduction. However, the traditional 'zero-risk tolerance' approach to the assessment of disease risk in these programmes is unattainable and unmanageable, often leading to an excessively cautious attitude towards the risks that are involved. It is therefore critically important to develop a comprehensive, unified and broadly applicable set of descriptive and analytical tools that can more realistically and accurately assess disease-based risks in conservation-based animal-movement programmes. The Conservation Breeding Specialist Group, of the IUCN – World Conservation Union, has brought together an international team of wildlife medicine professionals to construct a set of qualitative and quantitative tools to assess disease risk. The tools are flexible, intuitive and span a broad range of complexities. These tools are designed to enable professionals to incorporate not only published, statistically valid data but also to make reasonable decisions under conditions of uncertainty, and to capture valuable information from more basic field or clinical experience. Selected tools from the larger 'toolkit' are described here, with examples from actual case studies where available.

Key-words: decision analysis; disease; epidemiology; hazard identification; model; probability; risk assessment.

INTRODUCTION

Serious attempts to address disease risk and the role that such processes can play in the management of threatened wildlife populations date back to the mid-1980s (e.g. Dobson & May, 1986; May, 1988) and has since led to the recent publication of detailed studies of the subject from a broad diversity of perspectives (e.g. Daszak *et al*., 2000; Aguirre *et al*., 2002; Hudson *et al*., 2002; Collinge & Ray, 2006; Travis *et al.*, 2006). Through the emergence of conservation medicine as an important field of study in biodiversity management, we have come to appreciate that disease is often a significant risk factor in conservation programmes involving animal-movement protocols, such as translocation, transportation among zoos or reintroduction. Despite our ability to **recognize** these risks, however, professionals in the zoo and wildlife medicine community have historically been hard-pressed to find and apply appropriate tools that can effectively **analyse** these risks and use the resultant information to develop more sound programmes. With the absence of such tools, conservation medicine professionals would often adopt a 'zero-risk tolerance' approach to animal-movement recommendations. Using this approach, any perceptible risk of disease introduction or transmission is seen as excessive in the context of maintaining the health of managed individuals, and is therefore unrealistically strict as it fails to recognize that virtually any management action inherently involves risk.

Unfortunately, the 'zero-risk tolerance' philosophy has proved itself to be effectively unattainable for nearly all animal-movement protocols in wildlife-conservation programmes. Moreover, such an approach is not compatible with the current realities of disease management in an increasingly disturbed global ecosystem. It is therefore critically important to develop a comprehensive, unified and broadly applicable set of descriptive and analytical tools that can more

realistically and accurately assess disease-based risks in conservation-based animal-movement programmes.

In recognition of this need, staff, members and associates of the Conservation Breeding Specialist Group (CBSG), of the IUCN – World Conservation Union's Species Survival Commission, set out to engage zoo and wildlife conservation medicine professionals, as well as experts from academia, to establish the state of the science and to create the required tools for practical use. This article provides an overview of these tools, and gives the general philosophical framework for decision analysis within which the tools were created and refined.

A CHRONOLOGY OF TOOL DEVELOPMENT

CBSG's involvement in this effort began in 1991 as the convener of a working group meeting entitled 'Disease and Captive Conservation of Threatened Species' in Washington, DC, in collaboration with the American Association of Zoological Parks and Aquaria (now the Association of Zoos and Aquariums) and the American Association of Zoo Veterinarians. This gathering of 12 professionals represented one of the earliest attempts explicitly to address disease risk in integrated conservation programmes, and emphasized the immediate need for data assembly and distribution as a productive collaboration between the zoo and wildlife veterinary communities. The group also called for the organization of an international symposium on the topic as a means to extend this fledgling network.

The resulting International Conference on Implications of Infectious Disease for Captive Propagation and Reintroduction of Threatened Species was held in late 1992 in Oakland, CA, with more than 140 participants from 19 countries. Working groups provided expert insight and practical recommendations on monitoring, investigation and surveillance of disease in captive and free-ranging wildlife; infectious disease considerations in reintroduction programmes for captive wildlife; risk assessment and population dynamics; and diagnostic technology (Wolff & Seal, 1993). A major recommendation from the conference centred on the need to develop a set of quantitative risk assessment tools to assist in the decision-making process regarding the conservation value of animal movement programmes. To help accomplish this goal, participants also set forth a model for standardizing the collection of relevant information across a range of conservation disciplines. The full range of information collected and presented at the conference was published in a special issue of the *Journal of Zoo and Wildlife Medicine* in 1993.

Following on the success of these initial endeavors and further amplification of the professional network, CBSG organized and conducted additional meetings in 1999–2001 that were designed around the actual construction and initial testing of the tools described below. More than 70 experts across the zoo and wildlife medicine communities around the world participated in these workshops, with excellent open and collaborative spirit yielding outstanding results. This work culminated in the 2003 publication of a workbook entitled *Animal Movements and Disease Risk* (Armstrong *et al*., 2003) with subsequent field testing and training of local conservation professionals in Mexico, South Africa and Costa Rica in 2002–2003. The workbook is available in hardcopy directly from CBSG or via the Internet (www.cbsg.org). This article provides a summary of the key tools introduced in this workbook.

