IUCN

SSC
Species Survival Commission

Manual of Procedures for Wildlife Disease Risk Analysis

Richard M. Jakob-Hoff
Stuart C. MacDiarmid
Caroline Lees
Philip S. Miller
Dominic Travis
Richard Kock

WORLD ORGANISATION FOR ANIMAL HEALTH
Protecting animals, preserving our future

Edited and printed by the World Organisation for Animal Health
(OIE [Office International des Épizooties])
12, rue de Prony, 75017 Paris, France
Telephone: 33-(0)1 44 15 18 88
Fax: 33-(0)1 42 67 09 87
Electronic mail: oie@oie.int
www.oie.int
ISBN: 978-92-9044-957-7

Suggested citation:
Jakob-Hoff R.M., MacDiarmid S.C., Lees C., Miller P.S., Travis D. & Kock R. (2014). – Manual of Procedures for Wildlife Disease Risk Analysis. World Organisation for Animal Health, Paris, 160 pp. Published in association with the International Union for Conservation of Nature and the Species Survival Commission.

1. Bushmeat hunters returning to their village on the boundary of Odzala National Park, Republic of Congo, with a variety of duiker species harvested from the forest. Photo courtesy: Michael Kock
2. Oriental white-rumped vultures, Gyps bengalensis, feeding on a domestic water buffalo, Bubalus bubalis, in India. This species is now critically endangered as a result of ingesting the veterinary drug diclofenac used to treat buffalo and cattle for lameness and other conditions but highly toxic to vultures. Photo courtesy: Munir Virani – The Peregrine Fund
3. A Tasmanian devil, *Sarcophilus harrisii* with the cancerous growths typical of Devil Facial Tumour Disease which has decimated populations of this top predator on the Australian island state of Tasmania. Photo courtesy: Sarah Doornbusch
4. Zebra and domestic animals share a grazing area near a local village in the buffer zone of Limpopo National Park, Mozambique. Photo courtesy: Michael Kock

Manual of Procedures for Wildlife Disease Risk Analysis

Richard M. Jakob-Hoff
Stuart C. MacDiarmid
Caroline Lees
Philip S. Miller
Dominic Travis
Richard Kock

Co-published by OIE and IUCN

Disease risk analysis (DRA) process steps

Steps in the disease risk analysis (DRA) process

Risk communication (applies throughout all DRA steps)

Purpose: Engage with relevant experts and stakeholders in a way that will maximise the quality of analysis and the probability that the recommendations arising will be implemented.

Questions: 'Who has an interest, who has knowledge or expertise to contribute, and who can influence the implementation of recommendations arising from the DRA?'

1 Problem description

Purpose: Outline the background and context of the problem, identify the goal, scope and focus of the DRA, formulate the DRA question(s), state assumptions and limitations and specify the acceptable level of risk.

Questions: 'What is the specific question for this DRA? What kind of *risk analysis* is needed?'

2 Hazard identification

Purpose: Identify all possible health *hazards* of concern and categorise into 'infectious' and 'non-infectious' *hazards*. Establish criteria for ranking the importance of each *hazard* within the bounds of the defined problem. Exclude *hazards* with zero or negligible probability of release or exposure, and construct a scenario tree for the remaining, higher priority, *hazards* of concern, which must be more fully assessed (Step 3).

Questions: 'What can cause *disease* in the population of concern?', 'How can this happen?' and 'What is the potential range of consequences?'

3 Risk assessment

Purpose: To assess for each *hazard* of concern:

a) the likelihood of release (introduction) into the area of concern;

b) the likelihood that the species of interest will be exposed to the *hazard* once released;

c) the consequences of exposure. On this basis the *hazards* can be prioritised in descending order of importance.

Questions: 'What is the likelihood and what are the consequences of an identified hazard occurring within an identified pathway or event?'

4 Risk management

Purpose: Review potential risk reduction or management options and evaluate their likely outcomes. On this basis decisions and recommendations can be made to mitigate the risks associated with the identified *hazards*.

Questions: 'What can be done to decrease the likelihood of a hazardous event?' and 'What can be done to reduce the implications once a hazardous event has happened?'

5 Implementation and review

Purpose: To formulate an action and contingency plan and establish a process and timeline for monitoring, evaluation and review of *risk management* actions. The review may result in a clearer understanding of the problem and enable refinement of the DRA. (See 'Adaptive management' on p. 45.)

Questions: 'How will the selected *risk management* options be implemented?' and, once implemented, 'Are the *risk management* actions having the desired effect?' and, if not, 'How can they be improved?'

How to use this *Manual*

Users of this *Manual* will vary considerably in their level of knowledge and experience of *risk analysis* and the resources available to them. As such, the subject matter has been organised to enable users to work through it in a logical sequence or, for more experienced users, to rapidly find and turn to their specific items of interest.

Front and back

Two quick references have been incorporated into the layout:

– The process diagram inside the cover of this *Manual* is positioned for ease of reference to the stages of the DRA process, regardless of which part of the *Manual* is being used. Next to this is a succinct description of the purpose of each step and the questions they are designed to answer. The main steps in the DRA process are colour coded throughout the book.

– The glossary is located at the back of the book for quick reference. In addition, all terms used in the glossary are italicised in the text.

Overall design

Following a brief history of *disease risk analysis* (p. 15), this *Manual* is divided into five major sections:

1. **Key concepts for wildlife *disease risk analysis*** (pp. 17–20):

An outline of fundamental concepts that should be considered when analysing wildlife disease risks.

2. **Planning and conducting a wildlife *disease risk analysis*** (pp. 21–49):

A detailed description of each step in the DRA process with examples taken from published and unpublished sources. This section also includes guidelines for successful interdisciplinary collaboration, technical, social and political considerations and some of the associated challenges.

3. **Tools for wildlife *disease risk analysis*** (pp. 51–92):

Each of the DRA process step descriptions in the previous chapter is accompanied by a box listing the tools that may be useful in completing that step. This chapter provides detailed information on a representative array of the tools available to assist practitioners in working through a DRA. The tools included range from relatively simple drawing tools that help illustrate the disease system of interest and the main influences on it, to more complex, probability-based disease and population modelling programmes that can help with more detailed quantitative analyses. For ease of access, tools are categorised according to the step(s) in the DRA process to which they apply, and also according to their utility in situations in which resources, data or access to specialists, may be constrained.

4. **Appendices** (pp. 93–136):

The appendices include additional information, examples and references relevant to the topics covered in this *Manual*.

Appendix 1 provides a guide to further sources of information of value to *wildlife disease risk analysis*. Appendices 2, 3 and 4 provide information on disease surveillance, screening for pathogens and Monte Carlo modelling. These are large topics which are dealt with comprehensively in other texts. The purpose of the brief introductions included here is to help the broader audience of wildlife managers, policy makers and field biologists, who may be less familiar with these topics, to access a basic understanding and vocabulary in these areas.

Also included are guidelines for planning a DRA workshop (Appendix 5) and a DRA evaluation (Appendix 6). Three wildlife DRA case summaries that illustrate the application of the process to a range of scenarios are contained in Appendix 7, while Appendix 8 provides an example of a more comprehensive DRA utilising some of the tools featured in this *Manual*.

5. **References and Glossary**

A reference section on pages 137–143 is followed by a glossary of the technical terms used in this *Manual*. As the meaning of some of these words or phrases can vary between different disciplines (e.g. veterinary science vs ecology), it is advisable to check the meaning attributed to them by the authors of this publication. As noted above, to assist this, each of the terms featured in the glossary is italicised in the text.

Acknowledgements

The topic and practical nature of this *Manual* mean that it could only have been written through *transdisciplinary* collaboration. The editors are profoundly grateful and humbled by the generosity of the many individuals listed below who contributed their knowledge, skills and time to its development. This included some or all of the following: discussion and development of the vision, mission, overall structure and content through participation in a number of online meetings and, for some, participation in a face to face workshop in Auckland, New Zealand; following up on tasks assigned at, or after, the workshop; providing feedback on, and assistance with, the format, style and content of several drafts of the document over a two-year period; contributions of case studies and bibliographic materials; and assistance with enlisting contributors and supporters by 'spreading the word' through their personal and professional networks.

We thank you and hope you feel the resulting work is worthy of your efforts.

Acknowledgements to the following individuals for their valuable cooperation

– Amanda Fine, Wildlife Conservation Society, Mongolia
– Arnaud Desbiez, IUCN Species Survival Commission Conservation Breeding Specialist Group, Brazil
– Bethany Jackson, New Zealand Centre for Conservation Medicine, Auckland Zoo, New Zealand
– Craig Pritchard, New Zealand Centre for Conservation Medicine, Auckland Zoo, New Zealand
– Doug Armstrong, IUCN Species Survival Commission Reintroduction Specialist Group, Massey University, New Zealand
– Enkhtuvshin Shiilegdamba, Wildlife Conservation Society, Mongolia
– Fransiska Sulistyo, Borneo Orang-utan Survival Foundation, Kalimantan
– Hazel Hodgkin, Breakthrough Strategies, New Zealand
– Janelle Ward, Institute of Veterinary, Animal and Biomedical Sciences, Massey University, New Zealand
– John Ewen, Institute of Zoology, Zoological Society of London, United Kingdom
– Joseph K. Gaydos, UC Davis Wildlife Health Centre, Davis, California
– Kathy LaFauce, Department of Agriculture, Fisheries and Forestry, Australia
– Kevin Parker, Massey University, New Zealand
– Maggie Jakob-Hoff, Resonance Research, New Zealand
– Maj de Poorter, IUCN Species Survival Commission Invasive Specialist Group /Royal Forest and Bird Protection Society, New Zealand
– Nic Masters, Zoological Society of London, United Kingdom
– Rebecca Vaughn, Institute of Zoology, Zoological Society of London, United Kingdom
– Rob Jones, Aquarium Vet, Moorabin, Victoria, Australia
– Rodrigo Pinho Gomes Lopez, São Paulo Zoological Society, Brazil
– Rosalie Dench, Borneo Orang-utan Survival Foundation, Kalimantan
– Rosemary Barraclough, Massey University, New Zealand
– Shyama Pagad, IUCN Species Survival Commission Invasive Specialist Group, New Zealand
– Sue Bigwood, Zoos South Australia, Australia
– Susie Hester, Australian Centre of Excellence in Risk Assessment, Australia
– Tony Sainsbury, Institute of Zoology, Zoological Society of London, United Kingdom

Acknowledgements to the authors for their efficient and valuable contribution

- Verné Dove, BVSc Hons BAnimSc, MVS (Veterinary Conservation Medicine), MVS (Veterinary Disease Surveillance), Dip. Conservation
  PhD Candidate and Sea Shepherd Cetacean Field Veterinarian
  Murdoch University, Universidad de los Andes, and Sea Shepherd Conservation Society
  Coffs Harbour, Australia, and Bogotá, Colombia
  verne.dolphin@gmail.com

- Nigel French, BVSc MSc (Epi) DLSHTM, Dip. ECVPH, MRCVS, PhD
  Professor of Food and Safety and Veterinary Public Health
  Director of the Infectious Disease Research Centre and the Molecular Epidemiology and Public Health Laboratory in the Hopkirk Research Institute
  Massey University
  Palmerston North, New Zealand
  N.P.French@massey.ac.nz

- Tiggy Grillo, BVMS, MRCVS, PhD
  Projects Coordinator
  Australian Wildlife Health Network
  Taronga Conservation Society
  Sydney, Australia.
  tgrillo@zoo.nsw.gov.au

- Carly Holyoake, BSc, BVMS, PhD
  Senior Research Fellow, Marine Mammal Health
  Registrar in Wildlife Epidemiology and Conservation Medicine
  School of Veterinary and Biomedical Sciences, Murdoch University
  Perth, Australia
  c.holyoake@murdoch.edu.au

- Richard M. Jakob-Hoff, BVMS, MANZCVS (Wildlife Medicine)
  Senior Veterinarian, Conservation and Research
  New Zealand Centre for Conservation Medicine, Auckland Zoo
  Adjunct Associate Professor, School of Veterinary and Biomedical Sciences, Murdoch University, Co-convenor, Conservation Breeding Specialist Group Australasia
  Auckland, New Zealand
  richard.jakob-hoff@aucklandcouncil.govt.nz

- Richard Kock, MA, VMB, VMD
  Professor of Wildlife Health and Emerging Diseases
  Department of Pathology and Infectious Diseases, Royal Veterinary College
  Adjunct Professor, Faculty of Veterinary Medicine, University of Tufts, Grafton, Massachusetts
  Co-Chair IUCN Species Survival Commission – Wildlife Health Specialist Group
  London, United Kingdom
  rkock@rvc.ac.uk

- Ian Langstaff, BVSc, PhD
  Manager, Disease Surveillance
  Animal Health Australia
  Deakin, Australia
  ilangstaff@animalhealthaustralia.com.au

- Caroline Lees, MSc
  Programme Officer
  Co-convenor, Conservation Breeding Specialist Group Australasia
  IUCN Species Survival Commission Conservation Breeding Specialist Group
  Auckland, New Zealand
  caroline@cbsgaustralasia.org

- Stuart C. MacDiarmid, BVSc, PhD
  Principal International Adviser, Risk Analysis
  Adjunct Professor in Veterinary Biosecurity (Massey University)
  Member of the World Organisation for Animal Health International Standard Setting Commission
  Ministry for Primary Industries
  Wellington, New Zealand
  Stuart.MacDiarmid@mpi.govt.nz

- Kate McInnes, BVSc
  Veterinarian
  Department of Conservation
  Wellington, New Zealand
  kmcinnes@doc.govt.nz

- Philip S. Miller, PhD
  Senior Programme Officer
  IUCN Species Survival Commission Conservation Breeding Specialist Group
  Apple Valley, Minnesota
  pmiller@cbsg.org

– Noel Murray, BVSc, MACVSc
Senior Adviser, Risk Analysis, Domestic Policy Division
Canadian Food Inspection Service
Ottawa, Canada
Noel.Murray@inspection.gc.ca

– Andrea Reiss, BVSc, MSc (Zoo and Wildlife Medicine)
Regional Veterinary Officer
Zoo and Aquarium Association,
Sydney, Australia
andrea@zooaquarium.org

– Bruce A. Rideout, DVM, PhD
Director, Wildlife Disease Laboratories
San Diego Zoo Global
San Diego, California
brideout@sandiegozoo.org

– Shan Siah BVMS
Risk Analysis, Conservation and One Health Consultant
ConserveAction
Perth, Australia
Shan@ConservAction.org

– Lee Skerratt, BAnimSc, BVSc, PhD, MACVS
Senior Research Fellow
Tropical Infectious Diseases Research Centre
James Cook University
Townsville, Australia
lee.skerratt@jcu.edu.au

– Daniel M. Tompkins, BA (Hons), MA, DPhil
Wildlife Ecologist
Landcare Research
Dunedin, New Zealand
tompkinsd@landcareresearch.co.nz

– Dominic Travis, DVM, MS
Associate Professor of Epidemiology and Ecosystem Health
Department of Veterinary Population Medicine
College of Veterinary Medicine
University of Minnesota
St. Paul, Minnesota
datravis@umn.edu

– Steve Unwin, BSc, BVSc, MRCVS
Veterinary Officer (North of England Zoological Society), Veterinary Director (Pan African Sanctuary Alliance)
Conservation Medicine Division
Chester Zoo
Chester, United Kingdom
Steve.unwin@chesterzoo.org

– Mary van Andel, BVSc, MVS (Conservation Medicine)
Incursions Investigator, Animal Surveillance and Incursions Investigations Team
Ministry for Primary Industries
Wellington, New Zealand
Mary.vanAndel@mpi.govt.nz

– Simone Vitali, BSc, BVMS (Hons)
Senior Veterinarian
Adjunct Associated Professor, School of Veterinary and Biomedical Sciences, Murdoch University
Perth Zoo
Perth, Australia
simone.vitali@perthzoo.wa.gov.au

– Kristin Warren, BSc, BVMS (Hons), PhD, Dip. ECZM (Wildlife Population Health)
Senior Lecturer in Wildlife and Zoo Medicine;
Academic Chair, Postgraduate Studies in Conservation Medicine
Conservation Medicine Programme
School of Veterinary and Biomedical Sciences, Murdoch University
Perth, Australia
k.warren@murdoch.edu.au

Dedication

This work is dedicated, with great respect, to the late Ulysses S. Seal (Conservation Breeding Specialist Group Chairman 1979–2003) and to Doug Armstrong (Director of Animal Health, Henry Doorly Zoo) whose combined vision and work inspired its contributors and established the foundation on which this volume was built.

Workshop sponsors

We are deeply grateful to our sponsors: Auckland Zoo, New Zealand Department of Conservation, Landcare Research and the IUCN Species Survival Commission Conservation Breeding Specialist Group, who made the face-to-face workshop in Auckland, New Zealand, possible. This was a pivotal event in the development of this resource, enabling many of the contributors to cement their collaborative relationships, share perspectives and experiences and debate many of the issues relevant to the application of disease *risk analysis* to wildlife.

International Union for the Conservation of Nature (IUCN)

We also pay tribute to the following IUCN Species Survival Commission specialist group Chairs who gave their support to this project from the outset and facilitated the distribution of information regarding it through their networks:

Bob Lacy and, subsequently, Onnie Byers, Conservation Breeding Specialist Group;

William Karesh and Richard Kock, Wildlife Health Specialist Group;

Frederic Launay, Reintroduction Specialist Group;

Piero Genovesi, Invasive Species Specialist Group.

The World Organisation for Animal Health (OIE)

For their support and encouragement, we also thank:

Bernard Vallat, Director-General, World Organisation for Animal Health (OIE);

Alain Dehove, Coordinator, World Animal Health and Welfare Fund (OIE);

Barry O'Neil, Deputy Director-General (Acting) Verification, New Zealand Ministry of Agriculture and Forestry;

The Members of the OIE Working Group on Wildlife Diseases.

We also greatly appreciate the thoughtful and diligent assistance of the OIE publications team under the direction of Dr Daniel Chaisemartin – in particular Annie Souyri, Chief of the Publications Unit, and Gillian Whytock, copy-editor at Prepress Projects.

Contents

Boxes

Figures

Tables

OIE Preface

World Organisation for Animal Health
12, Rue de Prony - 75017 Paris, France

The need to fight animal diseases at the global level led to the creation of the Office International des Epizooties (OIE) through the signing of an international agreement on 25 January 1924. In May 2003 the Office became the World Organisation for Animal Health but kept its historical acronym, OIE.

The OIE is the intergovernmental organisation responsible for improving animal health worldwide and has 178 Member Countries (as at 2013). The OIE maintains permanent relations with 45 other international and regional organisations and has regional and sub-regional offices on every continent. The OIE is recognised as the international standard-setting organisation for animal health and zoonoses, under the World Trade Organization (WTO) Sanitary and Phytosanitary Agreement (SPS Agreement).

The complexity of disease emergencies in a globalised world calls for the identification of effective strategies, based on both science and proven practical experience, to reduce future threats. The H5N1 avian influenza crisis demonstrated how crucial it is to address persistent global threats at the interface among humans, animals and ecosystems. Moreover, it has shown how a concrete, transparent and consistent approach, based on high-quality scientific advice and practical experience, is vital for the management of these threats and for political credibility, at national, regional and international level. This *Manual of Procedures for Wildlife Disease Risk Analysis* provides a new resource that will be of great value to all those concerned with wildlife-related diseases.

In areas related to the animal–human–ecosystem interface, collaboration and cooperation among the various sectors is critical to ensure that efforts are efficient and effective. The OIE has been working to assist Member Countries with how they can best work at this interface. The OIE strongly supports the publication of this *Manual*, which will help to expand the scientific basis for effective intersectoral collaboration and identify ways to operationalise this interface in policy and in practice.

In recognition of the important role of wildlife as a reservoir of diseases of significance to domestic animals and human health, the OIE established a Working Group on Wildlife Diseases in 1994. The role of this body of international experts is to inform and advise the OIE on all health issues relating to wild animals, whether in the wild or in captivity.