THE DECISION ANALYSIS PROTOCOL – A UNIFYING PHILOSOPHY

The tools described in this article are best used as part of a holistic approach to the identification, analysis and management of disease risks in wildlife conservation programmes. This approach is rooted in the standard methodologies of decision analysis and emphasizes the importance of problem

formulation, system-level analysis and proper risk communication (Armstrong *et al.*, 2003). The specific steps involved in this protocol are listed below:

Step 1: Issue formulation – Provide a detailed description of the process (animal movement) under consideration, remembering to concentrate on the big picture from the beginning.

Step 2: Problem identification – What problems emerge from Step 1 that warrant further evaluation? Identify potential diseases of concern in the process. In addition to direct risks to the wildlife species under consideration, attention should be directed where appropriate to risks posed to other wildlife species, domestics, and humans during this phase.

Step 3: System visualization – Create a graphical flow diagram of the full movement pathway, including the animal source, quarantine procedures, transport methods, and end points.

Step 4: Hazard identification – Characterize and roughly prioritize the potential hazards at each appropriate point along the movement pathway.

Step 5: Hazard filtering – Reduce the list of potential hazards to those deemed "high-risk" at a coarse level and, therefore, require additional treatment in a more formal risk assessment.

Step 6: Risk assessment definition – Articulate a specific question for each high-priority hazard that forms the basis of the subsequent assessment. A general format for such a question would be 'What is the likelihood of introducing individuals of [*species, population, group*] that are positive for [*hazard*] from [*source*] to [*destination*] via [*transport method*] on [*pathway*]?'

Step 7: System-level risk assessment model construction – Refine the system visualized in Step 3, with the important addition of critical control points (CCPs) that define any point in the transportation pathway where the hazard may be introduced or released, depending on the question posed in Step 6.

Step 8: Qualitative risk assessment – The initial assessment should be conducted on a relative scale for each CCP, with categorical scales of severity used to identify such information as the prevalence of disease in the source population, the sensitivity of diagnostic tests, and the likelihood of disease transmission through human contact.

Step 9: Quantitative risk assessment (if required) – The decision to use deterministic or stochastic models for this more complex assessment is driven by an evaluation of the quality and quantity of available data, the extent of process variability in the estimates, and the amount of uncertainty in parameter estimation.

THE DISEASE RISK ASSESSMENT TOOLKIT

This section describes selected tools that are included in the toolkit outlined in Armstrong *et al*. (2003). While some of the tools here are original contributions from members of the CBSG community, others are based on commercially available software that is applied to specific needs within the species conservation domain. These distinctions are made clear in the following descriptions.

Rough assessment worksheet

Carefully describing and prioritizing hazards (diseases of concern) in a given animal management effort are critical early steps in the larger risk assessment process. Table 1 gives an example of a completed Rough Assessment Worksheet for the case of disease dynamics between Tsushima leopard cats *Felis bengalensis euptileura* and Domestic and Feral cats *Felis catus* on the island of Tsushima, south-western Japan (Murayama *et al*., 2006). The primary issue of concern here is

DISEASE	LIKELIHOOD OF SUSCEPTIBILITY	LIKELIHOOD OF EXPOSURE	LIKELIHOOD OF BECOMING INFECTED	LIKELIHOOD OF TRANSMITTING IT TO OTHERS	SEVERITY FOR INDIVIDUAL IF CLINICAL	SEVERITY FOR POPULATION	ESTIMATED SIGNIFICANCE TO PROGRAMME
Feline immunodeficiency virus	3	3	3	1	2	2	14
Feline parvovirus	2	3	2	3	2	2	14
Rabies	3	1	1	3	3	1	12
Feline leukemia	2	3	2	1	2	2	12
Aujeszky's disease	2	1	1	1	3	1	9
Pathogenic avian influenza	2	1	1	1	3	1	9
Feline coronavirus (captive population)	3	3	3	3	1	1	14
Coccidiosis (captive population)	2	3	2	2	1	1	11
Salmonellosis (captive population)	3	3	1	2	1	1	11
Ascariasis (captive population)	2	3	2	2	1	1	11

Table 1. Rough assessment workshop results for diseases of concern in the Tsushima leopard cat *Felis bengalensis euptileura* on the island of Tsushima, Japan. Table values: 1, low importance; 2, medium importance; 3, high importance. Adapted from Murayama *et al*. (2006).

the risk of transmission of disease from Domestic and Feral cats to the existing wild Leopard cat population, and the feasibility of a reintroduction programme from existing Leopard cat captive stock in the face of these disease threats.

The intent of this worksheet is to initiate easily the assessment process and to enable biologists and clinicians to begin to quantify and substantiate their intuitive information. The resulting list of disease hazards will provide an initial basis to start a risk assessment and will begin to rank the diseases so that the most significant hazards can be addressed as higher priorities. The list will be utilized in completing additional elements of the assessment process. It is likely that the disease list will be expanded as work progresses, as there is additional investigation and input from additional sources and as new information is revealed. The relative ranking and significance of diseases will change as more specific and accurate data are applied to areas that rely only on the intuition of the user.

Specific questions to be addressed through the worksheet include:

- What is the likelihood that an individual animal will be susceptible to a given disease?
- What is the likelihood that the animal will be or has been exposed to the disease?
- If an animal becomes exposed, what is the likelihood that the animal will actually become infected and subsequently capable of transmitting the disease?
- Is the disease likely to be transmitted to other individuals?
- If an individual in the wild population does become clinically ill with the disease, what is the usual outcome for that individual?
- If an individual in the wild population does become clinically ill with the disease, what is the usual outcome for the population as a whole? For example, rabies in wild dogs or canine distemper in lions may be severe for both the individual and the population, while brucellosis in wild cattle may not severely compromise individual survival but could have a profound impact at the population level through reproductive impairment.

The estimated significance to the programme will give valuable guidance on which hazards warrant additional attention in the more detailed risk assessment protocols to follow.

System-level modelling using STELLA, VENSIM

Once a given process has been adequately described and the relevant issues properly formulated, a visual depiction of the overall system is invaluable for helping those involved in the assessment to literally 'see the big picture'. We have found two similar system modelling platforms to be outstanding tools in this regard. Perhaps the more popular of the two is STELLA (current version 9 · 0; isee Systems, 2006, Lebanon, NH, USA), a software package that provides an environment to interactively visualize how complex systems are structured and how they function, thereby creating a graphical representation of our current beliefs and understanding of the problem being considered. Equally important is the ability to use this tool to communicate the system's structure to a wide audience more effectively through the use of diagrams, charts and associated text boxes that can be tailored to particular learning styles. Because of its relative ease of use and graphical nature, STELLA is an excellent tool for bringing together experts from diverse disciplines around the description of a given system. VENSIM (current version 5 · 6; Ventana Systems, 2006, Harvard, MA, USA) uses a very similar methodology for creating these visual models and can be obtained at a much lower cost in a scaled-down package for broader use. In addition, both packages can be used more intensively to quantitatively simulate the dynamics of a system to understand better the consequences of a particular activity within the system, such as the introduction of a disease to a naïve population.

An example of the use of this methodology for disease risk assessment is provided in Fig. 1. STELLA was used to construct a visual model of the dynamic relationship between Mountain gorillas *Gorilla beringei beringei*, human trackers operating as part of the