Publications of relevance to this topic include the OIE *Terrestrial Animal Health Code*. Chapter 2.1, Import Risk Analysis, provides OIE Member Countries with recommendations and principles for conducting transparent, objective and defensible risk analysis for international trade in animals and animal products. In addition, two earlier OIE publications, produced in collaboration with the Canadian Cooperative Wildlife Health Centre (CCWHC), are worthy of mention. *Health Risks Analysis in Wildlife Translocations*, published in 2004, provided step-by-step guidelines for health risk analysis for the movement of wildlife across or within national borders. In 2010 a practical *Training Manual on Wildlife Diseases and Surveillance*, authored by CCWHC Director, Dr F.A. Leighton, was published by the OIE and is used by the OIE within its capacity-building global programme of national focal points for wildlife. This was developed for use in training workshops, with a view to providing practical advice on wildlife diseases and surveillance and facilitating an interactive working session for participants.

Another OIE publication of relevance is the *Guidelines for Assessing the Risk of Non-native Animals Becoming Invasive*, published in 2011. This provides an objective and defensible method of determining whether imported animal species are likely to become harmful to the environment, animal or human health or the economy.

This IUCN/OIE *Manual of Procedures for Wildlife Disease Risk Analysis* adds another important resource by extending the application of the standardised OIE risk analysis methodology to the analysis of disease threats to biodiversity conservation. In the spirit of the cross-sectoral collaboration noted above, this document has been jointly developed by the OIE and the International Union for the Conservation of Nature (IUCN). The IUCN has also produced a complementary summary publication, the IUCN/OIE *Guidelines for Wildlife Disease Risk Analysis*, for use by policy and decision makers.

We are extremely grateful to Dr Richard Jakob-Hoff, his editorial committee and the contributing authors for sharing their specialist expertise in the compilation of this *Manual*.

December 2013
Bernard Vallat
Director-General OIE

IUCN Preface

International Union for the Conservation of Nature
7–9 North Parade Buildings - Bath BA1 1NS - United Kingdom

Founded in 1948, the International Union for Conservation of Nature (IUCN) is the world's oldest and largest global environmental organisation. Its membership comprises 12,000 voluntary scientists and experts representing over 200 government and 900 non-government organisations in some 160 countries.

The IUCN Species Survival Commission (SSC) is a science-based network of more than 8,000 volunteer experts from almost every country of the world, all working together towards achieving the vision of: 'A world that values and conserves present levels of biodiversity.' Most members are deployed in more than 130 specialist groups, Red List Authorities, sub-Committees, working groups and task forces.

The technical guidelines produced by the SSC provide guidance to specialised conservation projects and initiatives, such as reintroducing animals into their former ranges, handling confiscated specimens and halting the spread of invasive species. The development of this IUCN/OIE *Manual of Procedures for Wildlife Disease Risk Analysis* and its companion, the IUCN/OIE *Guidelines for Wildlife Disease Risk Analysis*, are fine examples of the benefits of collaboration among the global SSC voluntary network of experts. As outlined in the introduction, this work is the culmination of the collaborative effort of four of the SSC's disciplinary groups with a common interest in pathogenic organisms and their impacts on biodiversity conservation:

The Conservation Breeding Specialist Group (CBSG) aims to save threatened species by increasing the effectiveness of conservation efforts worldwide by:

- developing and disseminating innovative and interdisciplinary science-based tools and methodologies
- providing culturally sensitive and respectful facilitation that results in conservation action plans
- promoting global partnerships and collaborations, and
- fostering contributions from the conservation breeding community to species conservation.

The Wildlife Health Specialist Group (WHSG) serves as a first response for wildlife health concerns around the world and aims to enhance understanding of wildlife disease and its role in multispecies infections or other disease syndromes. It comprises a network of regional experts primarily conducting wildlife health work in the areas of health surveillance, reporting and response, wildlife disease management, disease ecology, diagnostics, epidemiology, pathology, toxicology, health policy and related health disciplines.

The Reintroduction Specialist Group (RSG) aims to combat the ongoing loss of biodiversity by using reintroductions as a responsible tool for the management and restoration of biodiversity through actively developing and promoting sound interdisciplinary scientific information, policy and practice to establish viable wild populations in their natural habitats. Recent RSG publications complimentary to the current volume include the fully revised *IUCN Guidelines for Reintroductions* and Ewen *et al.* (2012) *Reintroduction Biology: Integrating Science and Management* (Wiley-Blackwell).

The Invasive Species Specialist Group (ISSG) aims to reduce threats to natural ecosystems and the native species they contain by increasing awareness of invasive alien species and of ways of preventing, controlling or eradicating them. The ISSG promotes and facilitates the exchange of invasive species information and knowledge across the globe and ensures the linkage between knowledge, practice and policy so that decision making is informed. The two core activity areas of the ISSG are policy and technical advice, and, information exchange through networking and its online resources and tools, including the Global Invasive Species Database, which includes data on the distribution and biodiversity impacts of pathogenic organisms.

The present volume is the first formal collaboration among these four specialist groups on a topic of mutual interest and value. The increasing incidence of emerging and re-emerging disease threats to biodiversity conservation are a symptom of our species' increasing imbalance with our natural environment. In order to redress this imbalance, fundamental shifts in thinking and behaviour will need to be made. These include discarding disciplinary silos in favour of the transdisciplinary collaborations advocated in this *Manual* and modelled in its development.

The Species Survival Commission is grateful for the work of the authors and editors of this excellent volume and, in partnership with the World Organisation for Animal Health (OIE), proud to endorse it as a further, valuable resource for the global conservation community.

December 2013
Simon N. Stuart
Chair, IUCN Species Survival Commission

Introduction

R.M. Jakob-Hoff, S.C. MacDiarmid, C. Lees, P.S. Miller, D. Travis & R. Kock

Disease risk analysis (DRA) is a structured, evidence-based process that can help decision making in the face of *uncertainty* and determine the potential impact of infectious and non-infectious diseases on *ecosystems*, wildlife, domestic animals and people. Results from the DRA can help decision makers to consider an evidence-based range of options for the prevention and mitigation of disease risks to the population(s) under consideration.

‘One Health’ and another shift in focus

This *Manual of Procedures for Wildlife Disease Risk Analysis* (this ‘*Manual*’) builds on a large body of work on DRA in particular that of the World Organisation for Animal Health (OIE), and extends this to apply existing methodologies to the issues concerned with biodiversity conservation.

Thomas Kuhn, in his seminal 1962 work, *The Structure of Scientific Revolutions* (Kuhn 1962), described the stages through which our understanding of the world and how it works changes over time. Using examples such as the Copernican revolution that changed the dominant Western belief of the 15th Century from an Earth-centric universe to one in which the Earth orbits the Sun, Kuhn identified a consistent sequence of stages in which the prevailing world view or ‘paradigm’ is replaced by a new one. He found that such ‘revolutions’ happen over a considerable time period and are driven by a growing body of ‘anomalies’ that cannot be explained or understood within the framework of the current world view. In Kuhn’s analysis, there are long periods of ‘normal science’ in which research questions are pursued based on the existing paradigm. Observations that cannot be explained within this framework gradually accumulate until another, often radically different, world view is proposed that accounts for existing knowledge as well as these ‘anomalies’. A period of crisis follows in which there is strong resistance by the current ‘establishment’, (often accompanied by the ridicule of proponents of alternative paradigms) as the new thinking challenges prevailing beliefs and the social hierarchies and distribution of resources that have grown alongside them.

Such a ‘thought revolution’ is currently in progress as we are confronted with the realities of living in a world that is considerably more complex and integrated than suggested by the Newtonian *model* that has dominated Western thinking for the past 300 years. Through this world view natural phenomena are studied by reducing them to their component parts. This mechanistic paradigm has enabled (and continues to enable) extraordinary advances in medicine, technology and many other areas of human endeavour over the last three centuries. However, its limitations are becoming increasingly evident as we face a world dominated by the combined activities of 7 billion of our species. Human-induced or ‘anthropogenic’ effects on the planet are now radically changing *ecosystems* and the regulatory mechanisms (such as climate and the carbon cycle) that have become closely integrated over millions of years and provide the environmental conditions necessary to support the diversity of life we know today. If we are to understand (and manage) the drivers of wildlife disease in the dynamic, interdependent living systems of which we humans are a part, it is necessary to re-focus our view on the ‘big picture’ provided by the relatively modern science of ecology (the study of relationships between organisms and the environment) and epidemiology (the study of disease dynamics in populations).

The emergence of new diseases in people (e.g. bovine spongiform encephalitis or ‘mad cow disease’, human immunodeficiency virus/acquired immune deficiency syndrome, Severe acute respiratory syndrome,) and the re-emergence of diseases once thought to be controlled (e.g. tuberculosis) have prompted the re-establishment of the concept of ‘One Health’ and the development of associated disciplines such as ‘Ecosystem Health’ and ‘Conservation Medicine’ (Aguirre *et al.* 2002; Friend 2006, Rabinowitz and Conti 2010).

One Health is a comprehensive approach to health that focuses on:

1. improving health and well-being through the prevention of risks and the mitigation of the effects of crises (emerging diseases) that originate at the interface among people, animals and their various environments

2. promoting cross-sectoral collaborations and a 'whole of society' treatment of health *hazards*, as a systemic change of perspective in the management of risk.

This world view was encapsulated in the 'Manhattan Principles' at a 2004 conference at The Rockefeller University, New York, entitled 'One World, One Health: Building Interdisciplinary Bridges to Health in a Globalized World'. The Wildlife Conservation Society's Robert Cook, William Karesh and Steven Osofsky summarised these principles, now supported by many national and international bodies (e.g. see www.onehealthinitiative.com/supporters.php), in the closing statement of the conference report:

> *It is clear that no one discipline or sector of society has enough knowledge and resources to prevent the emergence or resurgence of diseases in today's globalized world. No one nation can reverse the patterns of habitat loss and extinction that can and do undermine the health of people and animals. Only by breaking down the barriers among agencies, individuals, specialties, and sectors can we unleash the innovation and expertise needed to meet the many serious challenges to the health of people, domestic animals, and wildlife and to the integrity of ecosystems. Solving today's threats and tomorrow's problems cannot be accomplished with yesterday's approaches. We are in an era of 'One World, One Health' and we must devise adaptive, forward-looking and multidisciplinary solutions to the challenges that undoubtedly lie ahead.*

The authors of this *Manual* have endeavoured to provide a practical resource that will enable wildlife conservation professionals and those who work within the health sciences – human, animal and environmental – to apply these principles to their analysis of disease risk. In so doing, we hope that they may be able to advance the inter-related causes of biodiversity conservation, biosecurity and domestic animal and public health through informed decision making when addressing the many situations in which wildlife disease is a critical factor.

The history and need for this *Manual*

Since 1992 the Conservation Breeding Specialist Group (CBSG) of the IUCN Species Survival Commission (IUCN SSC) has been facilitating collaboration between experts in zoo and wildlife veterinary medicine, disease ecology and population management to develop a set of tools for realistic and rigorous analysis of wildlife disease risks. This culminated in the publication of a workbook focused on disease risks associated with animal translocations (Armstrong *et al.* 2002) and available through the CBSG website (www.cbsg.org). In 2010, recognising that the range of concerns in relation to wildlife disease had broadened well beyond those associated with animal movements, CBSG, in partnership with three other IUCN SSC specialist groups (Wildlife Health, Reintroduction and Invasive Species), undertook a global needs analysis survey. The 290 responses from 40 countries represented 26 different occupation categories with an interest in wildlife disease (Box 1). As illustrated in Figure 1, human–wildlife interaction was the main issue of concern to the largest proportion of survey respondents, followed by domestic animal–wildlife interactions, management of wildlife in nature (in situ), wildlife translocations and management of wildlife in captivity (ex situ).

Box 1:
Occupations of respondents to the disease risk analysis needs analysis survey, 2010

Biologist
Biosecurity advisor
Captive breeding practitioner
Ecologist
Entomologist
Environmental toxicologist
Field manager
Herpetologist
Information management specialist
Marine biologist
Microbiologist
Nurse
Ornithologist
Pathologist
Planner/Manager
Policy officer
Public health physician
Research permit processing administrator
Researcher
Statistician
Student
Veterinary epidemiologist
Virologist
Volunteer
Wildlife ranger
Wildlife veterinarian

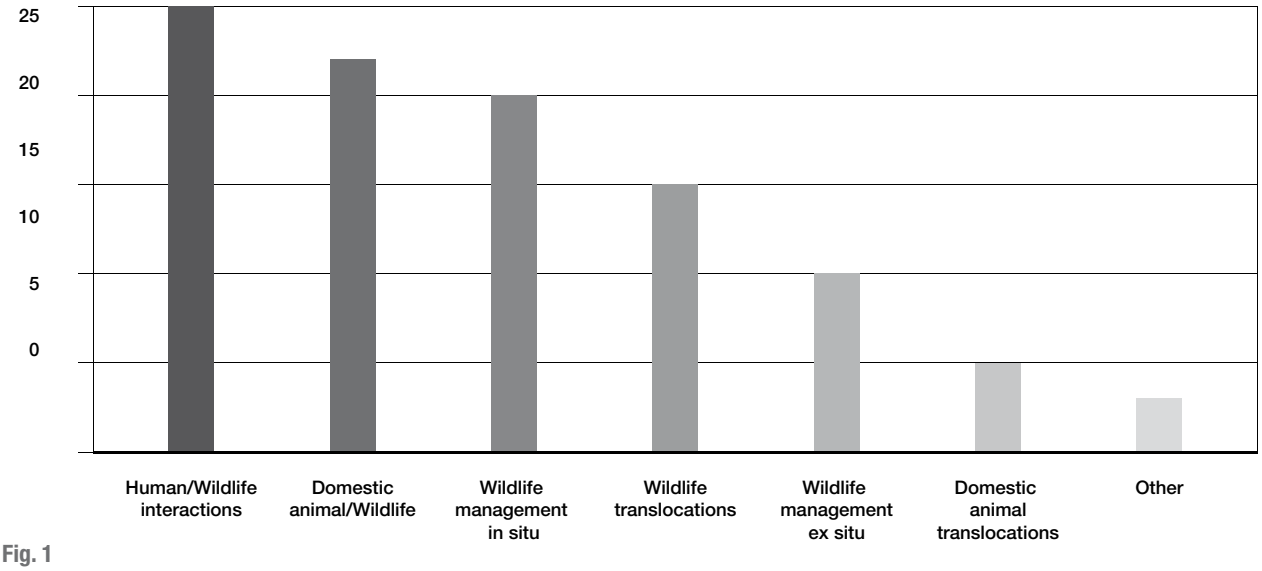


Fig. 1
Needs analysis survey respondents' main areas of wildlife disease concern (*n* = 290)

These results demonstrate that wildlife disease concerns are global, broad in scope and involve a wide diversity of people from multiple disciplines. This *Manual* was conceived and developed in response to this demand.

Prevention and collaboration

Fundamental to the understanding and management of wildlife disease risk are the concepts of 'prevention' and 'collaboration'.

The adage 'an ounce of prevention is worth a pound of cure' is nowhere more relevant than in addressing the impacts and management of wildlife disease. As outlined in this *Manual*, there are numerous examples in which infectious disease agents have inadvertently been transferred with the intentional and unintentional movement of wild and domestic animals, as well as people and animal products (Woodford and Rositer 1994; Wobeser 2006; Travis *et al.* 2011) . Examples include:

– the introduction of bovine tuberculosis into South Africa's Kruger National Park by domestic cattle, resulting in the rapid spread of infection through the park's African buffalo population, which now spreads the disease to other wildlife (Bengis *et al.* 1996; Michel *et al.* 2009)

– the introduction of invasive Australian brush-tailed possums, *Trichosurus vulpecula*, into New Zealand where they have become the major *reservoir* of tuberculosis for the cattle industry (Hickling 1991), and

– the spread of amphibian chytrid fungus, *Batrachochytrium dendrobatidis*, (now linked to mass amphibian extinctions), through legal and illegal trade (Travis *et al.* 2011).

As described in detail by Wobeser (2006), once the conditions needed for a *pathogen* to be released are established, (e.g. owing to changing populations, landscapes or ecological conditions) its control is invariably challenging and extremely expensive and eradication virtually impossible. For example:

– Despite over 40 years of efforts to eradicate bovine tuberculosis in possums in New Zealand, localised pockets of infected animals remain as *reservoirs* for cattle, and country-wide freedom, as at 2013, had not been achieved (Porphyre *et al.* 2008).

– The culling of 20,000 badgers, *Meles meles*, in England to control the spread of tuberculosis to cattle has resulted, in some cases, in the disruption of the social systems of these animals causing some infected badgers to disperse over greater distances (Donnelly *et al.* 2003).

Consequently there are major financial benefits in investing in the preventive strategy of conducting a DRA wherever wildlife is concerned – whether the object of concern be potential impact on wildlife conservation or the impact of wildlife as *reservoirs* or *vectors* of disease to people or domestic animals.

Transdisciplinary communication

Given the complexity of wildlife disease ecology, the relative scarcity of relevant published information and the involvement of multiple stakeholders, a major emphasis of this *Manual* is on *transdisciplinary collaboration*.

To make this resource as useful and accessible as possible to such a broad potential audience, an experienced multidisciplinary team, situated in many parts of the world, have freely and collaboratively contributed their knowledge and experience to the writing of this *Manual*. Through this collaboration it became evident that different disciplines sometimes use the same term but apply different meanings. This can present a language barrier when working in *transdisciplinary* groups. Consequently, there has been an effort to keep the language in this text plain and, where technical terms are necessary, to define each term in a glossary. The glossary of terms included herein has been developed and agreed upon by authors representing a range of disciplines in an effort to ensure consistent usage and interpretation by all users of this *Manual*. It is our hope that, over time, this publication will be translated into languages other than English so that this barrier to communication may also be overcome.

Disease risk analysis in the context of structured decision making

Analysing and managing disease risk in the context of animal population management involves many different decision points: What are the diseases of concern to my system of interest? How in particular do the species within that system – including humans – respond to the offending pathogenic agent? What are the best forms of treatment for the disease? What are the biological consequences of moving different species or populations of animals into or through the system of interest? This simple subset of questions helps to define the biological parameters of the larger problem, and the tools and processes described in this *Manual* are focused on analysing these in detail.

It is critical to realise, however, that species biology and disease epidemiology is only one of potentially many axes of information to consider when working to make the best decision to minimise the risk of disease introduction or transmission. Reducing financial cost, maximizing the extent of public support for a given management decision, or enhancing opportunities for gaining additional scientific knowledge of the system of interest can all be additional axes that might require consideration through the decision-making process. In fact, it is often necessary to make difficult trade-offs between the biologically optimal management decision and the allowable financial cost. How does the relevant decision-making authority balance these sometimes competing factors when trying to identify the best management decision?

The general field of structured decision making (SDM), sometimes referred to more specifically as multi-criteria decision analysis (MCDA), is ideally suited to address these types of complex, multidimensional problems. Structured decision making provides an organised approach to analysing the problem at hand, clarifies trade-offs between alternative potential courses of action and helps to communicate how people view these various options. Using a set of diverse tools and processes, SDM can integrate rigorous analysis and thoughtful deliberation in a fully transparent and accountable way. The process deals very explicitly with uncertainty, and can build significant capacity among included stakeholder domains for future decision-making abilities. For more information on SDM, see Clemen (1997), Gregory *et al.* (2012) and references therein.

Our goal with this *Manual* is not to provide the full breadth of information on the mechanics of putting DRA in the larger context of structured decision making. However, we recognise the potential value of incorporating elements of SDM when required for the specific decision at hand. If an expanded analysis becomes the desired approach, we recommend thoughtful consideration and application of the available SDM resources as an extension of the DRA analyses discussed here.