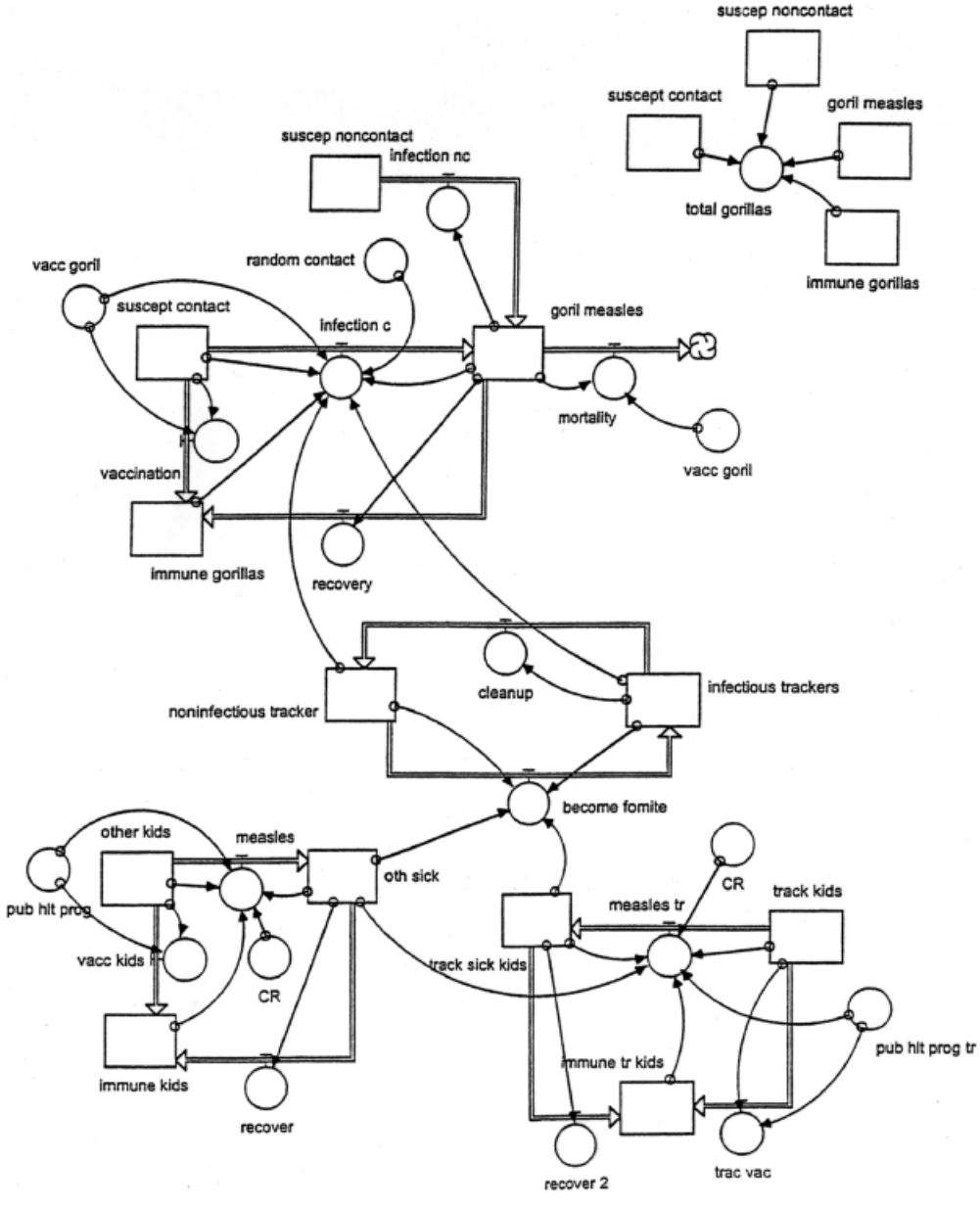

Fig. 1. Visual model, using the STELLA software platform, of the transmission of measles among Mountain gorillas *Gorilla beringei beringei* and human trackers. See Armstrong & Seal (2001) for more information on the development of this model.

ecotourism industry in south-west Uganda, and children within the villages who may be infected with measles (adapted from Armstrong & Seal, 2001). The underlying question driving the assessment was: 'Should the children of trackers be vaccinated for measles as a way to minimize risk of disease to the gorillas?' The system visualization led to detailed discussion about the probability that other children in the village, who were not members of tracker's families, could spread measles virus to the trackers. Preliminary results suggested that simply focusing on the families of trackers would not significantly reduce the risk of measles transmission to the nearby Mountain gorilla population. Major village- or region-wide public-health efforts would be necessary to make vaccination of children protective for gorillas. With a detailed graphical depiction of the system, deeper quantitative analysis of the risks involved with particular activities could proceed.

Figure 2 shows another simpler example of this general methodology. Generic flowcharting tools were employed to visualize the pathway involved in importing semen from wild Gerenuk *Litocranius walleri* in Kenya and to evaluate the risk of introducing rinderpest into the captive Gerenuk population in the United States through artificial insemination (Loskutoff *et al*., 2003). This example is used to illustrate the identification of critical control points at various stages along the semen importation pathway. For example, rinderpest could be present in the captured individuals, in the trucks used to transport the individual animals following capture or in the hospital facilities where the semen collection is to take place.

Decision analysis using PRECISION TREE

After the project has been described, hazards have been identified, and the system has been visualized with the inclusion of critical control points, it is possible to begin detailed analysis of the system through the use of models. Developing an explicit model of a given system can highlight the importance of critical information that is currently unknown, can be used to predict consequences of interventions, and can compare alternative programmes or policies in terms of their projected impacts on the system of study. An excellent example of this type of modelling approach in the field of conservation medicine is a technique known as decision analysis. This is simply a method for constructing another type of visual representation of the situation of interest, this time incorporating the decision maker's understanding regarding uncertainty within that system, so that the best decision can be made (i.e. the optimal outcome can be achieved). The formal result of a decision analysis is the preferred 'decision path', with a profile of the risks associated with each possible outcome.

PRECISION TREE (current version 1 · 0, Palisade Corporation, 2006, Ithaca, NY, USA) is a powerful 'add-in' to Microsoft EXCEL that allows a user to construct a decision tree within a simple computer spreadsheet interface. Decision trees provide a formal graphical structure in which decisions and chance events are linked from left to right in the order they would occur. (For example, before you decide whether to treat an individual for a disease, you need to determine if the individual tests positive for the disease.) The result is a tree structure with the 'root' on the left and branches for each chance event or decision extending to the right. Probabilities of events occurring and, optionally, payoffs for events and decisions are added to each node in the tree. The graphical nature of the tree provides an explicit visual understanding of the decisions being contemplated, as with the use of STELLA and VENSIM, with the added computational rigor necessary to justify the choice of a specific set of optimal choices. A decision analysis in PRECISION TREE generates a risk profile, which compares the payoffs and risks of different decision options. The cumulative risk profile graph displays a cumulative distribution showing the probability of an outcome less than or equal to a certain value. Where uncertainty exists in our depiction of the decision structure, sensitivity analysis options are available to test the impact of this uncertainty on our optimal decision.

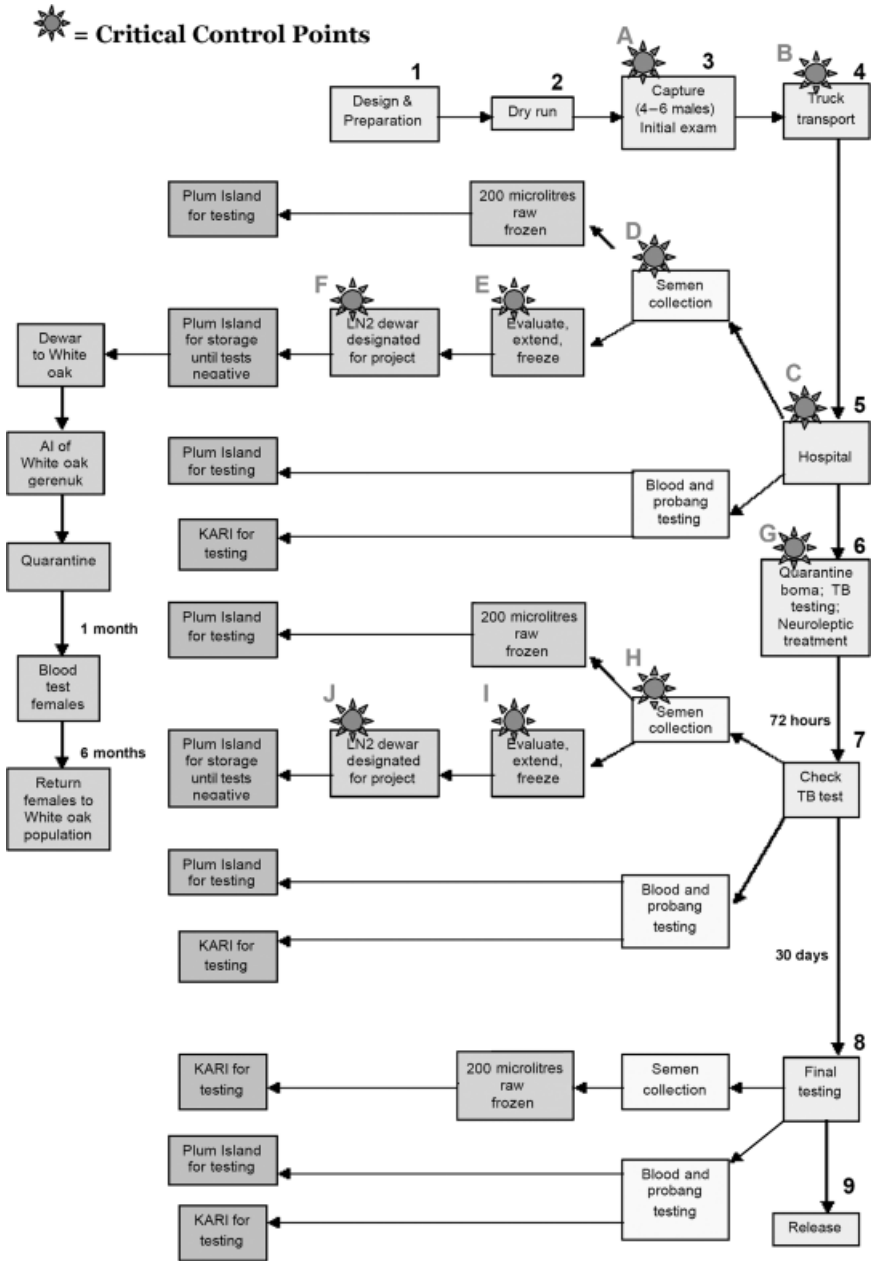

Fig. 2. Visual model of the collection, transport and utilization of semen collected from wild Gerenuk *Litocranius walleri* **in Kenya in the context of the risk of rinderpest introduction into the North American zoo population. Critical control points are indicated by stars. From Loskutoff** *et al***. (2003).**

A simple illustration of the use of PRECISION TREE-based decision analysis in disease risk assessment is shown in Fig. 3. Here, we quantitatively assess the risk of transmission of feline immunodeficiency virus (FIV) from Feral cats to the Tsushima leopard cat on the

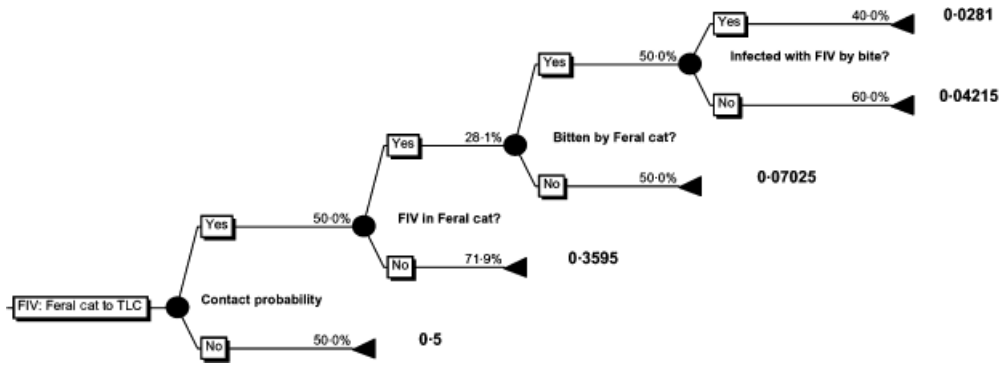

Fig. 3. Simple decision tree used to calculate the risk of feline immunodeficiency virus (FIV) infection of a Tsushima leopard cat *Felis bengalensis euptileura* through a bite from a Feral cat *Felis catus* in the Kamijima region of Tsushima island, Japan. Adapted from Murayama *et al*. (2006).

northern reaches of the island of Tsushima, south-west Japan (Murayama *et al*., 2006). Specifically, this analysis addresses the following question: 'What is the risk of an individual Tsushima leopard cat becoming infected with FIV in the northern region of Tsushima (Kamijima) through being bitten by an FIV-positive Feral cat?' This question emerged from a graphical visualization of the Leopard cat/Feral cat/Domestic cat system in the context of the high-priority diseases identified during the rough assessment phase (Table 1). The pathway from Feral cats to Tsushima leopard cats was seen as an important critical control point and, therefore, deserving of detailed quantitative analysis. In this analysis, we assume that in Kamijima:

- Fifty per cent of all cats contacted by a given Tsushima leopard cat will be Feral cats,
- The prevalence of FIV among Feral cats is 28 · 1%,
- If contact is made with a Feral cat, there is a 50% chance of being bitten,
- The probability of being infected with FIV after the Feral cat bite is 40%.