Wildlife DRA into the future

This *Manual* is a work in progress. We trust that managers and decision makers involved in land use planning that impacts wildlife, protected area managers, conservationists and those concerned with health in the broadest sense will see the benefits of this approach. Many of the examples used to illustrate the processes and tools described in the following pages are previously unpublished and are derived from the personal experiences of the authors. This exemplifies the current status of wildlife DRA with its considerable reliance on unpublished sources of information. However, there is a rapidly growing body of publications on the topics covered in this *Manual* and it is our hope that this resource will stimulate and encourage many more people to undertake wildlife DRAs and to publish and share their experiences. Only in this way will we broaden and refine our understanding of the complex systems of which wildlife disease is a manifestation and be able, collectively, to make decisions that benefit the health of all those who live on planet Earth.

December 2013

A brief history of disease risk analysis

D. Travis, S.C. MacDiarmid & R. Kock

The process of analysing risk has been a part of the human condition throughout history; every day, each of us assesses risk in the course of normal activities. However, it was not until 1654 when the French and Italian mathematicians Blaise Pascal and Luca Paccioli, exploring the issues of chance and *uncertainty* in gambling, developed what is now called the theory of probability, combining for the first time mathematics and rudimentary elements of today's concept of risk. In time, the theory of probability mathematics was further developed and refined by those in other disciplines attempting to assess risks and forecast the future (Berstein, 1996).

Veterinarians and veterinary services have traditionally based decisions regarding disease risks on experience and qualitative assessment.

In the late 20th Century, mathematicians, engineers, economists and health care professionals began to standardise techniques for qualitatively or quantitatively assessing and predicting measures of *risk* in their respective fields. As a result, a collection of methods known as *risk analysis* has emerged to support rational decision-making in the face of *uncertainty*. *Risk analysis* is not science *per se*, but is, instead an evidence-based process that is an organised and logical approach to identifying and using scientific information to support policy-making in the real world.

Numerous health-related organisations have published *risk analysis* frameworks for diseases caused by microbial organisms; most follow the generic *risk analysis* process but have differing *risk assessment* formats. A comparison of the intricacies of the formats can be found in the *ILSI Revised Framework for Microbial Risk Assessment* (International Life Sciences Institute 2000). A close inspection of the comparison provided by the International Life Sciences Institute (q.v.) shows that many *risk assessment models*, although evolving separately, converge into a similar format.

Box 2:
Recent landmarks in the development of disease risk analysis

In 1969, *quantitative risk assessment* methodology was advanced by Chauncey Starr who outlined a standardised format for the quantitative assessment of risk (Starr 1969).

In 1980, William W. Lowrance suggested that *quantitative risk assessment* methods should be applied to evaluate risks associated with infectious disease (Lowrance 1980).

In 1981, signs that *risk analysis* was becoming a formal discipline were evident as the journal *Risk Analysis* was created.

In 1983 the United States National Research Council of the National Academy of Sciences (NRC-NAS) standardised the format for the assessment of the effects of hazardous chemicals on human health in what is referred to as the Red Book. *Risk assessment* methodologies commonly used in animal and human health fields today can be traced back to this.

The World Organisation for Animal Health *risk analysis model* (Brückner *et al.* 2010) was developed from the environmental *risk assessment* methodology of Covello and Merkhofer (1993). Although developed primarily as a tool for import *risk analysis*, it has proven to be versatile in a number of diverse situations (Bartholomew *et al.* 2005). In this *Manual* we have adapted this globally used *model* to encompass the special features associated with *disease risk analysis* as it is applied to *wildlife* and biodiversity conservation.

Key concepts for wildlife disease risk analysis

D. Travis, S.C. MacDiarmid, K. Warren, C. Holyoake, R. Kock, R.M. Jakob-Hoff, I. Langstaff & L. Skerratt

People with a range of backgrounds and perspectives may apply *disease risk analysis* (DRA) to a broad spectrum of situations. To be successful, this *Manual* must communicate its contents effectively and consistently to all of these groups. In pursuit of this goal, we begin by describing a number of key concepts. Gaining an understanding of these is an important precursor to understanding the science and practice of DRA.

Risk

Risk is usually defined as the chance of encountering some form of harm, loss or damage. For this reason it has two components:

1. the likelihood[1], or probability, of something happening and, if it does happen,
2. the consequences of the deleterious activity.

Because of the element of chance, we can never predict exactly what will happen but, through an appropriate process, we can estimate the probability of any particular outcome occurring (Brückner *et al.* 2010).

Risk analysis

'*Risk analysis* is a formal procedure for estimating the likelihood and consequences of adverse effects occurring in a specific population, taking into consideration exposure to potential *hazards* and the nature of their effects' (Thrusfield 2007). It is a tool to enable decision makers to insert science into policy.

Disease

At the most basic level, disease is defined as any impairment of the normal structural or physiological state of an organism. The manifestation of disease is often complex and may include responses to environmental factors such as food availability, exposure to toxins, climate change, infectious agents, inherent or congenital defects, or a combination of these factors (Wobeser 1997).

Three important epidemiological concepts of disease to keep in mind are:

1. Disease never occurs randomly.
2. All diseases are multifactorial.
3. Disease is always a result of an interaction among three main factors: pathogenic agent, host and environment (Fig. 2).

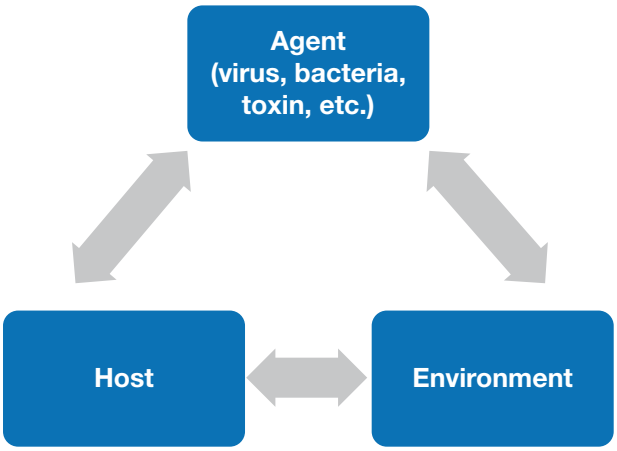


Fig. 2
Interaction among pathogenic agent, host and environment

Infectious microbes are a normal part of the *ecosystem* and thus disease plays an important role in maintaining the genetic health of populations and in regulating population numbers (Smith *et al.* 2009). However, in a highly disturbed environment, where significant and relatively permanent changes from earlier ecological states have occurred, disease may threaten the survival of an entire population.

Disease causes and impacts

Given that infectious microbes ('agents') occur normally in the environment, severe environmental events (natural or human induced) that alter the balance among agent, host and environment may result in the introduction, spread or manifestation of disease in a specific population. Some examples are given below.

1 The terms 'likelihood' and 'probability' may be used interchangeably. There is a tendency to use the term 'probability' when referring to quantified risk, and 'likelihood' when risk has been assessed qualitatively. However, both terms are correct

1. Human–wildlife interactions

Human–*wildlife* interactions can occur through hunting or harvesting, construction of roads, habitat modification, ecotourism, animal movement including global trade of animals and animal parts, pollution (e.g. organic contaminants, heavy metals, toxins, pharmaceutical drugs, sewage, oil spills, etc.). See Box 3 for an example.

Box 3:
How human pregnancy testing may have contributed to global amphibian decline

In 1934 urine from pregnant women, injected into African clawed frogs, *Xenopus laevis*, was found to stimulate ovulation and became the basis of a human pregnancy test.

Subsequently large numbers of this frog species were shipped to diagnostic and research laboratories worldwide.

African clawed frogs have since been found to be carriers of the amphibian chytrid fungus, *Batrachochytrium dendrobatidis* but usually remain disease free.

Mass extinction of amphibians in multiple geographic regions has subsequently been associated with the spread of the disease chytridiomycosis caused by this fungus.

The accidental or deliberate release of infected *Xenopus* frogs is one mechanism proposed for the dissemination of this pathogen. One retrospective study demonstrated that the fungus was introduced to Mallorca through the release of captive-bred Mallorcan midwife toads, *Alytes muletensis*, which had been in contact with chytrid-infected Cape platanna, *Xenopus gilli*, an endangered frog native to Western Cape, South Africa.

References: Weldon et al. *2004; Skerratt 2007; Walker* et al. *2008*

2. Livestock–wildlife interactions

Interactions between *wildlife* and domestic livestock (cattle, sheep, pigs, etc.) can occur, for example, through direct or indirect contact, erection of fences, use of pesticides or use of veterinary drugs (Box 4).

Box 4:
How pain relief for cattle increased the risk to people from rabies

Diclofenac (a non-steroidal anti-inflammatory drug) was used to provide pain relief for cattle in India, Pakistan and Nepal where these animals are allowed to die naturally, in accordance with Hindu beliefs.

Vultures scavenged the carcases of cattle left to decay in the open.

Diclofenac residues in the tissues of treated dead cattle have been found to be highly toxic to vultures, resulting in up to 99% mortality in some species.

The decline in vultures has favoured an increase in packs of rabies-carrying feral dogs scavenging cattle remains.

The number of cases of rabies in people due to dog bites has since increased.

References: Oaks et al. *2004; Sharp 2006; Markandya* et al. *2008; see also Appendix 7 (p. 119) of this* Manual

3. Wildlife management

Wildlife management actions may include animal movements, reintroductions, veterinary treatments, *vaccination*, fencing (e.g. creation of a *wildlife* reserve). For instance, see Box 5.

Box 5:
The spread of crayfish plague by fisheries management

Healthy North American signal crayfish, *Pacifastacus leniusculus*, are carriers of a fungus, *Aphanomyces astaci*.

These apparently healthy crayfish were translocated and released into European crayfisheries in the 1970s.

European white-clawed crayfish, *Austopotamobius pallipes*, had no immunity to the fungal organism which, in these previously unexposed animals, caused 'crayfish plague', leading to mass mortality.

In Britain since 1970 native crayfish populations from 88.6% of sites have either been eliminated, or are directly threatened, by crayfish plague infection, or habitat invasion by signal crayfish or pollution.

References: Holdich and Reeve 1991; Alderman 1996; Daszak et al. *2000*

4. Climatic events

Climatic events that may be associated with *wildlife* disease emergence include climate change, El Niño and La Niña events, fire, flooding and drought (Box 6).

Box 6:
Examples of disease spread associated with climatic events

1. Impacts of climate change on sheep parasites in Northern Ireland

'The results of this [10 year study] … revealed shifts in seasonal abundance and appearance times of parasites during the calendar year, which are likely due to the effects of climate, specifically: an increased abundance of trichostrongylosis/ teladorsagiosis and strongyloidosis in the south and west of the Province.'

Reference: McMahon et al. *2012*

2. Mosquito-borne malaria and El Niño

Ecuador, Peru and Bolivia suffered serious malaria *epidemics* after heavy rainfall in the 1983 El Niño. The *epidemic* in Ecuador was exacerbated by displacement of populations due to the flooding.

Reference: World Health Organization 2000

3. Plant diseases favoured by drought

'Drought reduces the breakdown of plant residues. This means that inoculum of some [*pathogens*] does not decrease as expected and will carry over for more than one growing season. The expected benefits of crop rotation may not occur.

Bacterial numbers decline in dry soil. Some bacteria are important antagonists of soil borne fungal diseases. These diseases can be more severe after drought'.

Reference: Murray et al. *2006*

The consequences of pathogen introduction or spread at the individual level may be obvious (e.g. overt *clinical signs* of ill health or death), or may be more subtle such as a reduction in immune function, impaired reproduction, subtle behavioural changes that may render individuals more prone to predation or accident, or decreased growth rate (Wobeser 2006).

As illustrated in Figure 3, diseases that affect many individuals may result in adverse effects on the population. These effects may be driven by multiple factors such as changes in birth rates, death rates, immigration and emigration. The population effect exerted by disease may, in turn, result in *ecosystem*–scale consequences through changes in community composition (competitors, predators, prey), productivity and stability (Tompkins *et al.* 2011).

The examples described in Boxes 3 to 6, illustrate that sometimes the less visible and longer term effects of disease on individuals or populations can have a profound impact. Consequently these potential impacts need to be considered in a *wildlife* DRA.

Objectivity

It is often said that *risk analysis* is an 'objective' process. The reality is that in disease risk analyses there are often so few data available that the analyst begins, unconsciously, to substitute value judgments for facts. Indeed, in assessing the consequences of disease introduction a degree of subjectivity is almost unavoidable. Risk analyses are seldom truly *objective* and for this reason *transparency* in declaring all assumptions made is essential (MacDiarmid 2001).

Proportionality

Actions taken to prevent or minimise disease risks to *wildlife* populations or biodiversity conservation must be in proportion to the likely consequences of disease entry. For instance, a *risk analysis* may conclude that there is a significant likelihood that an introduction of animals into a new area would introduce a particular disease agent. However, if there are other, unmanaged movements of animals, people or their chattels into the same area, the application of risk mitigation measures to the planned introduction may not be warranted.

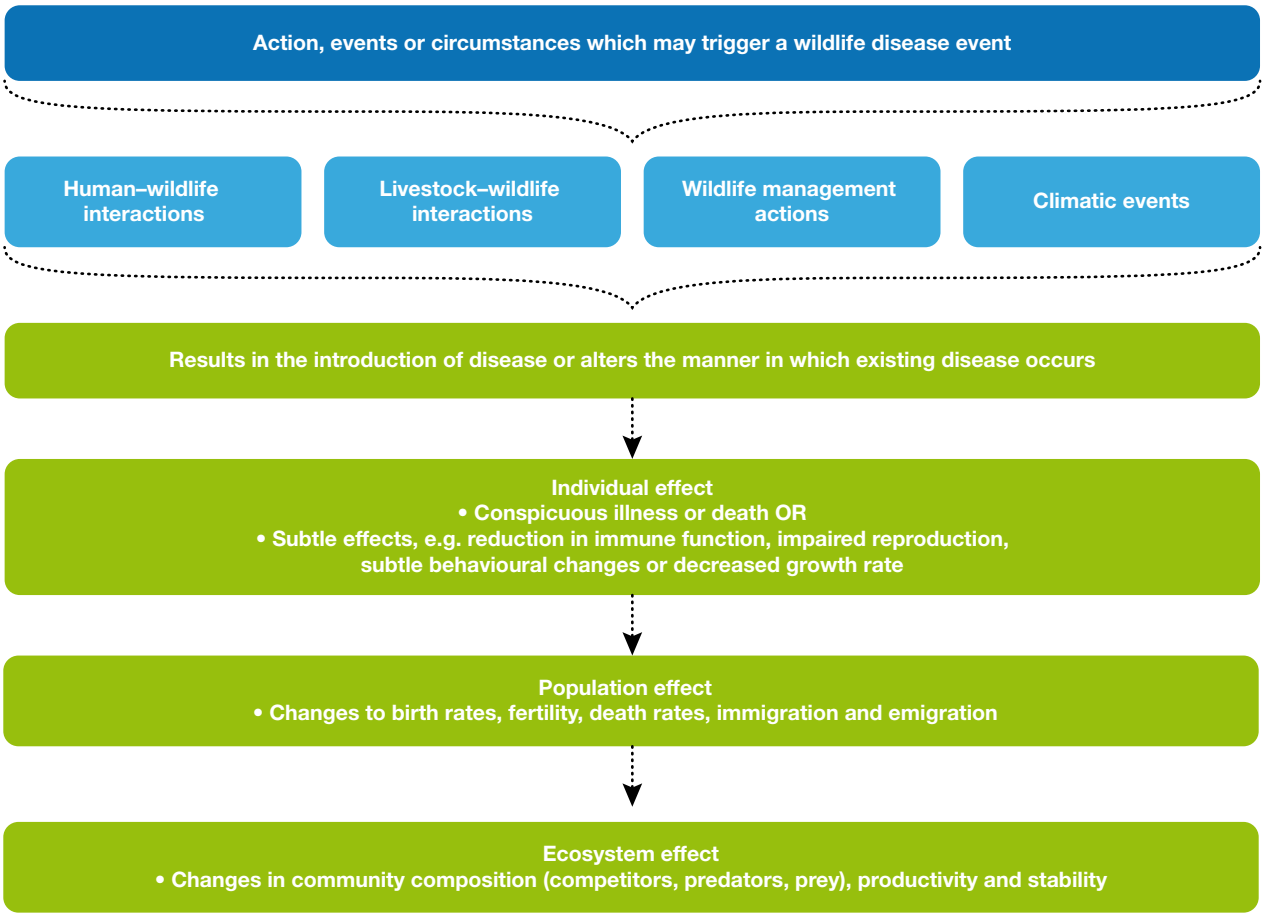


Fig. 3
Possible drivers of disease introduction and associated consequences

Worthington and MacDiarmid (2011) pointed out that it is important to consider this issue of proportionality in an analysis of the disease risks posed by the importation of non-human primates into zoos. As an example they considered a situation in which there is some likelihood of an imported primate carrying a *pathogen* that is equally likely to be carried by a human. It would not be justified to impose stringent measures on the importation of a few primates when there are no meaningful preventive measures that could be applied to the hundreds of thousands of humans who enter the country each year. In this situation, the imposition of risk mitigation measures to the primate importation would do nothing to significantly reduce the biosecurity risk to the importing country. (However, the manager of the zoo might well impose measures to reduce risks to other animals in the zoo.)

Acceptable risk

The *risk communication* process is essential in helping decision makers to deal with one of the most difficult problems encountered during the *risk analysis* process, namely determining what constitutes an 'acceptable risk' (MacDiarmid and Pharo 2003).

Zero risk is seldom, if ever, attainable and some degree of risk is unavoidable. For this reason, deciding whether or not a particular risk is acceptable is generally a societal or political decision because the benefits of a particular activity for one stakeholder group may have adverse consequences for another (MacDiarmid and Pharo 2003; Thrusfield 2007).

For example, when considering the disease risks to an unspoiled *ecosystem* posed by the construction of a road, risks considered acceptable by a government agency tasked with economic development may be quite unacceptable to the government agency tasked with *wildlife* conservation.

Similarly, the disease risks posed by relocation of wild animals into a conservation reserve may be acceptable to those ecologists concerned with maintenance of a genetically diverse population of endangered animals but be considered unacceptable to neighbouring farmers or ranchers concerned with the health of their livestock.

An example of an acceptable disease risk may be the translocation of kiwi harbouring a low number of coccidian intestinal parasites providing that other, specified, health indicators (e.g. body condition, behaviour, haematology parameters, etc.) are within the range considered healthy for the species.

The 'precautionary principle'

In situations in which there is significant scientific *uncertainty* regarding a risk and its consequences, such as a cause-and-effect relationship not being fully established, the 'precautionary principle' may be invoked. This principle holds that the implementation of preventive measures can be justified even in the absence of such a risk. This precautionary approach has a useful protective effect as the initial response to a new potential threat and may be an appropriate reaction to complex problems such as loss of biodiversity, where more formal *risk analysis* may not be adequate (Thrusfield 2007).

Assumptions

A *risk assessment* may sometimes be criticised because some of its inputs are based on assumptions. However, all decision making is based on assumptions, and *uncertainty* and subjectivity do not mean that valid conclusions cannot be drawn. Although many of the inputs of a *risk assessment* are surrounded by *uncertainty*, one may be able to have confidence that the 'true risk' is unlikely to exceed the estimate resulting from a careful and conservative analysis (MacDiarmid 2001).

Planning and conducting a wildlife disease risk analysis

R.M. Jakob-Hoff, T. Grillo, A. Reiss, S.C. MacDiarmid, C. Lees, H. Hodgkin, K. McInnes, S. Unwin & R. Barraclough

Collaboration

A *robust risk analysis* involving *wildlife* disease is usually beyond the scope of a single individual and is more effectively approached as a collaborative exercise.

Typically, a conservation manager, veterinarian or public health practitioner is tasked with responding to a request for a *wildlife disease risk analysis* (DRA) within a very short time-frame and with few relevant data. Even in this situation, however, it is advisable to consult and seek input from key people with relevant knowledge or expertise or relevant decision-making responsibility.

At the 'ideal' end of the DRA spectrum is a well-prepared and -funded workshop in which an appropriate range of experts, stakeholders and decision makers are gathered for a facilitated, structured review and analysis of the scenario, over one or more days. This group of individuals may meet only once but be engaged in dialogue with each other over a more extended time, both before and after the workshop. Table I lists some of the benefits and limitations of a collaborative versus an individual approach to *wildlife* DRA. Appendix 5 (p. 112) provides some additional guidance on planning a workshop and developing and maintaining a DRA team.

Technical, social and political considerations

This *Manual* has been written with the aim of enabling anyone tasked with conducting a *wildlife* DRA, or implementing its recommendations, to do so with the confidence that they are basing their work on the 'best practice' possible within the constraints of their circumstances. This includes the application of scientific rigour and the most appropriate tools and technology available. However, even the best science does not guarantee that the findings of a *wildlife* DRA will be translated into actions in the 'real world'. Taking into consideration relevant technical, social and political aspects of the DRA scenario and implementing an appropriate *risk communication* strategy from the outset, will help to ensure that time and effort is well spent and the recommendations of the *risk analysis* are more likely to be implemented.

Technically, more often than not, data on disease in *wildlife* populations are very limited or completely absent. Relevant information, where it exists, is more likely to be unpublished and in the heads or files of a few key individuals. The selection and use of the most appropriate DRA tools and interpretation of results may also require the help of individuals with those skills. Therefore, enlisting the collaboration of people with relevant knowledge and expertise will help ensure that the *wildlife* DRA is as technically *robust* as possible within the circumstances.

Table I
Benefits and limitations of individual and collaborative approaches to a wildlife disease risk analysis (DRA)

DRA by a single individual		DRA by collaboration	
Benefits	**Limitations**	**Benefits**	**Limitations**
– Supports rapid decision making – Cheap – No disputes – Relatively minimal effort	– Individual bias – Knowledge and skill limitations – More prone to errors – Less likely to get decision maker support – May alienate other stakeholders not consulted	– Less influenced by individual bias – Broader understanding of problem – Wider knowledge and skills – Less prone to errors – More likely to get stakeholder and decision maker support	– Slower – May be more expensive – Can involve conflicts – Significantly more effort

Socially, disease in *wildlife* and its management has the potential to impact a wide range of people who may have many different and, sometimes, conflicting concerns. These 'stakeholders' may have significant influence on the ability to conduct a meaningful *risk analysis* or the implementation of recommendations arising from it. Each individual or group may have very different concerns, interests and levels of knowledge of the situation. However, as noted by Westley and Vredenburg (1997) and Brückner *et al.* (2010) stakeholders who have been involved in the decision-making process from the outset are more likely to support the outcomes and become involved in implementing the resulting activities.

Politically, the recommendations of the DRA will need to convince those with the necessary policy or decision-making authority, especially if significant changes in social behaviour (e.g. restricting access to previously accessible sites, changes in farm practices, etc.) or commitment of resources are required. Consequently, understanding the political factors at play and the support that may be needed is important. The DRA *risk communication* strategy should identify and involve key decision makers from the outset to help them make informed decisions and thereby help to ensure the success of the DRA exercise.

Some challenges in wildlife disease risk analysis

Before embarking on a *wildlife* DRA it is important to be aware of some of the special challenges associated with analysis of situations involving *wildlife* disease risks.

Complexity There are always multiple variables influencing the introduction, establishment and spread of disease-causing agents within and between populations of single or multiple species. The collaborative, *transdisciplinary* approach recommended in this *Manual* is one way of addressing this challenge. Taking an adaptive management approach in which the DRA includes a schedule to monitor and review its findings and implementation will also help to ensure that new information is captured to expand knowledge and refine decision making over time.

Uncertainty As in all complex situations not all the relevant facts are available when dealing with *wildlife* disease. As noted above, more often than not, available data are scant. Consequently, qualitative analysis is the most common approach used. A comprehensive literature review, the use of appropriate analytical and decision-making tools (such as those provided in this *Manual*) and the explicit recording of assumptions and limitations will ensure the best use of available information, identification of significant data gaps for further research and the level of *uncertainty* decision makers should take into consideration.

Multiple stakeholders As mentioned, invariably there will be a range of people and organisations with diverse and sometimes conflicting interests in any situation involving *wildlife* disease. Identifying key stakeholders and developing an appropriate communications plan at the outset will help to avoid conflicts and ensure that the best available expertise has been incorporated into the analysis.

Transdisciplinary terminology Differences in interpretation of terms will inevitably emerge in a collaborative process involving individuals from a number of disciplines (e.g. veterinary science, ecology, *risk analysis*, etc.). A glossary of commonly used technical terms associated with *wildlife* DRA is included in this *Manual* to help consistency of language and avoid misunderstandings.

Resources Time, money, equipment, people and relevant expertise for a *wildlife* DRA are among the resources often in short supply. The systematic process outlined in this *Manual* is designed to enable a single person with some knowledge of *wildlife* management and access to relevant information and expertise to conduct a basic *wildlife* DRA. However, for situations in which the consequences of disease *transmission* are severe (e.g. threatening the viability of an endangered species) or in which there is a high level of public interest (e.g. threatening human health or economics), a collaborative approach is highly recommended. This will invariably produce a DRA that is more *robust* and better able to withstand critical scrutiny.

The risk analysis process

Figure 4 hereafter provides an overview of the systematic process of DRA described in this *Manual*. For easy reference this figure is also included at the front of the book. When applied in the sequence depicted, each step and its sub-steps build on the work of the previous step.

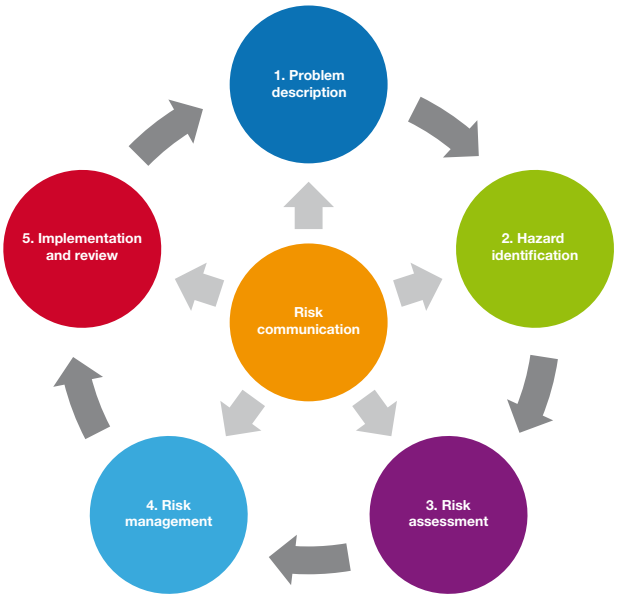


Fig. 4
Steps in the disease risk analysis process

However, insights gained in later steps may suggest a review of assumptions or questions formulated in earlier steps. For this reason it is valuable to constantly keep the context or 'big picture' of the problem in mind. A detailed description of each step in the process follows.

Risk communication

The risk communication step asks 'Who has an interest in, who has knowledge of value to, and who can influence implementation of recommendations arising from the DRA?'

Risk communication is the practice of continuous communication between interested stakeholders and experts and, as depicted in Figure 4, runs throughout the DRA process. Its purpose is to engage with relevant experts and stakeholders in a way that will maximise the quality of the analysis and the probability that recommendations arising will be implemented. It is also essential to determine the level of risk that is acceptable to stakeholders. (See 'Problem description', p. 24).

Tools that can help

- DRA Worksheet, p. 58
- Graphical models, p. 60
- Decision trees, p. 63
- Influence diagrams, p. 66
- Fault trees, p. 68
- Scenario trees, p. 69
- GIS, p. 75
- OIE Handbook, p. 76
- Risk communications plan template, p. 91

Effective communication involves both listening and speaking. The messages heard are influenced by both the content and the manner in which they are delivered and received. While it is beyond the scope of this *Manual* to review the theory and methods of effective communication, some familiarity with this topic is recommended. A useful resource relevant to this text is Jacobson (2009), *Communication Skills for Conservation Professionals*.

Stakeholder and expert identification

The first step in developing a *risk communications* strategy is the identification of stakeholders, experts and key decision makers associated with the issues to be considered. These are identified by answering the questions 'Who has an interest in, and who has knowledge of value to, the DRA topic?' and 'Who may have influence to support or block recommendations resulting from the analysis?' Where communication between relevant experts and stakeholders can be facilitated, opportunities can arise to share information and gain insights that might not otherwise be possible. As all *wildlife* DRA scenarios attract interest from a range of people this applies whether the *risk analysis* is conducted by a single individual or a group. An example of a stakeholder and expert list developed for a DRA focused on Tasmanian devils is provided in Table II.

While it is not always possible to involve a wide range of experts and stakeholders, consideration of who could potentially assist and who might be impacted by the results will be of value in framing the DRA report and its recommendations in a manner appropriate to the audience.

Communications strategy and plan

Following the identification of appropriate stakeholders and experts it is useful to develop a communications strategy and plan (see Table III for an example). This is a helpful tool for thinking through the communication issues associated with a *wildlife* DRA. It is useful to map this out at the start of each *risk analysis* and to continually update it as needed.

The communication plan is developed in consultation with the stakeholders and experts and should include what information they may be able to provide, what information they are interested in receiving and how frequently and in what form it should be delivered.

An example taken from the same Tasmanian devil DRA is provided in Table III. Once the list of stakeholders has been completed the names of specific individuals and their contact details can be added.

Table II
Stakeholder and expert list for Tasmanian devil disease risk analysis workshop, Hobart, 2008

Stakeholder groups and organisations represented	Wildlife disease expert participants
Researchers School of Zoology, University of Tasmania Macquarie University **Captive breeding** Taronga Conservation Society Australia (TCSA) Latitude 42 Environmental Consultants Pty Ltd East Coast Natureworld Trowunna Wildlife Park Australasian Regional Association of Zoological Parks and Aquaria (ARAZPA) Healesville Sanctuary Australian Reptile Park **Indigenous communities** Tasmanian Aboriginal Land and Sea Council (TALSC) **Government departments** Office of the Minister of Primary Industries and Water Department of Primary Industries and Water (DPIW) Department of the Environment, Water, Heritage and the Arts (DEWHA) Reserve and Wildlife Conservation Branch (DECC) Wildlife and Marine Conservation Section (DPIW) **Funding agencies** Foundation for Australia's Most Endangered Species Inc. **Media:** local and national	Cytogeneticist Conservation geneticist Government Veterinary Officer, State of Tasmania Wildlife veterinary pathologist Medical immunologist Field veterinary officers, Save the Tasmanian Devil Programme Representatives of the Steering Committee, Save the Tasmanian Devil Programme and the Australian Wildlife Health Network

Communication etiquette

Communication etiquette should include appropriate acknowledgement of contributors and sources of information and respect of issues of confidentiality and intellectual property. The method of communication should always be tailored to the audience. Where individuals from different disciplines or cultures are involved the use of technical terms should be avoided wherever possible. Where such terms must be used for clarity their meaning should also be explained in non-technical language.

As noted above, the messages received by people are influenced by both the content and the manner of communication. What may be clear to one person may be confusing to another. Misunderstandings can be avoided through initial discussion of the forms of communication best suited to each person or organisation and their specific needs or interests. These could include face-to-face or telephone conversations, meeting minutes, formal reports, oral presentations to groups, a press release, newsletter, email, etc. The emphasis is on effective two-way communication. A periodic survey of stakeholders to monitor the effectiveness of the communications methods employed can be of great value.

Problem description

The problem description step asks 'What is the specific question for this DRA?' and 'What kind of risk analysis is needed?'

The problem description step (sometimes referred to as 'problem formulation' or 'problem identification') outlines the background and context of the problem, and identifies the goal, scope and focus of the DRA. To ensure *transparency*, assumptions and limitations are documented and a statement on the acceptable level of risk formulated, bearing in mind that there are no 'zero risk' options.

Tools that can help

- DRAT, p. 52
- DRA Worksheet, p. 58
- Graphical models, p. 60
- OIE Handbook, p. 76

The *risk communications* plan outlined above is developed concurrently during this phase.

Table III
Extract of a communications plan from the Tasmanian devil disease risk analysis, Hobart, 2008

Group role	Stakeholder/Expert	Information needs	Communication method(s)	When	Responsibility
Operational/ implementation	Managers of devil captive facilities, e.g. wildlife parks	Biosecurity protocol/ animal movement requirements Details of individual animal movements Timing of moves	Personal direct (email, phone, fax, etc.)	Need most lead-in time	Individual coordinator for each movement
	Veterinarians associated with devil health care	As above plus: – Specific *diagnostic tests* required – Medical histories	Personal direct (email, phone, fax, etc.)	Two weeks in advance of movement	As above
Governance	Steering Committee	Overarching information on: protocols, plans, implementation/ update reports, issues	Formal reporting to committee	At three month intervals	Insurance population coordinator
Compliance, auditing and monitoring	Chief Veterinary Officer, Tasmanian *quarantine*, Australian Quarantine Inspection Service	Protocols Movements Issues around biosecurity Reports of breaches	Personal direct (email, phone, fax, etc.) (formally provided with translocation and biosecurity protocols)	Advise at time of movement	Planning team Individual coordinator for each movement
Public	Media (press, radio, television)	Need to have information available so that public can know how to minimise their impact General information on conservation strategy: – Ways to prevent disease spread – Point of contact for information	Via media liaison officer Press release Save the Tasmanian Devil Website (public area) Newsletter	In advance of significant events/ moves that may impact public	Department of Primary Industry and Water media liaison officer

Establishing the goals, scope and focus of the DRA at the outset will provide useful points of reference for ensuring that the DRA, as it proceeds, remains consistent with its original intent. Ultimately, conducting separate problem description and *hazard* identification exercises helps to protect the scientific evaluation of risk (*hazard* identification and *risk assessment* steps) from being overly influenced by political and social issues that may arise during problem description (US Environmental Protection Agency 1998).

There is little consensus in the literature regarding the stage at which this step is completed (Power and McCarty 2002). Problem description is sometimes included within the first step of the *risk analysis* framework along with *hazard* identification (e.g. US Environmental Protection Agency 1998) or is a step undertaken prior to commencing a *risk analysis* (e.g. US Food and Drug Administration 2002). For the purpose of this *Manual*, problem description is the first step in the DRA process (Fig. 4, p. 23).

In the end, whether solutions are difficult or easy to understand or implement, minimising disease risk to *wildlife* is a policy problem for decision makers. Framing the issues within their bigger context and logically describing and organising them will help to determine if a DRA will add value to the policy decision-making process. The problem description step consists of logically describing the overall policy issue at hand in order to define specific questions that need to be thoroughly assessed using the *risk analysis* process. Depending on the complexity of the issues and the information and resources available, this analysis may be conducted in a single meeting or may require a well-facilitated workshop or series of workshops.

Once a problem has been described it will be possible to estimate the level of detail required in the DRA. For example, when conducting a DRA for a *wildlife* translocation programme, fewer *hazards* may need to be assessed in detail if the translocation pathway does not cross an ecological or geographical barrier (Sainsbury *et al.* 2012). In these

relatively short distance translocations source and destination *hazards* can effectively be considered equal. (See Tool 1 in this *Manual* for an example of a process to assist this decision making).

Questions to assist problem description

In an effort to direct this step the US Environmental Protection Agency (1998) poses a series of questions. These questions are listed below, with some having been adapted for the purposes of this *Manual*:

- What is the nature of the problem?
- What are the management goals and decisions needed, and how will the *risk analysis* help?
- What is the ecological level of concern (population, community, *ecosystem*)?
- Are there any policy or regulation considerations?
- What precedents are set by similar DRAs and previous decisions?
- What is the cultural and political history and current context of the problem as represented through the eyes and values of different stakeholders?
- What resources (e.g. personnel, time, money) are needed and available?
- What level of risk is acceptable?
- What documents or data exist to describe the state of knowledge of the problem?

Addressing these questions may highlight other types of information not previously recognised as needed. DRAs frequently proceed without all the information one might wish for and extrapolations from what information is available must be made. It is important to make explicit the areas and extent of *uncertainty* that is likely given the available information and resources. Subsequent steps of the DRA may aid in the identification of missing data or knowledge gaps and can thereby help to direct future research. The following two examples of a DRA problem description are provided to illustrate the application of these concepts to actual *wildlife* DRA scenarios.

Problem description example 1 Disease risk analysis for tuberculosis infection in an orang-utan (*Pongo pygmaeus*) reintroduction programme

Based on a DRA submitted by Fransiska Sulistyo and Rosalie Dench, The Borneo Orang-utan Survival Foundation at Nyaru Menteng

Note that this and other examples are specific to the site and circumstances described and may not be appropriate for other locations.

Context

The Central Kalimantan Orang-utan Reintroduction Program of The Borneo Orang-utan Survival Foundation at Nyaru Menteng (CKORP-NM BOSF) is taking care of more than 600 orang-utans in the centre. At the moment there are 14 orang-utans (2.3%) that have been identified as non-clinical carriers of the bacterial agent of tuberculosis, *Mycobacterium tuberculosis*. They are kept in an isolated facility within the centre but are taken care of by technicians (keepers) who also care for the rest of the population. Resources are not available to assign dedicated technicians to the exclusive care of the infected orang-utans.

Tuberculosis is a *contagious disease* that may cause serious illness in primates, including humans and orang-utans. The disease is *endemic* in the human population, especially in the region of Palangkaraya, within the province of Central Kalimantan.

Goal of the DRA

The risk assessment question is: 'What is the risk of transmission of tuberculosis to and between the orang-utans within, and living near to, the Nyaru Menteng Reintroduction Centre?'

The goal of the DRA is to develop a plan to minimise the risk of spread of tuberculosis to those orang-utans in the Nyaru Menteng centre currently considered to be uninfected, and to improve confidence that orang-utans selected for reintroduction to the wild are free of tuberculosis.

Scope and focus

- To identify disease transmission pathways to healthy orang-utans in the centre from the infected orang-utans and from other potential carrier mammals living in and around the centre (orang-utans and other *wildlife*: macaques, rodents, domestic animals, etc.) including workers and local villagers.

– To assess the relative risks of the tuberculosis transmission pathways to uninfected orang-utans and identify critical control points at which to apply risk mitigation actions.

– To evaluate risk mitigation options and develop an implementation and review plan.

Assumptions

– That tuberculosis is not present in the general population of orang-utans in the centre, nor in the wild population of orang-utans living near to the centre, and

– that tuberculosis is not present in *wildlife reservoirs* at sites selected for orang-utan reintroduction, and

– that disease has the potential to cause mortality in orang-utans.

Limitations

– There is no standardised procedure or 'gold standard' for diagnosis of tuberculosis infection in orang-utans. Screening and diagnostic methods available either have low sensitivity (culture may detect only 60% of active cases) or low specificity (tuberculin skin test can show 60% positive in apparently healthy orang-utans with no known exposure to tuberculosis [Calle 1999]). The resources for more advanced molecular diagnostic tests are lacking, and these methods have not been validated for use in orang-utans.

– The long-term effect of a tuberculosis infection in orang-utans is unknown.

– Risk mitigation strategies must ensure that the welfare of the infected orang-utans is not compromised. This includes keeping them in a healthy condition and enabling them to express natural behaviours with sufficient stimulation to maintain their mental and physical welfare.

– Euthanasia of clinically healthy carriers of *Mycobacterium tuberculosi*s is, politically, unacceptable.

Acceptable levels of risk

It is acknowledged that there is a population of tuberculosis-infected, but healthy, orang-utans within the reintroduction centre. Given the limitations to management of these animal outlined above, this is unlikely to change in the short to medium term. Therefore, the continued presence of a small number of infected orang-utans held in isolation from other orang-utans is considered an acceptable level of risk.