Combining these probabilities in a simple multiplicative model yields a 2 · 81% risk of a contact with a Feral cat resulting in FIV transmission to an individual Leopard cat. Identical procedures indicate that the risk of transmission from a Domestic cat is much lower – just 0 · 4%. Given the precarious future for this species on the island of Tsushima as concluded from other analyses and discussions of population viability, local wildlife managers immediately initiated an aggressive programme of Feral cat removal and Domestic cat registration and monitoring to dramatically reduce the density of Feral cats on the island and the associated FIV-based risks.

Considerably more complexity can be added to these types of analyses in order to take true advantage of the capabilities of the software platform. For example, if disease is known to exist in a given wildlife population, it is often important to determine the relative financial and/or biological costs and health benefits of different types of treatment regimes. By easily adding value information to the tree, the user can interactively optimize these trade-offs to determine the best course of action.

Health assessment worksheet and database

This worksheet was originally developed by Dr Richard Jakob-Hoff and his colleagues at the Auckland Zoological Park and the New Zealand Department of Conservation. By constructing this detailed data collection tool, we intend to provide an overall framework for developing quarantine and health screening protocols aimed at minimizing disease risks during the movement of wildlife.

Wildlife managers and veterinarians are able to consider the specific disease risk issues associated with each planned animal movement project, and to communicate this more effectively to all parties involved. It is recognized that resources for wildlife management are generally constrained and the data needed to make a quantitative assessment of risk is often incomplete. However, in conjunction with the graphical and analytical tools already discussed here, this worksheet enables managers to work within these constraints and to begin the process of identifying knowledge gaps that can be filled as opportunities are presented.

The electronic version of this worksheet, developed by Dr. John Williams as an application for Microsoft ACCESS, makes possible Internet-based communication of disease risk information rapidly and easily (see Fig. 4). Through collaboration with our growing network of wildlife medicine professionals, we intend to populate this database with a variety of real-world cases that can serve to inform and instruct the larger community in search of this type of data. At a late date, the emerging database will be published on the CBSG website (www.cbsg.org) as a service to the global community.

Data collected in some of the other tools briefly discussed here and in more detail in Armstrong *et al*. (2003) can be directly transferred to this larger database for more effective synthesis. Moreover, the details of specific outcomes that emerge from a formal decision analysis – for example, whether to treat, or to quarantine, or to release – can be evaluated in considerably greater detail in this

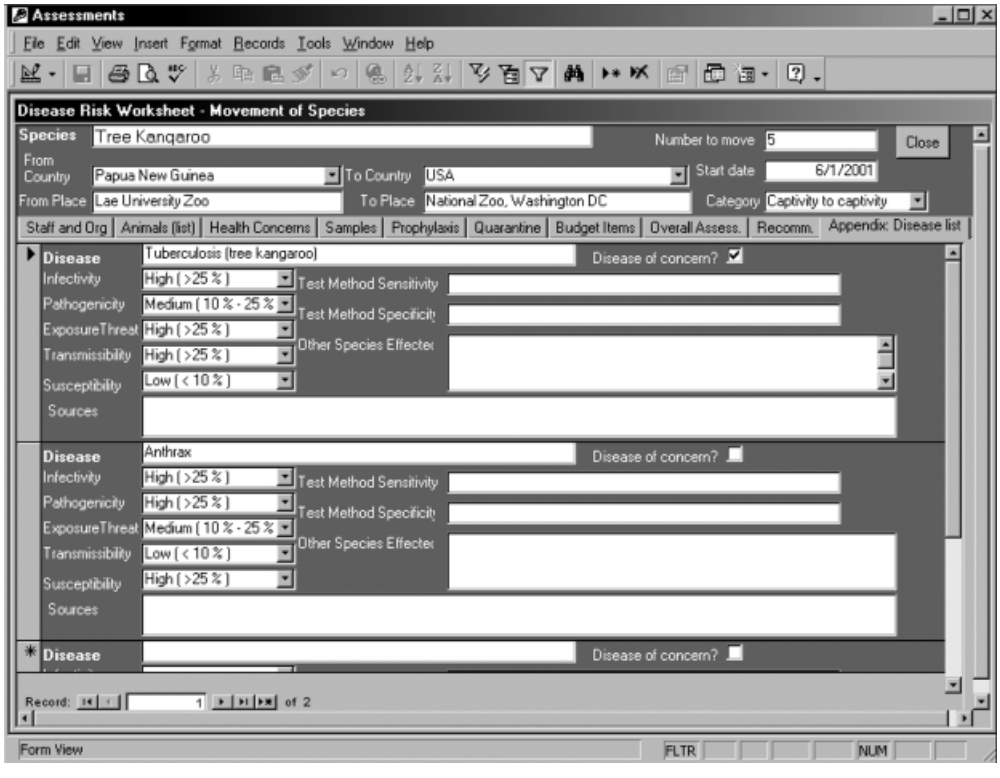

Fig. 4. Sample screen of the Health Assessment Database, showing the details of identifying and characterizing diseases of concern for a hypothetical animal movement of Tree kangaroos from Papua New Guinea to the United States.