Problem description example 2 Foot and mouth disease risk analysis in Mongolian gazelles (*Procapra gutturosa*) on the Eastern Steppe of Mongolia

Based on a DRA submitted by Enkhtuvshin Shiilegdamba and Amanda Fine, Wildlife Conservation Society (WCS) Mongolia Country Programme, Ulaanbaatar, Mongolia

Context

Mongolian gazelles are one of Asia's last *wildlife* migration spectacles, with herds of over 1 million individuals moving nomadically across the Daurian Steppe Eco-region, concentrated in the Eastern Steppe of Mongolia. Mongolian gazelle are listed as endangered in the Mongolian Red List of Mammals (Clark *et al.* 2006) owing to decreases in both the range and the numbers of this species in recent decades. The Mongolian gazelle herds are a source of pride for local people, a source of protein for subsistence hunters and a potential focus of nature-based tourism in the region (Heffernan 2005). Overhunting, habitat loss, die-off due to disease and competition with livestock for forage have contributed to the species' decline, and recent investments in the extractive industries (oil and mineral extraction) have put additional pressures on the landscape (Lhagvasuren and Millner-Gulland 1997; Olson 2007; Heiner *et al.* 2011).

Although the role of mining in Mongolia's economy is growing, the livestock sector remains a major component and will continue to employ the majority of Mongolians. On Mongolia's Eastern Steppe, Mongolian gazelle are an important part of the grazing eco-system and there is a strong desire among government agencies and conservation organisations to co-manage the rangelands for *wildlife* and livestock (Garratt and Chimed-Ochir 2001; Heffernan 2005; Wildlife Conservation Society 2009; Olson *et al.* 2010; Wildlife Conservation Society 2010).

To achieve this, a number of issues must be addressed, including the potential fragmentation effects of roads, railroads and other infrastructure developments in the region. However, the subject of this case study is managing the risk of livestock/*wildlife* disease transmission with a focus on foot and mouth disease virus (FMDV). Foot-and-mouth disease is one of the major threats to livestock and *wildlife* such as Mongolian gazelle on the Eastern Steppe. Foot and mouth disease is a highly contagious, viral disease that affects most ruminant and porcine species. Periodic outbreaks on Mongolia's Eastern Steppe affect Mongolian gazelles as well as livestock such as cattle, sheep, goats and camels.

At least four new FMDV incursions occurred in Mongolia between 2000 and 2010: three belonging to serotype O and a single Asia 1 introduction in 2005. These introductions were part of an Asian pandemic that affected many countries.

Country-wide livestock *surveillance* conducted in 2007 indicated that FMD was not *endemic* in livestock populations in Mongolia. Serological surveys of gazelles conducted by the Wildlife Conservation Society (WCS) in 1998–1999 and 2005–2008 (Bolortsetseg *et al.* 2012) demonstrated that antibodies were either not present in gazelle populations before livestock outbreaks (1998–1999) or declining to non-detectable levels between livestock outbreaks (2005–2008). However, during an FMD outbreak in livestock in 2001, researchers detected antibodies in 67% (22/33) of gazelles tested (Nyamsuren *et al.* 2006). Although sample sizes were not large, this finding suggests that, during widespread FMD outbreaks in livestock across the Eastern Steppe of Mongolia, Mongolian gazelle do become exposed to the virus.

Foot and mouth disease may threaten the long-term persistence of the Mongolian gazelle. The threat is both direct, through morbidity and mortality, and indirect, through disease management actions that may have additional negative impacts on the species (Nyamsuren *et al.* 2006; Thomson 2011; Bolortsetseg *et al.* 2012). While mass culling of gazelle has been discussed as a management option during outbreaks of FMD in livestock, it has never been carried out as the perceived financial and biodiversity costs have been considered too high. Management actions directed at gazelle in Mongolia to date have included:

- chasing gazelle suspected of being exposed to FMD away from livestock or disease quarantine zones
- selectively culling gazelle that appear to be clinically affected by FMD (weak and lame).

Calls for science-based national policy approaches to FMD control, which take into account the conservation value of species such as the Mongolian gazelle, have been made by local and national conservation organisations in Mongolia including the Wildlife Conservation Society, the Worldwide Fund for Nature (WWF), The Nature Conservancy (TNC) and citizens through the media (*Daily News*, 5 October 2010, p. 12; *Daily News*, 9 October 2010, p. 6; *Udriin Shuudan*, 5 October 2010, p. 11; *Unuudur*, 4 October 2010, p. C2; *Unuudur*, 11 October 2010, p. A6).

Reviews of the literature and official FMD disease reports suggest that one of the seven FMD outbreaks that occurred between 2000 and 2010 may have been introduced by Mongolian gazelles but that the six other outbreaks were introduced by other means (Thomson 2011). To date there has been no clear epidemiological investigation of the role of *wildlife* in FMD introduction in Mongolia and further study is needed.

Goals, scope and focus

The DRA question is 'What is the risk of Mongolian gazelles facilitating FMDV transmission to domestic livestock on the Eastern Steppe of Mongolia?'

The goal of this WCS-led DRA is to develop a science-based FMD control and management policy for the Eastern Steppe of Mongolia incorporating appropriate actions for the conservation of Mongolian gazelles.

The scope will be confined to analysis of relevant published and unpublished information on FMD and the population biology of Mongolian gazelles, combined with the input of relevant experts and stakeholders.

The focus is the long-term sustainability of Mongolian gazelle populations on the Eastern Steppe along with free ranging livestock.

Assumptions

- The control of FMD will remain a high priority for the Mongolian government, given the important role of the livestock sector in the national economy and the livelihoods of the majority of Mongolian people.
- Serological *surveillance* in both livestock and Mongolian gazelle populations will remain an important part of FMD management and control in Mongolia.
- There is general acceptance that FMDV spills over to Mongolian gazelle populations during livestock outbreaks and these populations may transmit the disease among *wildlife* and livestock populations as the gazelle exposure to FMD was confirmed during FMD outbreaks on the Eastern Steppe.
- Mongolia is currently free from FMD with an ongoing livestock FMD *vaccination* programme.

Limitations

Population-based longitudinal studies of FMD on Mongolia's Eastern Steppe (in Mongolian gazelle and livestock) are lacking. Consequently this DRA must draw upon the limited studies and FMD outbreak reports from Mongolia that are available. Comparable studies of populations in similar systems must be

used for this risk analysis pending further research within the Eastern Steppe.

Discussion of acceptable levels of risk

Owing to the huge economic, social, animal welfare and conservation impacts of FMD there is a low risk tolerance associated with this disease in Mongolia. A national FMD-free status is the government's ultimate objective. (The Mongolian Government has already applied to the World Organisation for Animal Health for an FMD-free zone status in the western part of the country where this disease has not been reported since 2002).

Hazard identification

The hazard identification step asks 'What can cause disease in the population(s) of concern?', 'How can this happen?' and 'What is the potential range of consequences?'

A *hazard* is defined as a biological, chemical or physical agent in, or a condition of, an animal or animal product with the potential to cause an adverse effect on health.

When embarking on the process of *hazard* identification it is important to consider both the problem of concern as well as the broader environmental context within which the *wildlife* population resides (see Fig. 3).

Tools that can help

- DRA Worksheet, p. 58
- Paired ranking, p. 59
- Graphical models, p. 60
- Decision trees, p. 63
- Influence diagrams, p. 66
- Fault trees, p. 68
- Scenario trees, p. 69
- Cmap, p. 74
- GIS, p. 75
- OIE Handbook, p. 76

The purpose of the *hazard* identification step is to identify all possible health *hazards* of concern. Criteria are established for ranking the importance of each *hazard* and its possible direct and indirect consequences within the bounds of the defined problem. Exclude hazards that have a zero or negligible probability of release or exposure and construct a scenario tree for the remaining, higher priority hazards of concern. These can then be further investigated using tools for *risk assessment* (Harvey *et al.* 1995; Sarnet *et al.* 1998; Armstrong *et al.* 2002; Clancy *et al.* 2009).

The completion of this step involves a thorough review of published literature and unpublished sources and consultation with relevant experts.

The previous 'Problem description' step may have resulted in two different scenarios:

1. There is already a problem identified that is specifically associated with one or more well-defined hazards that stakeholders believe need to be assessed (e.g. an outbreak of salmonellosis in an island population of an endangered bird species; the introduction of rabies into a rabies-free island; the spread of West Nile virus after its emergence in North America) OR

2. The problem is broader in scope and specific priority hazards have not yet been defined (e.g. a widespread population decline due to unknown factors).

In the latter case, the *hazard identification* process should list all potential hazards. In the former scenario, the *hazard identification* step may be relatively simple but performing and documenting this step provides additional *transparency* to the process. It also helps to validate or challenge assumptions that may have been made during the problem description step. For instance, in a mass mortality of free-living penguins due to the fungal disease aspergillosis, discussion during the problem description step revealed that this infection was not the primary hazard (as originally thought) but a consequence of chronic stressful environmental disturbances due to multiple off-shore mining and fishing activities.

If a specific aspect of the *hazard identification* step is omitted the decision should be justified. For example in a DRA undertaken for a translocation that does not cross an ecological or geographic barrier, it should be stated that source hazards have been discounted for this reason.

Hazard categorisation

In order to minimise the risk of overlooking any potential hazards it can be helpful to consider the following categories:

- *Infectious* (i.e. the entry and development or multiplication of a parasite in the body of a host, where it may or may not cause disease):
  - viral
  - bacterial
  - fungal
  - parasitic (external and internal *macroparasites*)
  - prions (infectious agents responsible for transmissible spongiform encephalopathies).

– *Non-infectious* (i.e. diseases that cannot be transmitted between organisms):
  - toxic
  - genetic, developmental
  - degenerative
  - neoplastic (cancer causing)
  - nutritional
  - metabolic
  - traumatic (e.g. road kill)
  - immune-mediated (e.g. allergic)
  - environmental (e.g. pollution of air, soil, water, radiation, climatic events such as floods or droughts).

Hazard consequences

Considering the potential direct and indirect consequences of each hazard is a useful exercise when deciding which hazards should be subjected to a full risk assessment. This is discussed in some detail in a Council of Canadian Academies 2011 publication 'Healthy Animals Healthy Canada' and summarised below. These authors suggest the categories of consequences for consideration illustrated in Figure 5.

Examples of the listed consequences include:

– **Animal health** – direct consequences on the individual health of animals.

– **Animal welfare** – animal suffering either directly associated with the hazard or indirectly associated as a result of efforts to mitigate the effects of the hazard such as holding in quarantine and handling for collection of diagnostic samples.

– **Human health** – direct consequences from zoonotic disease or indirect effects such as food security due to loss of *wildlife* or domestic animal populations or ecosystem services such as pollination by bees afflicted by colony collapse disorder.

– **Social and psychological** – a component of human health that can be severely impacted by loss of animals or measures to control outbreaks such as mass culling, restrictions on movements and loss of income.

– **Environmental and ecological** – often the most complex and difficult to predict. Examples include the increase in rotting carcases associated with the decline in top predators such as Tasmanian devils in Australia or scavengers such *Gyps* spp. vultures in Asia.

– **Economic** – massive losses of jobs, income and animals have been associated with measures to control outbreaks of animal diseases such as bovine spongiform encephalopathy (BSE) and highly pathogenic avian influenza

Fig. 5
Categories of consequences associated with animal health hazards
(From Council of Canadian Academies, 2011)

– **Political** – as previously discussed there are always political consequences to disease in *wildlife*, the extent of which will vary with the species involved, the severity of impacts and the level of public concern. In considering the range of consequences of various risk management options it should be recognised that actions that benefit some stakeholders may disadvantage others.

– **National Security** – these consequences are usually associated with widespread impacts of animal disease on human health, economics, social stability and the associated politics. A good example is a pandemic due to highly pathogenic avian influenza.

Sources of information and transparency

In addition to an extensive literature review, efforts should be made to access unpublished information (e.g. from diagnostic laboratories, researchers, etc.) and seek expert opinion from a multidisciplinary group of stakeholders with relevant expertise. If this process of consultation is undertaken, it is important that it be done in a formal and structured manner (such as an official workshop forum or questionnaire). It should be transparent and inclusive in nature to ensure that viewpoints from all participants are heard and considered (See Tool 17: Formal elicitation of expert opinion as an example of one such process).

Hazard identification example 1 Kakapo (*Strigops habroptilus*) disease risk analysis and management planning workshop, 2008

R.M. Jakob-Hoff, CBSG Australasia; NZCCM, Auckland Zoo, New Zealand

The kakapo is an intensively managed critically endangered *endemic* species restricted to a small number of predator-free offshore islands in New Zealand. Emphasis at this DRA workshop was placed on the risks associated with anticipated movements of people and birds between Codfish Island/Whenua Hau and the New Zealand mainland owing to the major kakapo breeding event anticipated for the summer of 2008–2009. From a review of published and unpublished sources circulated prior to the workshop the following hazards of concern were identified for kakapo (Table IV).

For each disease a brief synopsis was provided as a basis for discussion by stakeholders. An example is provided below.

Table IV
Disease hazards identified for kakapo

Infectious	Non-infectious
Viral Psittacine beak and feather disease virus (BFDV) Psittacine polyomavirus Psittacine herpesvirus (Pacheco's disease) Highly pathogenic avian influenza Psittacine pox Avian paramyxovirus 1 (Newcastle disease) **Aetiology unknown but suspected viral** Myeloproliferative disease of Antipodes parakeets **Bacterial** Salmonellosis Yersiniosis Erysipelas Chlamydiosis/Psittacosis Macrorhabdosis (Megabacteriosis) **Fungal** Aspergillosis **Internal parasitic** Avian malaria Coccidiosis Trichomoniasis Cryptococcosis **External parasitic** Mites Ticks Lice Fleas Hippoboscid flies	Aflatoxicosis

Salmonellosis

Organism: The zoonotic bacterium *Salmonella enterica* subsp. *enterica* serovar Typhimurium is one of the most common species of *Salmonella* found in psittacine birds.

Clinical signs: Asymptomatic carriers are common. The disease can manifest in many forms but the most common is diarrhoea or sudden death.

Incubation period: As a carrier state is common, the time from infection to onset of *clinical signs* in birds can be highly variable; in humans it is 8 to 48 hours.

Sources of infection: The intestinal tract of a wide range of vertebrate animals including other birds, rodents and people

Transmission: The infection is usually transmitted by ingestion of faecally contaminated material but some serotypes (e.g. *S.* Pullorum in poultry) can also be transmitted in utero.

Wildlife disease in New Zealand: Salmonellae are widespread throughout New Zealand although some strains have a more local distribution. *S.* Typhimurium DT195 caused deaths in the *endemic* passerine, hihi (*Notiomystis cincta*) in 2006, as did DT160 in house sparrows (*Passer domesticus*) in 2007. Both serotypes were also isolated from sick people in New Zealand around the same time.

Control: The organism is susceptible to most disinfectants and to temperatures over 60°C.

Prevention:

- Avoid exposure to rodents.
- Personnel working with kakapo should observe strict hand hygiene.
- Avoid overcrowding in captivity.
- Test for the organism during *quarantine*.

References

Alley *et al.* 2002; Hirsch 2004; Alley and Gartrell 2006.

Hazard identification example 2 Risk analysis for the import of sand tiger (grey nurse) shark (*Carcharias taurus*) into New Zealand (Prepared for the New Zealand Ministry of Agriculture and Forestry)

R. Jones, The Aquarium Vet, Moorabin, Australia

In order to identify all the diseases, *pathogens* and parasites associated with the sand tiger shark, a comprehensive literature review was undertaken utilising the services and databases of the Commonwealth Scientific and Industrial Research Organization (CSIRO) Australian Animal Health Laboratory (AAHL) at Geelong, VIC, Australia.

The initial literature search revealed very few diseases recorded in the sand tiger shark and so the search was extended to include diseases in sharks in general particularly with respect to viruses and bacteria. Another two resources used extensively were the *Elasmobranch Husbandry Manual* by Smith *et al.* (2004) and *Fish Medicine* by Stoskopf (1993). The author also contacted a network of professional colleagues in public aquaria and other institutions around the world, in particular the United States and South Africa (these were listed in Appendix 2 of the original document but are not included here).

For each organism identified the epidemiology is briefly discussed, including a consideration of the following questions (Table V):

1. whether the imported sand tiger sharks could act as a vehicle for the introduction of the organism, and

2. if the organism requires a *vector*, whether competent *vectors* might be present in New Zealand, and

3. whether the organism is *exotic* to New Zealand but likely to be present in exporting countries, and

4. if it is present in New Zealand:

   – whether it is under official control, which could be by government departments, by national or regional pest management strategies or by a small-scale programme, or
   – whether more virulent strains are known to exist in other countries.

For any organism, if the answer to question 1 is 'yes' (and the answer to question 2 is 'yes' in the case of organisms requiring a *vector*) and the answer to either question 3 or 4 is 'yes', it is classified as a potential hazard requiring *risk assessment*.

Under this framework, organisms that are present in New Zealand cannot be considered as potential hazards unless there is evidence that strains with higher *pathogenicity* are likely to be present in the sand tiger sharks to be imported. Therefore, although there may be potential for organisms to be present in the imported sand tiger sharks, the risks to human or animal health are no different from risks resulting from the presence of the organism already in this country.

Table V
Hazard identification for proposed importation of sand tiger sharks (extract)

Disease name	Scientific name	Recorded in sand tiger shark	Recorded in other sharks	Vector of a hazard	Already in NZ	Potential hazard	Reference
Virus							
Dusky smooth-hound viral dermatitis	Herpesvirus	No	Yes	No	No	No	Terrell (2004)
Viral erythrocytic necrosis	Iridovirus	No	Yes	No	No	Yes	Terrell (2004) Johnston (1975) Khan and Newman (1981)
Bacteria							
Shark meningitis	*Vibrio carchariae* (syn. *V. harveyi*)	Yes	Yes	No	Yes	No	Grimes *et al.* (1984)
Vibrio spp.	*Vibrio* spp.	Yes	Yes	No	Yes	No	Terrell (2004) Tuttle *et al.* (2008)
Furunculosis	*Aeromonas salmonicida* subsp. *Salmonicida*	No	Yes	No	No	Yes	Briones *et al.* (1988)
Aeromonas hydrophila	*Aeromonas hydrophila*	Yes		No	Yes	No	Gál *et al.* (2005)
Flavobacterium spp.	*Flavobacterium* spp.	No	Yes	No	Yes	Yes	Terrell (2004)
Miscellaneous bacteria	*Citrobacter freundii*	Yes		No	Yes	No	Stoskopf (1993)
	Pseudomonas aeruginosa	Yes		No	Yes	No	Stoskopf (1993)
	Pseudomonas fluorescens	Yes		No	Yes	No	Stoskopf (1993)
	Staphylococcus epidermidis	Yes		No	Yes	No	Craig A. Harms, North Carolina State University, pers. comm. November 2009
	Enterococcus faecalis	Yes		No	Yes	No	Craig A. Harms, North Carolina State University, pers. comm. November 2009

Example disease synopsis:

Shark meningitis

Aetiological agent: *Vibrio carchariae* (syn. *Vibrio harveyi*).

OIE listing: This disease is not OIE listed.

New Zealand status: *V. harveyi* is already present in New Zealand.

Epidemiology: *V. carchariae* was originally cultured and then identified as a new species from a brown shark or sandbar shark (*Carcharhinus plumbeus*) that died in an aquarium (Grimes *et al.* 1984). It was the first recorded *Vibrio* spp. in an elasmobranch. In brown sharks, meningitis is a prominent feature of the disease and *V. carchariae* has been isolated from cerebrospinal fluid. There has been natural infection in the sand tiger shark. It is important to note that all cases have been in captive sharks originally from the mouth of the Delaware Bay (Stoskopf 1993).

In a study by Pedersen *et al.* (1998), *V. carchariae* was shown to be a junior synonym of *V. harveyi*. This is confirmed by the National Centre for Biotechnology Information (2009).

Conclusion: As *V. harveyi* is already present in New Zealand (Biosecurity New Zealand, 2005), it will not be considered further in this import risk assessment.

Hazard identification example 3 Tasmanian devil disease risk analysis

Initially a list of over 60 infectious and non-infectious potential hazards were identified from a search of the literature (including references provided by Dr Philip Ladd and Dr Peter Holtz) and unpublished cases recorded in the Australian Wildlife Pathology Registry (supplied by Dr Karrie Rose, Taronga Zoo, Sydney). An excerpt is shown in Table VI below.

In this case, the expert knowledge of a group of *wildlife* veterinarians and researchers working with Tasmanian devils was combined in a workshop setting to review this list and identify a subset for further analysis based on their understanding of which were the most probable and significant health hazards to the Tasmanian devil. Those chosen are highlighted in bold in the following list.

Infectious hazards

- **Devil facial tumour disease (DFTD)**
- **Salmonellosis**
- **Pseudotrichinosis (Trichinella)**
- **Ectoparasites (mites, *Uropsylla*, ticks)**
- Sarcocystosis (muscle condition)
- Toxoplasmosis?
- Fungal infections
- Intestinal helminths (cestodes, nematodes)
- Protozoa (Giardia, Entamoeba, Sarcocystis sporocysts, coccidia)
- Bacterial infections (abscess, septicaemia etc)
- Viral infections (herpesvirus, endogenous retroviruses)
- Mycobacterial diseases

Non-infectious hazards

- **Young age onset neoplasia (other than DFTD)**
- **Other neoplasia (other than the above)**
- **Lymphoproliferative diseases**
- Metabolic diseases (eg osteodystrophy)
- Degenerative diseases (eg spondylosis and osteoarthritis in aged animals)
- Nutritional disease (eg obesity)
- Allergic dermatitis
- Road accidents (note devils are attracted to scavenge other road kill so are more at risk)[2]
- Persecution (poisoning – mostly with organophosphates)
- Predation by dogs (especially two dogs together)
- Shooting.

Reference

Conservation Breeding Specialist Group, 2008.

Table VI
Excerpt from Tasmanian devil (non-devil facial tumour disease) hazard review

Disease Category	Disease	Comment	Author	Year	Title	Journal/Publisher
Allergy	Hypersensitivity dermatitis	Adult female	Rose Karrie	2007	Australian Registry of Wildlife Pathology, Taronga Conservation Society, Australia, pers. comm.	Tasmanian Devil – Australasian wildlife pathology register
Bacterial	Salmonellosis	Comment that this is one of the most common conditions in larger dasyurids but reference does not mention Tasmanian devil (also note high carrier rate in marsupials)	Finnie Edward P.	1988	Diseases and Injuries of Other Australian Mammals	in Proceedings No. 104 'Australian Wildlife', University of Sydney Post-Graduate Committee in Veterinary Science
Neoplasia	Neoplasms	Review	Griner Lynn A.	1979	Neoplasms in Tasmanian Devils (*Sarcophilus harrisii*)	J. Nat. Cancer Inst. 62, 589–595
Non-infectious	Ulcerated alimentary canal	Ulcers in stomach, pylorus or duodenum and anaemia. Possible association with stress in captivity	Griner Lynn A.	1983	Pathology of Zoo Animals – Ch 35 Mammals	Zoological Society of San Diego

2 Road kill mortality can be very high in local areas, e.g. 50% devils and 100% quolls in one area where a road was upgraded and average vehicle speed increased from 40 to 80km/hour. Furthermore, 20% mortality was recorded in Fraycinet National Park in a drought year.

Risk assessment

The risk assessment step asks 'what is the likelihood and what are the consequences of a specified hazard occurring within an identified pathway or event?'

The purpose of the *risk assessment* step is to assess:

- the likelihood of release (introduction) into the area of concern
- the likelihood that the species of interest will be exposed to the hazard once released, and
- the consequence of exposure.

On this basis the hazards can be prioritised in descending order of importance.

Tools that can help

- Stella and Vensim, p. 57
- DRA Worksheet, p. 58
- Paired ranking, p. 59
- Graphic models, p. 60
- Cmap, p. 74
- OIE Handbook, p. 76
- @Risk, p. 78
- OUTBREAK, p. 78
- PopTools, p. 80
- Formal elicitation of expert opinion, p. 84
- Netica, p. 86
- Precision tree, p. 87
- Vortex, p. 88
- RAMAS, p. 90
- Monte Carlo modelling, p. 103

Stated another way, disease risk assessment is the process of estimating the likelihood of a pathogenic agent (from any defined source) entering, establishing or spreading in a country, zone or population and its accompanying impact(s) on animal or human health, the environment or the economy. It is important that this be specifically laid out during the problem description step.

Risk assessment may be qualitative, expressed in terms such as 'high', 'medium' or 'low' risk, or quantitative, expressed in numerical terms such as 'one disease outbreak per 100 animal introductions' or 'failure to correctly identify one diseased herd out of 100'.

For each hazard identified in the preceding step, the best available information is used to assess the likelihood of introduction into the environment of concern (*release assessment*) and exposure of the population of interest to the hazard (*exposure assessment*). If there is a significant risk of exposure an assessment is made of the consequences (biological, environmental, social, economic) of the entry, establishment or spread of the hazard, together with an estimate of the likely magnitude of the consequences. This process provides the basis for prioritising hazards to determine whether or not risk mitigation measures are warranted.

Valid risk assessments are:

- based on a specific question
- transparent
- fully disclose the assumptions made
- include a discussion of factors that add to the uncertainty surrounding conclusions

Example risk assessment questions (from Unwin and Travis 2009):

'What is the likelihood of introducing TB (tuberculosis) into lemurs in Betampona given that the population is TB-free?'

'What is the probability of introducing chimpanzee x into the wild with pathogen y?'

In the *risk analysis* methodology adopted by the World Organisation for Animal Health (OIE), *risk assessment* follows *hazard identification*, and comprises four steps: *release assessment*, *exposure assessment*, *consequence assessment* and *risk estimation* (Brückner *et al.* 2010).

The assessments commonly associated with the OIE usually revolve around international trade in animals or animal products. In the biodiversity conservation and *wildlife* health arena, this basic framework needs to be adapted to many different kinds of scenarios. The output of the *risk assessment* can then be used to decide whether the risk is acceptable as it stands or whether mitigation measures are required to reduce the risk to an acceptable level. This method is versatile and can be applied to various risk questions, making it the system of choice for many risk assessors (Brückner *et al.* 2010).

Scenario trees

Prior to embarking on the disease risk assessment itself, it can be helpful to draw a scenario tree (see Fig. 6 and DRA Tool 10, Scenario trees) for each hazard under consideration. This will facilitate the identification of the various biological pathways leading to exposure of the susceptible animals or people to the hazard as well as potential 'outbreak' scenarios (sometimes called 'pathways analysis'; see Fig. 6).

Uncertainty

As in all complex situations, not all the relevant facts are available, and this is always so when dealing with *wildlife* disease where available data are generally scant. Consequently, qualitative analysis is the most common approach used in *wildlife* disease risk assessments. A comprehensive literature review, the use of appropriate analytical and decision-making tools (such as those provided in the Tools section of this *Manual*) and the explicit recording of assumptions and limitations will ensure the best use of available information and identification of significant data gaps for further research and the level of *uncertainty* that decision makers should take into consideration.

However, it is important to distinguish the precision of a risk assessment from its accuracy. For instance the population management software, Vortex (see Tool 20), can calculate population growth rates to any number of decimal places in a very repeatable way. But the predicted rate could be highly inaccurate, i.e. very different from the 'true' rate expected in the 'real' system under study. In a DRA it is more important to estimate and discuss the *accuracy* of the assessments, rather than the precision.

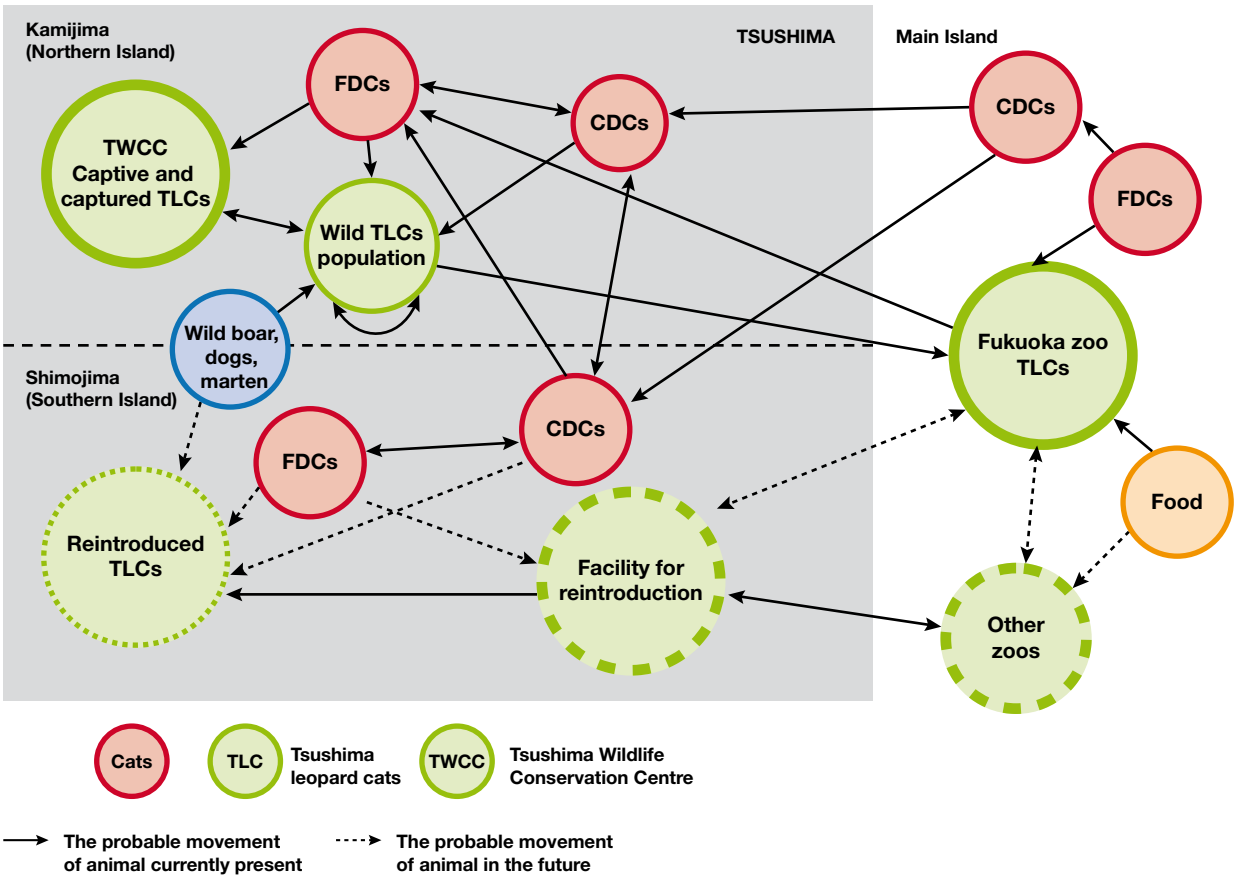


Fig. 6
Possible pathogen transmission pathways relating to Tsushima leopard cats
Diagram of possible pathways of transmission of infectious disease agents between Tsushima leopard cats (TLCs), feral domestic cats (FDCs) 'captive' (pet) domestic cats (CDCs) and other animals within specified geographic regions in Japan (Murayama *et al.* 2006)

Qualitative vs quantitative risk assessments

In *qualitative risk assessments* the likelihood of the outcome, or the magnitude of the consequences, is expressed in terms such as 'high', 'medium' or 'low'[3]. In *quantitative risk assessments* the likelihood is expressed in terms such as 'one disease outbreak per 100 animal introductions' or 'failure to correctly identify one diseased animal out of 100'. Both qualitative and quantitative approaches to *risk assessment* are valid and, in practice, all *risk assessments* are usually first conducted qualitatively (MacDiarmid 2001; MacDiarmid and Pharo 2003). Only if further insight is required is it necessary to attempt to quantify the risk (Brückner *et al.* 2010). As North (1995) explains, quantitative '… *risk analysis* is best used to develop insights, and not to develop numerical results which might mistakenly be considered to be highly precise. The discipline of numerical calculation can help to sharpen thinking about risks involving high levels of complexity and *uncertainty*, and thereby enable conclusions to be drawn which could not have been reached solely on the basis of qualitative reasoning.'

Semi-quantitative risk assessment

Semi-quantitative methods have been promoted by some as being more *objective* than strictly qualitative techniques. These methods involve assigning numbers in the form of probability ranges, weights or scores to qualitative estimates and combining them by addition, multiplication, etc. with the goal of achieving a greater level of objectivity. While superficially appealing, there are, however, significant problems with such semi-quantitative methods when the numbers are assigned and combined arbitrarily without adequate *transparency*. Inconsistent outcomes frequently arise and conclusions are reached that may be statistically and logically incorrect. These methods do not offer any advantages over a well-researched, transparent, peer-reviewed qualitative approach and seldom stand up well in adversarial situations (Brückner *et al.* 2010)

However, provided that there is an explicitly stated interpretation of a numerical scale and that it is consistently applied, the assignment of a 'score' to the designations of a qualitative assessment can be a useful means to gain consensus on relative risk from a diverse group of experts when discussing and assigning levels of risk across a range of criteria. An example in which such a scoring system was used to rank disease hazards is provided in Table VII below.

The rankings against each disease in this table were based on consideration of published and unpublished data combined with expert opinion elicited at a DRA workshop. To ensure *transparency* an explanation of the ranking ascribed to each disease was provided. An example of this for the disease erysipelas is given below.

Disease: Erysipelas

Erysipelas is caused by infection with the bacterium *Erysipelothrix rhusiopathiae*. This organism is shed in the faeces of affected animals, and may survive for long periods in the environment.

Table VII
Excerpt of semi-quantitative assessment for diseases hazards to kakapo, *Strigops habroptilus*, on Codfish Island, New Zealand

Disease	1. Likelihood of susceptibility	2. Likelihood of exposure	3. Severity for the population	Impact *(columns 1 × 2 × 3)*
Erysipelas (*Erysipelothrix rhusiopathiae*)	5	5	3	75
Psittacine circovirus (BFDV)	5	2	5	50
Salmonellosis	3	5	3	45
Chlamydiosis (Psittacosis)	5	3	2	30
Psittacine polyomavirus	5	1	5	25
Trichomoniasis (*Trichomonas* spp.)	5	4	1	20
Aflatoxicosis	3	1	3	9
Myeloproliferative disease of Antipodes parakeets	1	1	1	1
Pacheco's disease (Psittacine herpesvirus)	5	0	5	0

(Scale for columns 2 and 3: 0 = zero probability; 1 = highly unlikely; 2 = unlikely; 3 = moderately likely; 4 = likely; 5 = highly likely)
(Scale for column 3: 0 = nil, 1= very low; 2 = low; 3 = moderately severe; 4 = severe; 5 = very severe)
From Jakob-Hoff 2008

3 As these terms are context specific, definitions of each should be included whenever they are used in a DRA.

Likelihood of susceptibility (5): Kakapo have been shown to be highly susceptible, particularly young birds when stressed.

Likelihood of exposure (5): Given the widespread occurrence in seabirds on Codfish Island, exposure is highly likely. This is supported by serological surveys of kakapo.

Severity for the population (3): Moderate – an outbreak severely impacting the population is unlikely.

Reference

Gartrell *et al.* 2005.

Release assessment

The *release assessment* results in an estimate of the likelihood that the hazard of concern is present or will be introduced into the environment of concern, or exit its source or *reservoir*, and thus be 'released' into an environment where susceptible animals or humans may be exposed.

Depending upon the natural history of the disease, release may result in contamination of the environment or in risk of direct exposure between animals or humans. Examples include the reintroduction or translocation of animals carrying a novel infectious organism into a new environment, the accidental release of non-native species into a new environment or a change in land use resulting in greater contact between previously isolated species. The *release assessment* includes a description of the biological pathways necessary for that hazard to be introduced into the area or population under consideration. For each step, one should list the relevant biological, ecological or geographical factors considered and the assumptions made.

The *risk assessment* may be concluded at this point if there is a negligible likelihood of the *wildlife* of interest being affected by the hazard at the time under consideration.

Example of a qualitative release assessment for West Nile virus (WNV) as a hazard to the reintroduction of white-tailed sea eagles (WTSEs, *Haliaeetus albicilla*) to the United Kingdom from Eastern Europe (from Sainsbury *et al.* 2012)

'Serological surveys in Eastern Europe suggest that there is a low likelihood that WTSE, like other birds, will be infected with WNV through contact with ornithophilic [bird-favouring] mosquitoes, and the latter are present in Eastern Europe (McLean and Ubico 2007). Fatal infection in raptors (including red-tailed hawks [*Buteo jamaicensis*] and great horned owls [*Bubo virginianus*]) has been reported (Saito *et al.* 2007) but other bird Orders, including Passeriformes, are more susceptible to the infection and the disease (McLean and Ubico 2007). No cases of WNV disease have been reported in birds in Eastern Europe, which suggests that disease is rare. However, viraemia may occur without disease. Therefore there is a low likelihood of infection in a translocated WTSE.'[4]

Exposure assessment

An *exposure assessment* consists of assessing the likelihood that the susceptible animal(s) will come into contact with the hazard in a manner in which transmission may potentially occur. For each step, one should again list the relevant biological, ecological and geographical factors which were considered and the assumptions made. The risk assessment for this hazard may be concluded at this point if the likelihood of exposure is negligible.

Example of a qualitative exposure assessment for WNV as a hazard to the reintroduction WTSEs (*H. albicilla*) to the United Kingdom from Eastern Europe (from Sainsbury *et al.* 2012)

'Falconiformes are known to develop a sufficient viraemia for infection to be transmitted to mosquitoes (Defra 2009) and viraemia has a duration of approximately one week and so the arrival of a viraemic WTSE is possible. Since other bird species, particularly passerines, are highly susceptible to West Nile virus infection there is a high likelihood that these species will be exposed from ornithophilic mosquitoes (which are present in the United Kingdom) in contact with WTSE. There is a high probability that highly susceptible bird species will be infected. There is a high probability of dissemination of WNV through susceptible bird species because at the time of importation in the summer, ornithophilic mosquitoes will be common. Humans are susceptible to infection and there is a low probability that they may be exposed through vector-borne transmission (Zeller and Schuffenecker 2004)'.

Consequence assessment

A *consequence assessment* identifies the biological, environmental and economic consequences associated with the entry, establishment or spread of the hazard, together with an estimate of their likely magnitude and likelihood of occurrence. For each step, one should list the relevant direct and indirect consequences that were considered. The *risk analysis* may be concluded at this point if either consequences are not identified or the likelihood of all the consequences is negligible.

4 In addition it is also important to assess the risk of the translocated birds being exposed to the hazard(s) of concern at the destination site.

Example of a qualitative consequence assessment for WNV as a hazard to the reintroduction of WTSEs (*H. albicilla*) to the United Kingdom from Eastern Europe (from Sainsbury *et al.* 2012)

> 'There is a high probability that disseminated infection would occur if the virus is introduced because many passerine birds will be in the vicinity of WTSE at the release site. West Nile virus has given rise to epidemic disease in Passeriformes in the United States, where birds were naive to infection (McLean and Ubico 2007) and, assuming the epidemiological parameters are similar in the UK, epidemic disease would be predicted. However, antibodies to WNV in UK bird populations have been detected without signs of epidemic disease. Such evidence suggests that differing epidemiological parameters (possibly cross-protection from other flaviviruses [Gubler 2007 cited by Defra 2009] in the UK and incidentally also in continental Europe) have reduced the likelihood of disease outbreaks. An epidemic would have a major economic, environmental and biological impact, as witnessed by the effect of the WNV outbreak in North America over the last ten years (McLean and Ubico 2007), but the evidence suggests that there is a low [probability] of this happening in the UK.'

Risk estimation

The *risk estimation* step summarises the results or conclusions arising from the *release assessment*, *exposure assessment* and *consequence assessment* of all hazards evaluated. It is a prerequisite, before moving on to the *risk management* step that determines whether or not risk mitigation measures are warranted. In weighing up the results of the risk assessment it is important to consider the broader context identified in the problem formulation step. The objective is to ensure that any *risk management* recommendations are appropriately proportional to the risks within the 'real world' situation of concern (see Proportionality, p. 19).