worksheet. There is particular attention given to the specifics regarding quarantine of animals, including specification and associated justification for the duration of quarantine. This kind of information is invaluable to others when planning future movements of the same species at a later date or under similar circumstances. The subject of diagnostic sample collection, storage and transport is also given ample attention in the worksheet. In recognition of the fact that in many cases the persons collecting diagnostic samples from animals in the field will not be veterinarians, a simple guide to sample collection and handling is provided as an attachment to the hardcopy version of the worksheet. It is highly recommended that the techniques are practiced – preferably under veterinary supervision – before samples are collected in the field. The value of the samples will directly reflect the quality of the processes used to collect and handle them. Finally, appendices to the worksheet include notes on qualitative and quantitative risk analysis methods, diagnostic test specificity and sensitivity and choice of optimal sample size for developing baseline data.

Simulation modelling of disease epidemiology using Outbreak

While substantial effort is directed towards constructing demographic models of wildlife population viability with greater realism and mathematical sophistication (e.g. Sjögren-Gulve & Ebenhard, 2000; Beissinger & McCullough, 2002; Reed *et al*., 2002; Miller & Lacy, 2003a), there is considerably less attention directed at the larger ecological factors that influence population persistence. One such factor is infectious disease and its transmission dynamics among co-existing human and animal populations. Typically, models of wildlife population viability do not adequately reflect the demographic effect of disease on a population, which can vary considerably depending upon the structure of the host population, the characteristics of the infectious agent, and environmental variables such as habitat condition and availability (but see Haydon *et al*., 2006, for an outstanding exception to this generality).

Similarly, the great majority of epidemiological models of infectious disease focus primarily on the disease status of the individuals in the population (e.g. susceptible, infected, recovered) and assume a static population size or use only very simple models of population change. As a result, these models produce estimates of morbidity and mortality without considering the important effects of random demographic, environmental and genetic factors. In other words, they lack the core components that make effective population viability analysis (PVA) models inherently useful: an explicit treatment of the intrinsic and extrinsic stochastic forces that put small populations of wildlife at risk of extinction. By developing a detailed, individual-based simulation modelling package of the epidemiology of wildlife disease [see Barlow (1995) for a discussion of the value of individual-based models], and by studying the impacts of disease on population viability through its linkage with an existing PVA model, our understanding of (1) the process of disease transmission in small wildlife populations subject to unpredictable demography and (2) the interactions that occur among demographic factors, environmental variables, disease pathogens and host genetics to impact endangered population persistence, could be greatly enhanced. This integrated product would provide an outstanding opportunity for productive collaboration between the wildlife ecology and veterinary communities. Moreover, such a package could serve as a unique teaching vehicle for students in these fields of study. Through this process, an effort like this can also promote a more intimate integration of scientific disciplines – an endeavor that has recently been argued as vital to the success of biodiversity conservation and its inherent complexity (Redman, 1999; Lacy & Miller, 2002; Nyhus *et al*., 2002; Westley & Miller, 2003).

In order to fulfil this need, the CBSG team of disease risk-assessment experts has developed a stochastic simulation model of the

dynamics of disease epidemiology in small wildlife populations. The resulting Microsoft Windows software package, titled OUTBREAK, simulates SEIR – style disease dynamics, using the basic conceptual algorithms of Anderson (1982) and May (1986) as a foundation. The prevalence of infectious disease in wildlife populations is dependent on the number of individuals already infected, as well as on the numbers of susceptible and exposed individuals. To model infectious processes, the state of each individual in the population is tracked, and the probabilities of transition among states are specified as functions of the number of individuals currently in each state and of other relevant parameters, such as contact rate and the latent period of infection. Multiple iterations of a given dataset are used to generate mean population characteristics as model output for analysis.

As the user clicks on different elements of the model or, alternatively, selects one of the many corresponding model tabs, the interface provides general information on the specific model element (disease state or transition) along with the appropriate equations that make up the mathematical treatment of that element (Fig. 5). Moreover, the fields (composed of dropdown boxes, radio buttons, etc.) necessary to parameterize the elements are organized cleanly by disease state. In this way, the user moves through the graphical depiction of the model to construct a complete epidemiological specification of the disease model.

The mathematical algorithms run on a simulated daily time-step in order to model the details of disease transmission dynamics. In addition, relatively simple demographic information, such as breeding rates and non-