Example of a risk estimation for WNV as a hazard to the reintroduction of WTSEs (*H. albicilla*) to the United Kingdom from Eastern Europe (from Sainsbury *et al.* 2012)

'The likelihood of release through importation in a WTSE is low but the likelihood of exposure of susceptible species to infection is high. Evidence suggests that the likelihood of a significant epidemic disease is low. Therefore the overall risk level is considered low.'

Risk management

> *The risk management step asks 'What can be done to decrease the likelihood of a hazardous event?' and 'What can be done to reduce the implications once it has happened?'*

The purpose of this step is to review the potential risk reduction or management options and evaluate their likely outcomes. On this basis decisions and recommendations can be made to mitigate risks associated with the identified hazards.

Risk management is the process of identifying and selecting measures that can be applied to reduce the level of risk. Hazards can be further prioritised based on the likelihood and magnitude of their adverse consequence in relation to the level of *acceptable risk*. *Risk management* options for each significant hazard are then reviewed according to their likely effectiveness and feasibility.

Tools that can help

- Stella and Vensim, p. 57
- DRA Worksheet, p. 58
- Graphical models, p. 60
- Decision trees, p. 63
- Influence diagrams, p. 66
- Fault trees, p. 68
- Scenario trees, p. 69
- GIS, p. 75
- OIE Handbook, p. 76
- OUTBREAK, p. 78
- Precision tree, p. 87
- Vortex, p. 88
- RAMAS, p. 90

Risk evaluation

The first step is to consider whether or not *risk management* measures are needed given the level of *acceptable risk* agreed to in the problem description step. The result can be displayed using simple or complex matrices depending upon the level of data and the complexity of the *risk assessment* (see 'Implementation' step below). In addition, the level of *uncertainty* in the *risk assessment* should be taken into account at this time.

Option evaluation

The second step is to review and evaluate the effectiveness and feasibility of options available to mitigate risks at the critical control points identified in the biological pathway for each hazard of concern.

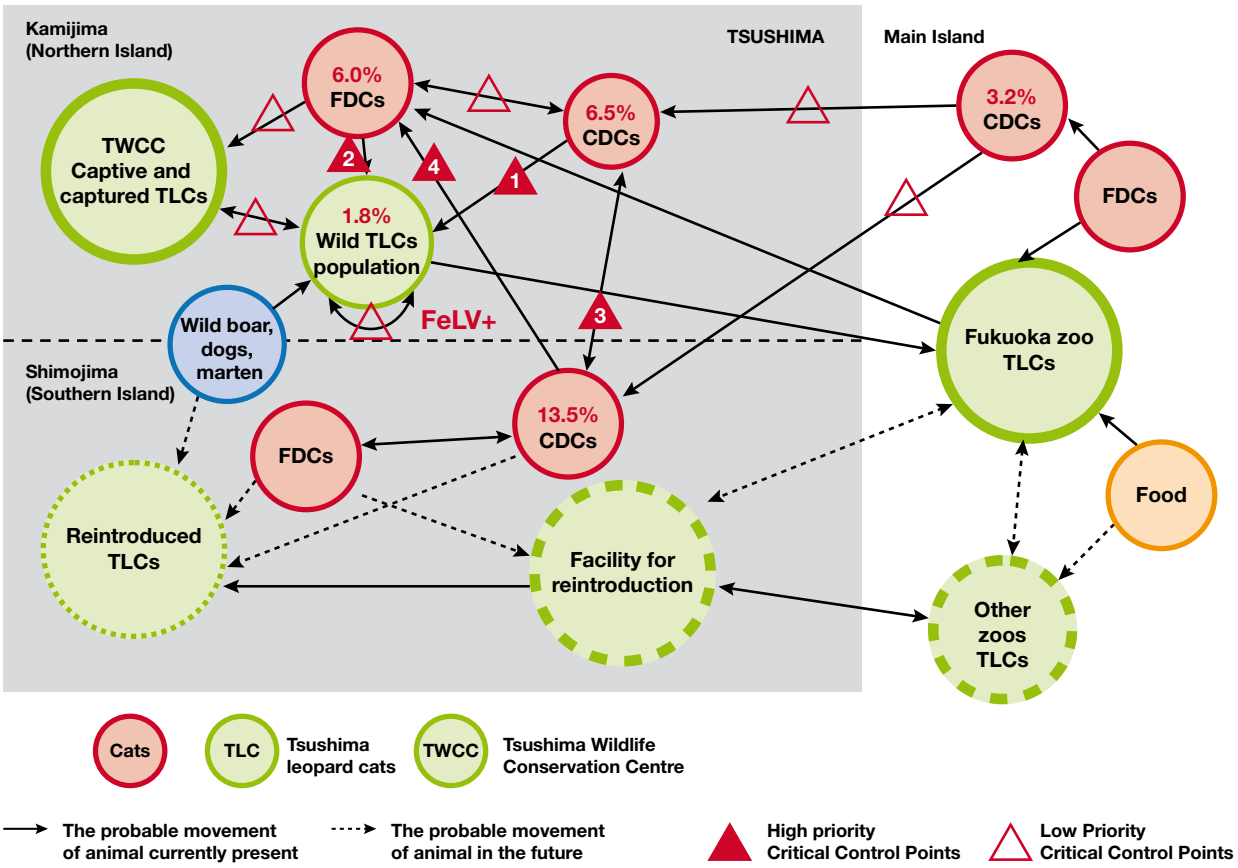


Fig. 7
Example of the application of critical control points (CCPs)

The effectiveness is the degree to which an option reduces the likelihood or magnitude of the potential adverse consequences (health, economic, etc.). Each option should be evaluated according to the expected outcome when implemented against the acceptable level of risk.

The feasibility takes into consideration technical, operational and economic factors affecting the implementation of the *risk management* options. In addition, the management of risks to and from *wildlife* must consider the cultural, ethical and political acceptability of the various *risk management* options.

Critical Control Points

Critical Control Points (CCPs) are identified as points in a hazard's biological pathway (see Figs 6 and 7) at which practical risk reduction or prevention strategies could be implemented. This graphical analysis can assist managers to make decisions on where to focus interventions and consider which *risk management* options are feasible at these points in the pathway.

In this case, using Figure 7, CCPs (△) have been identified for feline leukaemia virus (FeLV) *transmission* routes to the Tsushima (TLCs). Solid numbered triangles indicate priority CCPs (Murayama *et al.* 2006)

Risk management decisions

A matrix such as the one shown below can be a useful tool to assess a range of risk management options according to their feasibility and effectiveness (Table VIII). This can provide a valuable starting place for decision making before specific measures are developed and evaluated further:

Table VIII
Option evaluation decision matrix

Option	Feasibility	Effectiveness	Decision
A	H	H	Yes
B	H	M	Possible
C	H	L	No
D	M	H	Yes
E	M	M	Possible
F	M	L	No
G	L	H	Possible
H	L	M	No
I	L	L	No

In this table, options with a medium to high feasibility and high effectiveness (A and D) are the most desirable options. An option with low feasibility but high effectiveness (G) might be considered but would probably need further investigation before making a decision.

Risk management contingency planning

I. Langstaff

In situations in which diseases pose a significant threat to animals or humans, cost–benefit analysis of management and policy solutions may delay the implementation of an adequate response. Thus, predetermined strategies, or contingency plans, for emergency response are useful parts of the *risk management* implementation plan. For instance, once disease risks have been categorised and compared with previously agreed levels of *acceptable risk*, thresholds may be established above which risks will not be tolerated and above which a response will be made. Alternatively, response planning can focus on the highest and most extreme risks first, working though to lower risks as resources allow.

Disease categorisation

With both approaches it can be useful to group the risks into some broad categories. Structuring response planning around these categories is one operational approach that enables common risk pathways of many diseases to be identified and managed simultaneously. For instance, diseases could be categorised as follows:

1. Disease risks attributable to *pathogen pollution*
   This category refers to risks posed by diseases that may have recently arrived and those that are not known to be in the country of interest (*'exotic'*) but are a risk as a result of human activities. (e.g. spread of *exotic* diseases such as foot and mouth disease to Australia)

2. *Endemic* disease risks
   These diseases, by definition, have a long history of occurrence, and a constant presence in the *wildlife* populations of interest. Factors attributable to human activities pose little risk for further spread relative to the interaction among *wildlife* hosts, the disease agent and the environment (e.g. rabies and foot and mouth disease in parts of Africa)

3. Unknown or novel emerging *pathogens*
   Diseases that have not previously been recognised anywhere (e.g. white nose syndrome in North American bats).

A framework for contingency planning for these *wildlife* disease risks is outlined in Table IX (p. 43). This table shows contingency planning options for addressing each of these categories with a colour code used to illustrate the priority of each component relative to the others within the category.

The components of the strategy are:

- Risk analysis: an evaluation of the probability of disease entry and spread and potential consequences as outlined in this *Manual*.
- Passive *surveillance*: *monitoring* of *wildlife* for clinically diseased cases.
- Targeted *surveillance*: collecting specific information about a defined disease.
- Research: to understand the epidemiology of the disease.
- *Wildlife* health expertise: to implement the *wildlife* disease management strategy.
- Recording incident investigations: information management during *wildlife* disease incidents.
- Data storage and analysis: enhancing baseline *wildlife* disease information.
- Communication and education: dissemination of information on *wildlife* disease.
- Biosecurity measures: for managing disease risks associated with *wildlife* translocations.
- Hygiene standards: biosecurity measure to reduce the risk of disease spread (*pathogen pollution*).

An approach to managing pathogen pollution or spread of known exotic disease

Pathogen pollution refers to the introduction of *pathogens* to novel environments and hosts through human activities (Daszak *et al.* 2000), and most cases are considered to be related to trade and travel (Morrell 1999). *Pathogens* are known to be disseminated by trade in commodities, including livestock and their products, as well as trade in *wildlife* (MacDiarmid 2011; Travis *et al.* 2011).

Wildlife species are considered to be particularly vulnerable to introduced *pathogens* with which they have not evolved (Daszak *et al.* 2000) and therefore the consequence to *wildlife* from *pathogen pollution* can be the emergence of disease *epidemics* such as chytridiomycosis in frogs (Daszak *et al.* 2003). Examples of global human health risks from *pathogen pollution* include sudden acute respiratory syndrome (SARS) and highly pathogenic avian influenza ('bird flu').

A *disease risk analysis* (DRA) (Heading 1) utilising relevant *wildlife* health expertise (Heading 5) is an excellent process for identifying potential risk pathways for the spread of *pathogens* of concern, while the application of biosecurity measures (Heading 9) and appropriate hygiene standards (Heading 10) are the principal management options for mitigating the risk of *pathogen pollution*. These measures should be applied where high-risk human

activities (critical control points) have been identified through the DRA. Targeted *surveillance* projects (Heading 3) are required to evaluate the efficacy of biosecurity standards while research (Heading 4) is needed to fill information gaps on risk pathways for human-mediated introduction and spread of *wildlife pathogens* and their potential consequences. (See Appendix 2, p. 95: Surveillance, monitoring and outbreak investigations as a source of information).

Passive *surveillance* (Heading 2) and incident investigations (Heading 6) are activities that reinforce targeted *surveillance* in detecting where biosecurity measures fail to limit the introduction or spread of *pathogens*. For example, investigating mortality in free-living *wildlife* may detect the occurrence of a disease thought to be *exotic* to a population and reveal the occurrence of a human activity previously thought to be at low risk of introducing disease or identify previously unknown disease *transmission* pathways.

Necessary information gathering, management and dissemination activities include storage and interpretation of *surveillance* data and communication of these data to other *wildlife* users and managers (Headings 6 to 8).

An approach to managing unknown or novel emerging pathogens

'Novel emerging *pathogens*' is a term used here to identify previously unknown disease agents detected for the first time, such as the Tasmanian devil facial tumour, or diseases caused by a *pathogen* infecting a species previously not considered susceptible. Susceptibility may emerge to typically benign microbes undergoing evolutionary changes in virulence or due to a reduced genetic pool or poor immune resistance in the host associated with a decline in environmental quality (Carey *et al.* 1999).

Causal factors contributing to the emergence of novel *pathogens* are typically poorly understood and are the focus of research in *ecosystem* health. *Risk factors* highlighted for emergence of disease in human and domestic animal populations are also likely to be *risk factors* for emerging disease in *wildlife* and include the expansion of human populations influencing agricultural development, urbanisation, deforestation and habitat fragmentation. These *risk factors* are considered to influence disease emergence by changing the density and ecology of disease hosts, *vectors* and *pathogens* (McMichael 2004).

The commonality of human activities influencing these *risk factors* suggests that management opportunities may lie in changes to human behaviour. However, a decision to attempt to influence these changes inevitably depends upon a good understanding of disease epidemiology. The priority components in this strategy for managing novel emerging *pathogens* are therefore passive *surveillance* to detect such diseases (Heading 2) and research (Heading 4) to understand them. A DRA (Heading 1) engaging *wildlife* health expertise (Heading 5) is then an effective method of analysing the information to provide stakeholders and decision makers with recommended options for *risk management*. In addition, applying the precautionary principle, such an analysis should be a component of environmental impact assessments (EIAs) for any new developments associated with important biodiversity or *wildlife* protected areas.

An approach to managing *endemic* pathogens

Endemic pathogens, by definition, are those established and sustained within an area or animal population. For example, *Toxoplasma gondii* (causative agent of toxoplasmosis) is a common *endemic pathogen* in most parts of the world and is spread by its definitive hosts, members of the cat family, Felidae. The lifecycle of *T. gondii* can involve a range of *wildlife* species and is commonly maintained by the presence of feral cats. *Endemic pathogens*, which are restricted in their geographic range to a local area, may also have the potential for further spread through various human activities (described above as *pathogen pollution*).

The threat from *endemic pathogens* arises as increases in their virulence, host range or geographic range may occur, for instance, owing to climatic shifts (Cowell 1997). Feasible management options can be identified and justified only through a good understanding of the interaction among the disease host, agent and their environment over time (i.e. their epidemiology).

Key components for understanding and managing *endemic* disease threats are a *risk analysis* (Heading 1), utilising *wildlife* health expertise (Heading 5) to identify and describe high-risk pathways of disease spread and research (Heading 4) designed to fill knowledge gaps identified through the *risk analysis*. Targeted *surveillance* (Heading 3) is a priority for species considered to be at risk of significant consequences from an *endemic* disease (such as a threatened species). Passive *surveillance* (Heading 2) can be complementary in gathering baseline incidence data. Management of *endemic* disease data (Headings 6 and 7) is important for identifying trends in disease incidence and *risk factors* for disease occurrence that can inform management decisions. Communication of information on *endemic* diseases (Heading 8) is vital for supporting the passive *surveillance* network, as *endemic* diseases are those most encountered

Table IX
Example of contingency planning to address three categories of infectious wildlife disease threat

	1. Risk analysis (DRA)	2. Passive surveillance	3. Targeted surveillance	4. Research projects	5. Wildlife Health Expertise	6. Recording incident investigations	7. Data storage and analysis (information management)	8. Communication and education	9. Biosecurity measures	10. Hygiene standards
Pathogen pollution	Identify and describe high-risk pathways for exotic disease entry and inform decisions to limit entry. Identify information gaps	Back-up to targeted surveillance and biosecurity measures	Surveys of a defined species to detect diseases or their pathogens identified as a priority by risk analysis	To understand risk pathways for anthropogenic introduction and spread of wildlife pathogens	Risk analyses and surveillance, disease intelligence and biosecurity measures	Morbidity and mortality incidents detected by scanning surveillance	Provide records of surveillance information	Communicate disease intelligence to wildlife users and managers	Identify and mitigate the risks from animal imports, exports and movements	Critical management activity for mitigating the risk of pathogen pollution
Novel emerging diseases	Identify and describe high risk pathways, e.g. for intensification of livestock systems next to wildlife habitats	A key system for detecting novel emerging diseases	For species and at sites identified as a priority owing to the potential consequence of a disease	To understand causal factors for disease emergence	Risk analyses and surveillance, disease intelligence and biosecurity measures	Morbidity and mortality incidents detected by scanning surveillance	Provide records of surveillance information, analyse research project data	To facilitate scanning surveillance networks by providing feedback on incidents	Not applicable	Not applicable
Endemic diseases	Identify and describe high-risk pathways of endemic disease spread and inform decisions to limit further spread. Identify information gaps	To gather baseline incident data	For species considered to be at risk of significant consequences from an endemic disease	To fill knowledge gaps identified through the risk analysis	Risk analyses and surveillance, disease intelligence and biosecurity measures.	Morbidity and mortality incidents detected by scanning surveillance	Identifying trends in disease incidence and risk factors for disease occurrence	To support the scanning surveillance networks by providing feedback on incidents	Identify and mitigate the risks from animal movements	To limit the prevalence of disease (e.g. in captive programmes)

Key: Colour codes to illustrate the priority of each component relative to other components within a wildlife disease threat category

Priority category	Highest	High	Medium	Lowest	Not applicable

and most problematic to members of the *wildlife* disease investigation network . Biosecurity actions (Headings 9 and 10) are a lower priority as they are likely to have limited impact if an *endemic* disease is widespread. However, it is prudent to implement biosecurity actions to limit further spread of *endemic* diseases through animal translocations and limit the *prevalence* of disease in populations at risk through appropriate hygiene practices.

Implementation and review

> *The implementation step asks 'How will the selected risk management options be implemented?' and, once implemented, 'Are the risk management actions having the desired effect?' and, if not, 'How can they be improved?'*

The purpose of the implementation and review step is to formulate an action and contingency plan and establish a process for *monitoring*, evaluation and review of risk mitigation strategies. The review may result in a clearer understanding of the problem and enable refinement of the DRA (see 'Adaptive management' on p. 45).

Tools that can help

- DRA Worksheet, p. 58
- OIE Handbook, p. 76

Previous sections have framed the context of disease risk in *wildlife* populations and described a practical *risk analysis* framework for application to identified hazards. If this process has been followed a list of high-priority hazards will have been generated with an estimation of risk based upon the specific *risk assessment* question and some potential management strategies identified. In addition, the *risk assessment* process has helped place these risks into a larger context. This is in order to understand risk pathways for disease spread and identify *wildlife* species and geographic areas that are at risk of suffering significant consequences from disease. It also serves to identify gaps in our knowledge of disease threats. These insights are essential in communicating risk and planning for the implementation of possible management solutions.

Action and contingency plan

Implementation is initiated by the development of a *risk management* action and contingency plan for ensuring the *risk management* measures are in place and followed through.

This plan should include details of what actions are to be taken, why, when and by whom, the associated resource costs (time, money, people, equipment, etc.). Responsibility, with deadlines for actions, must be assigned to, and accepted by, individuals directly involved in the *risk management* discussions.

The contingency plan identifies corrective actions that may be taken if the risk manifests itself under the conditions that were accepted as a part of the *risk management* process. Although this is a real-world application, many of the contingencies can be modelled during the *risk management* step in order to help further prioritise actions. See the preceding section and Table IX (p. 43) for one approach to contingency planning.

Monitoring and review

This is the ongoing process by which the *risk management* measures are continuously monitored to ensure that they are achieving the results intended(see 'Adaptive management' on p. 45). A process must be developed to evaluate the effectiveness and practicality of *risk management* options. To enable this, measurable criteria must be established against which to base decisions to continue to monitor (if favourable outcomes are being achieved) or modify the *risk management* strategy (if the risk is not being adequately mitigated). It is recommended that even 'acceptable' risks are monitored as DRAs are very dynamic processes. If the question was important enough to ask, and the hazard prioritised sufficiently to model, the situation probably warrants *monitoring* and evaluation. Either way, this must be addressed in the conclusions of the *risk analysis* report to ensure *transparency* and proper communication to stakeholders.

Evaluation

Considering the question 'How will success be measured?' during the problem description step will help to identify the data to be gathered to evaluate the DRA and consider refinements to increase its effectiveness. Involving all participants in the development of an evaluation plan and review of its findings helps ensure a common understanding of the issues and project goals.