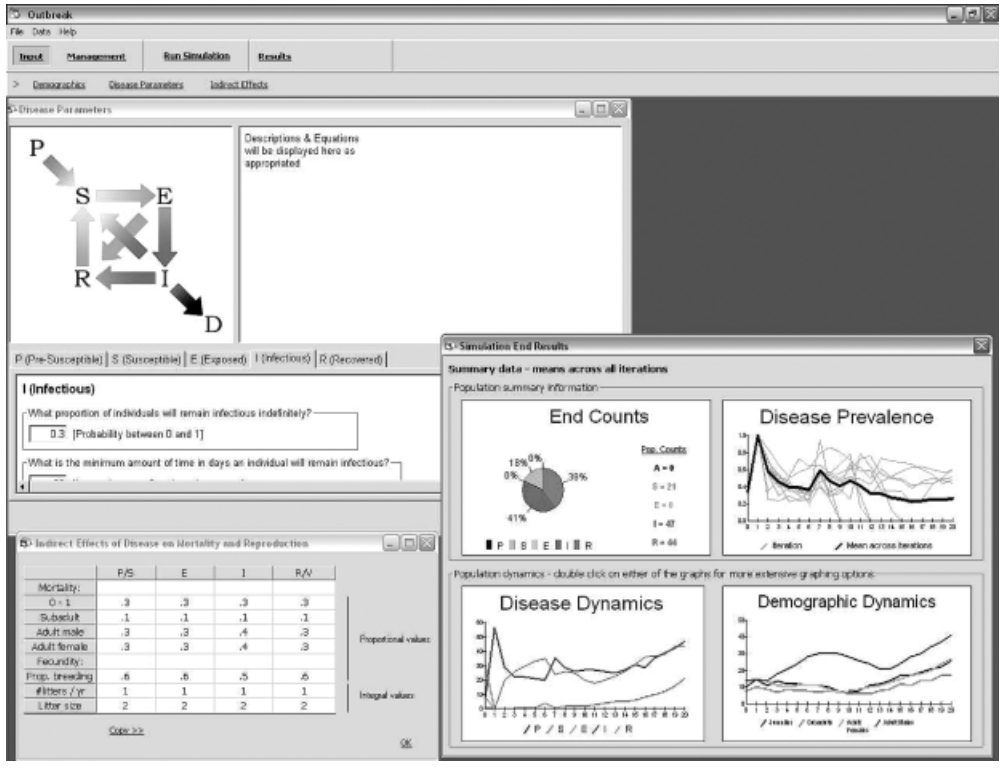

Fig. 5. Sample screen from the OUTBREAK epidemiology simulation modelling platform, showing representative input (left) and output (right) windows.

disease mortality for general sex-specific stages (juveniles, sub-adults and adults), is user-specified and used to project total population size. In addition to basic disease analysis, we allow the user to include vaccination as a means of controlling disease dynamics. Model output across multiple scenarios includes real-time graphical depictions of metrics like the relative mean proportion of the population within a given disease state, mean population size, etc.

In addition to using OUTBREAK as a standalone application, a user has the option to physically link the model with the popular PVA package VORTEX (Lacy, 2000; Miller & Lacy, 2004). VORTEX is an individual-based stochastic simulation of the extinction process that requires highly specific and detailed data on a variety of demographic and ecological parameters of the population under consideration. Almost all demographic input values can be constant over time, can change over time, or can be specified to be functions of population density, age, sex, degree of inbreeding, other individual characteristics of the population.

If one intends to use VORTEX to investigate the projected viability of small wildlife populations impacted by disease, OUTBREAK is called up to parameterize the disease of concern, and this information would then be passed on to VORTEX in order to allow modification of population demographic rates as a function of an individual's disease state. In this way, an individual's demographic behavior will change over the duration of the simulation as they are exposed to the infectious agent, contract the disease and later acquire resistance (if applicable for the disease of concern). All other aspects of population dynamics unrelated to disease, such as annual variation in demographic rates, catastrophic events that dramatically reduce reproduction and/or survival, dispersal and migration between metapopulations, will be handled directly within VORTEX. This flexibility allows the user to develop any number of sophisticated population viability modelling scenarios with or without the additional complexity of detailed infectious disease epidemiology, and to graphically compare the results. The flexibility of this 'meta-modelling' process (Miller & Lacy, 2003b) results in a versatile PVA modelling environment that is of considerably greater depth than other packages currently available and greatly facilitates the creation of interdisciplinary collaborative teams that are so important to effectively address today's complex issues in conservation medicine (Westley & Miller, 2003).

CONCLUSION: FUTURE DIRECTIONS

While the *Animal Movements and Disease Risk* workbook as it stands at time of writing is a highly effective toolkit for the conservation medicine community, there are areas of continued research and improvement that can enhance its value. Specifically, we intend to expand our network of experts, to compile datasets appropriate for the rigorous testing of existing tools, to train the larger conservation community in the use of these tools and to continue to explore the development of new tools to serve better the wildlife disease management community. In this regard, the integration of geographic information system (GIS) tools, the application of rigorous economic models for cost–benefit analysis of management alternatives, and even the use of tools for collecting information on disease from outside the scientific community, such as participatory rural appraisal techniques, show particular promise. As wildlife health managers around the world show interest in mastering these tools and techniques, our goal is to continually improve the means by which the world's threatened biodiversity can survive and flourish.

ACKNOWLEDGEMENTS

A full list of those who have contributed their knowledge and expertise to the creation of this workbook is beyond the scope of this work. Their talents, however, are no less appreciated. Special thanks go to Douglas Armstrong, Richard Jakob-Hoff, Dominic Travis, Laura Hungerford, Jon Ballou, Patti Bright, J.P. Pollak, John Williams, Bob Lacy, Don Janssen and Alberto Páras for their special efforts in the intellectual and technical contributions to this project. Finally, a singular note of thanks to the late Dr Ulysses Seal, CBSG Chairman, who displayed the creativity and wisdom to bring us all together.

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Manuscript submitted 17 December 2006; revised 12 April 2007; accepted 12 April 2007