Evaluation questions and sources of data to answer them should be included in the *risk management* action plan. When working with scarce and valuable resources (always the case with *wildlife* conservation scenarios), some means of measuring the effectiveness of the activity on a periodic basis is essential. This is standard practice in many businesses and government services and, increasingly, funding agencies are requiring documented evidence of progress against agreed

goals. Regular structured analysis of project performance also provides valuable data to identify performance issues as they occur with opportunities for adjustments and refinements. An example and further information is provided in Appendix 6 (p. 118).

Adaptive management

As outlined in this *Manual*, the DRA should start with a clear statement of the problem(s) being addressed and the question(s) to be answered. In virtually all risk analyses, including those focused on *wildlife* disease, there will be a considerable degree of *uncertainty* and a need to make a range of assumptions. Assumptions will be based on the available information and current understanding of the problem and must be stated explicitly. As more information is gathered, assumptions can be tested and modified or reinforced depending on the outcome. In turn, *risk management* actions can be refined and re-tested. This is a process of adaptive management also referred to as 'learning by doing'.

An adaptive management or continuous improvement cycle is illustrated in Figure 8 and can be applied to any project. This cycle continues through the life of the project, ensuring adaptation to changing circumstances and the incorporation of new information and insights

In Figure 8 the initial plan (Plan I) is implemented and monitored. At regular, pre-determined intervals, monitoring data is used to evaluate the project against its objectives. New insights and changes in circumstances identified in the evaluation enable the initial plan to be refined (Plan II) and so on.

Scientific peer review

Many *wildlife* disease risk analyses are conducted in response to an immediate need with the expectations of a rapid turnaround which may not allow time for scientific peer review prior to submission. However, any *risk management* recommendations will gain credibility if the DRA document has been reviewed by one or more appropriate experts. This is worth doing even if publication of the work is not intended.

Wildlife conservation agencies or universities with departments involved in *wildlife* studies and associated disciplines (such as veterinary science, ecology or epidemiology) can be good places to start looking for appropriate reviewers. Written feedback from individuals who are regarded as authorities in their field will have the greatest credibility with stakeholders.

Given that reviewers are being asked for a significant allocation of their time, the draft should be as close to a final copy as possible and should clearly explain the thinking and assumptions behind each step of the DRA. It is important to let reviewers know the deadline for receipt of comments (and check that this is acceptable) and to clarify what aspects of the DRA report you would like comment on. This could include comments on the technical robustness of the DRA, validity of the assumptions made, effectiveness of the communications, and how the work will withstand the criticism of stakeholders who may have opposing views (Brückner *et al.*, 2010).

Those involved in producing the DRA should be open and responsive to any feedback from independent peer review. A defensive attitude, while understandable at times, can undermine the benefits of such a review. Not all comments and criticisms from reviewers are valid or need to be

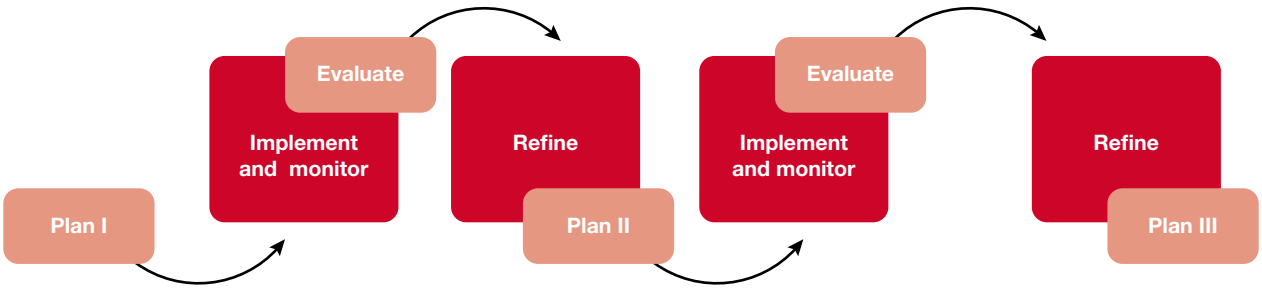


Fig. 8
A depiction of an adaptive management cycle

acted upon, but it is beneficial to accept that they are made in good faith and are worthy of serious consideration before making a decision to accept or reject one or more aspects of the feedback.

An example template for documenting an implementation and review plan is provided in Table X below.

Table X
Example implementation and review plan template

Problem/goal	Objective	Actions	Responsibility	Collaborators	Timeline	Cost	Evaluation	Obstacles
Problem 1: Contacts between feral domestic cats and wild Tsushima leopard cats **Goal 1:** No contact between feral domestic cats and wild Tsushima leopard cats	Remove all feral cats	**1.** Capture and remove feral cats in Kamijima especially where FIV infection rate is high **2.** Start capturing feral cats based on local agreement **3.** Launch 'No stray cat' campaign (implementation of good husbandry and veterinary care programme) **4.** Ensure shelters for captured cats, and find new owners for them	Tsushima city, Social Welfare Division (name or representative at workshop)	Liaison Conference for Implementation of Good Husbandry and Veterinary Care for Domestic Cats in Tsushima (LC)	Start within three years	To be determined: depends on the availability of a cat shelter	Monitor FIV infection rate Estimate size of population of feral cats	Domestic cat ownership is not clearly defined (need for a cat registration system). Both in and out of Tsushima, shelters and a system to find new owners for the captured feral cats has yet to be developed

Based on Murayama *et al.* 2006

A checklist for conducting a wildlife translocation disease risk analysis[5]

S.C. MacDiarmid

1. Problem description

1.1 Determine the scope of the *risk analysis*

Define as precisely as possible the animals (or germplasm) which are the subject of the *risk analysis* by specifying:

- ☐ the scientific names of the animal species
- ☐ the nature, source(s) (including country) and intended purpose of the animals (or germplasm)
- ☐ the likely number of animals to be moved and the frequency of such translocations.

Based on these, draft a suitable title for the *risk analysis*.

1.2 State the goal of the *risk analysis* clearly

The purpose of the *risk analysis* should be stated in an appropriate form, for example:

> 'To identify and assess the likelihood of (*the hazard(s)*) being introduced and spreading or becoming established in (*the area of translocation*) together with the likelihood of, and the likely magnitude of, the potential consequences for wild animal, domestic animal or human health as a result of (*the activity*).'
>
> 'To recommend risk mitigation measures, if appropriate.'

1.3 Identify sources of information for the *risk analysis*

Information to assist in identifying hazards, assessing risks and exploring options to manage risk can be found in a variety of sources (see Appendix 1, p. 93).

5 Adapted from: Brückner G., MacDiarmid S.C., Murray N.., Berthe F., Müller-Graf C., Sugiura K., Zepeda C., Kahn S. & Mylrea G. (2010). – Handbook on Import Risk Analysis for Animal and Animal Products, Volume I. Introduction and Qualitative Risk Analysis. Second edition. World Organisation for Animal health (OIE), Paris, 88 pp.

2. *Risk communication*

2.1 Develop a *risk communication* strategy

The risk communication strategy should:

- identify interested parties (stakeholders and experts)
- determine when you need to communicate with them
- determine the appropriate means of communication.

3. Hazard identification

3.1 Identify the hazards likely to be associated with the species under consideration:

- Draw up a preliminary list of the infectious and non-infectious *pathogens* associated with the species under consideration and, based on the following criteria, determine whether or not they can be classified as a hazard for further consideration in a *risk assessment*.

3.2 Is the live animal or germplasm under consideration a potential vehicle for the pathogenic agent?

If the answer is YES proceed to step 3.3, otherwise the pathogenic agent is not a hazard.

3.3 Is the pathogenic agent present in the area from which the animals or germplasm are sourced?

- If the answer is YES proceed to step 3.4.

- If the answer is NO, do you have sufficient confidence in the capacity and capability of the Competent Authority responsible for the source area or country to satisfactorily substantiate a claim that the pathogenic agent is absent?
  - If the answer is YES the pathogenic agent is not a hazard.
  - If the answer is NO, contact the Competent Authority to seek additional information or clarification and proceed to step 3.5, assuming that, until otherwise demonstrated, the pathogenic agent is likely to be present in the source area.

3.4 Are there zones from which the animals or germplasm will be sourced that are free of the pathogenic agent?

- If the answer is YES, do you have sufficient confidence in the capacity and capability of the Competent Authority to satisfactorily substantiate a claim that the pathogenic agent is absent from and ensure that the animals or germplasm are derived only from these zones or compartments?
  - If the answer is YES the pathogenic agent is not a hazard.
  - If the answer is NO, contact the Competent Authority to seek additional information or clarification and proceed to step 3.5), assuming that, until otherwise demonstrated, either the pathogenic agent is likely to be present in these zones or the animals or germplasm are likely to be derived from other areas.

- If the answer is NO proceed to step 3.5.

3.5 Is the pathogenic agent already present in the area to which animals or germplasm are to be translocated and which will be affected by the planned activity?

- If the answer is YES proceed to step 3.6.

- If the answer is NO, are you or the Competent Authority of your country able to satisfactorily substantiate a claim that it is absent?
  - If the answer is YES the pathogenic agent is classified as a hazard.
  - If the answer is NO, proceed to step 3.6.

3.6 For a pathogenic agent reported in both the source area and the area of translocation, if:

- it is subject to an official control programme, OR

- there are zones of different animal health status, OR

- local strains are likely to be less virulent than those reported in the source area,

THEN pathogenic agent may be classified as a hazard. Proceed to step 4.

A risk analysis may be concluded at this stage if none of the pathogenic agents considered are classified as potential hazards.

3.7 Has a previously conducted *disease risk analysis* for the same translocation or activity provided risk mitigation measures for the hazard under consideration?

– If the answer is YES, are you required by legislation, policy or other considerations within your country to undertake a complete *risk analysis*?
  - If the answer is YES, proceed to step 4 and conduct a *risk assessment*.
  - If the answer is NO, apply the risk mitigation measures prescribed in the previously conducted *disease risk analysis*.

4. Risk assessment

Conduct a *risk assessment* for each hazard:

☐ Identify the populations of interest:
– Potentially susceptible species need to be identified to ensure that all the appropriate biological pathways are considered in the *risk assessment*.
– Susceptible species may include terrestrial and aquatic animals in the wild or in captivity or being farmed, as well as humans if the hazard has zoonotic potential.

☐ Draw a scenario tree to identify the various biological (risk) pathways leading to:
– the translocated animals or germplasm harbouring the hazard when moved or animals impacted by the planned activity harbouring the hazard
– susceptible animals or humans being exposed
– potential 'outbreak' scenarios.

☐ Conduct a *release assessment* to estimate the likelihood of the animals or germplasm or activity introducing the hazard into the environment, *ecosystem* or area of concern:

List the relevant biological, environmental and animal factors that you considered in each step:

– Is the likelihood that the animals or germplasm to be translocated or which will be impacted by the activity are carrying the hazard negligible? If the answer is:
  - YES, the risk estimate (step 5.1) is classified as negligible and the *risk analysis* may be concluded at this point
  - NO, proceed to the next step.

☐ Conduct an *exposure assessment* to estimate the likelihood of susceptible animals or humans being exposed to the hazard.

List the relevant biological, environmental and animal factors that you considered in each step:

– Is the likelihood of susceptible animals or humans being exposed to the hazard via each and every exposure pathway negligible? If the answer is:
  - YES, the risk estimate (step 5.1) is classified as negligible and the *risk analysis* may be concluded at this point
  - NO, proceed to the next step.

☐ Conduct a *consequence assessment* to estimate the likely magnitude of potential biological, environmental and economic consequences associated with the entry establishment or spread of the hazard and the likelihood of their occurrence.

List the relevant direct and indirect consequences that you considered:

– Is the likelihood of each and every significant biological, environmental or economic consequence associated with the hazard negligible? If the answer is:
  - YES, the risk estimate (step 5.1) is classified as negligible and the *risk analysis* may be concluded at this point
  - NO, proceed to the next step.

☐ *Risk estimation:* summarise the results or conclusions arising from the release, exposure and consequence assessments and proceed to step 5.

5. Risk management

5.1 Risk evaluation:

– Is the risk estimate greater than *risk communication* has determined to be acceptable to stakeholders? If the answer is:
  - YES, proceed to step 5.2
  - NO, the risk mitigation measures are not required and the *risk analysis* may be concluded at this point.

5.2 Option evaluation:

– Formulate an objective that clearly states the intended outcome of the risk mitigation measure(s) by taking into account the risk pathways leading from the likelihood of introducing the hazard, the exposure of susceptible animals or humans and of significant consequences arising.
– Identify possible risk mitigation measures.

– Select an option or combination of options that will achieve an acceptable level of risk by ensuring that:
  - option(s) are not chosen or applied arbitrarily but are based on scientific principles and a *risk analysis*
    · evaluate the likelihood of the entry, exposure, establishment or spread of the hazard together with an estimate of the likely magnitude and likelihood of occurrence of biological, environmental and economic consequences according to the measure(s) that might be applied
    · choose measures that are technically, operationally and economically feasible
  - apply measures only to the extent that is necessary to protect human or animal life or health
  - avoid situations where some parts of a risk pathway are over managed
  - consider each measure from the overall perspective of the entire risk pathway, not in isolation
  - if the contribution of a particular measure to the overall reduction in risk is insignificant or negligible, it is effectively redundant and should not be included
  - it is unlikely to be necessary to apply a risk mitigation measure at each and every step in the risk pathway in order to achieve the *acceptable risk*.

6. Implementation

☐ Undertake a scientific peer review to ensure that the *risk analysis* is technically *robust* and that the risk mitigation measures chosen are appropriate to the circumstances.

☐ Make the final decision and implement the risk mitigation measure(s).

☐ Monitoring and review:
– Monitor factors that may have an immediate impact on the risk, for example changes in the animal disease status of the source population or related populations in neighbouring regions.
– Monitor factors associated with each *risk analysis* that may need to be reviewed periodically as updated or new information becomes available.
– Monitor the implementation of risk mitigation measures to ensure they are achieving the results intended.

Tools for wildlife disease risk analysis

C. Lees, P.S. Miller, B. Rideout, V. Dove, S.C. MacDiarmid, M. van Andel, D. Tompkins, K. McInnes, R.M. Jakob-Hoff, L. Skerratt, N. French & S. Siah

Introduction

This section will direct you to appropriate tools for your *disease risk analysis* (DRA) and to pertinent case studies illustrating their use. It is important to understand the DRA process as it is outlined in this *Manual* before exploring these complementary tools, and we refer you to the previous sections for this insight.

The library of tools presented here is representative rather than exhaustive, and highlights, where possible, tools that are well tested and readily accessed. We hope that this will provide most practitioners with the tools they need for most DRA scenarios, while recognising that more work is needed in this area to build a fully comprehensive resource.

The role of tools in disease risk analysis

The analysis of disease risk in biological systems is complex, involving many types of data with a variety of relationships among them. We can not necessarily rely on our own 'mental models' to evaluate such risks. Experimental studies on humans (e.g. Towse *et al.* 2000; Oberauer and Kliegl 2006) show that, at any given time, our 'working memory' can hold only a small number of specific pieces of information pertinent to a particular problem. Holding the necessary information on the relationships between these pieces of data poses an additional challenge to our already strained faculties. To solve complex problems, then, we must turn to other means, or 'tools' for assembling, relating and analysing information.

Tools for *disease risk analysis* range in complexity from simple, yet powerful spreadsheets for compiling and organising data, to sophisticated simulation *models* for exploring the impact of *variability* and *uncertainty* on our ability to predict future outcomes of alternative *risk management* strategies. Despite their differences, all tools have something in common: they serve as independent instruments of investigation (Morgan and Morrison 1999).

By representing some aspect of the real world (often in the form of *models* or simplified representations of complex systems), tools can teach us something about the world that they represent. The more we interact with those tools in our analysis of a system, the more we learn about that system. Further, because most tools are based on both theory and data, they can mediate between these two realms and connect them in meaningful ways.

In applying tools it is important to recognise that no tool is perfect in its design, and no accompanying dataset is without gaps. Consequently, tools will not accurately predict the future, nor will they necessarily provide a single 'right answer' to a specific problem. Uncertainty is a constant feature of DRAs that must be recognised and addressed. The advantage of using tools will often lie in helping us to make relative rather than absolute predictions, for example when assessing the risk of disease agent introduction or *transmission* under different circumstances. This kind of comparative assessment is often referred to as *sensitivity analysis* and it allows us to make much more *robust* predictions about disease dynamics in host populations under alternative management scenarios. Many of the predictive tools discussed here can be used effectively in a comparative framework, in addition to their use in a more traditional (and often more problematic) absolute predictive context.

Disease risk analysis tools, properly applied, should help us to learn more about the system we are studying: to understand what we know and do not know about the system; to understand what we most need to know in order to intervene effectively where needed; and to assess the comparative merits of different *risk management* approaches. We offer the tools discussed in this section in the firm belief that they will provide such benefits.

Figure 9 illustrates some of the tools that can be used in *wildlife* DRA, and how they fit into the DRA framework described.

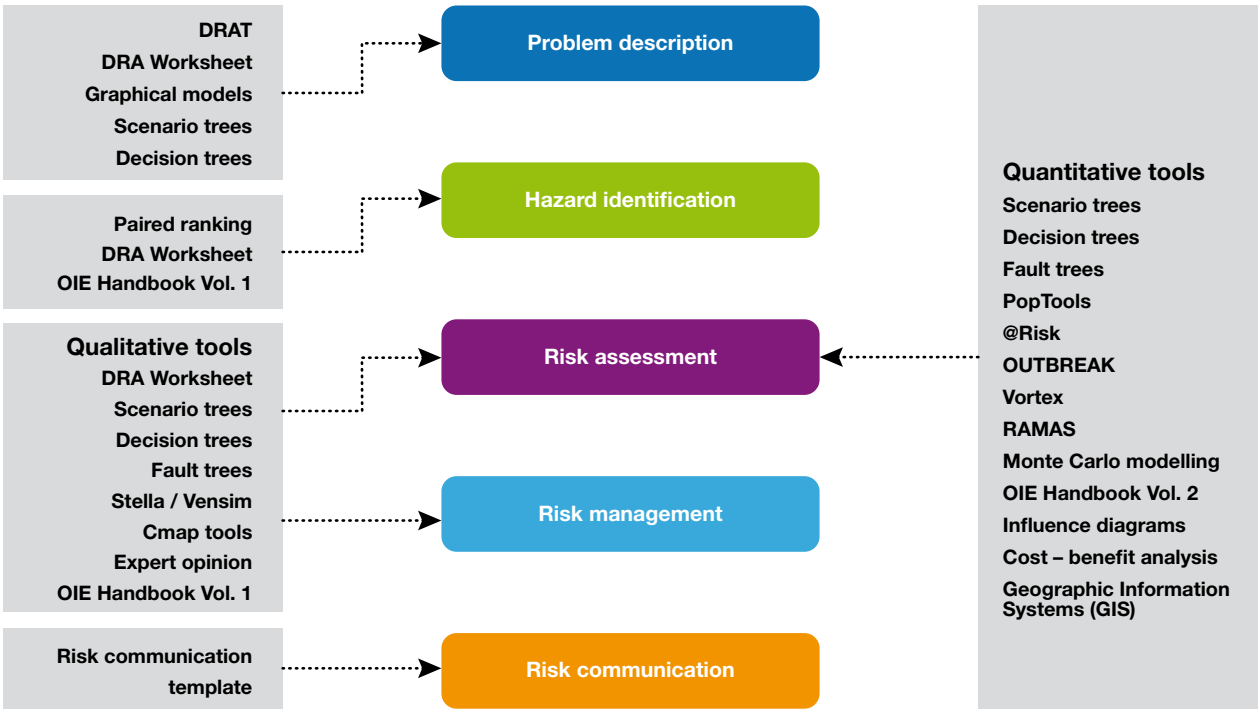


Fig. 9
Flow chart to illustrate where selected tool types can assist the disease risk analysis

Finding the right tool

Locating an appropriate tool for a specific scenario requires an understanding of what the tool will be required to do, some knowledge of the range of options available, and an understanding of any limitations in the areas of funding, data or expertise that might constrain your choice.

The tools matrix in Figure 10 is designed to point the user quickly and easily to tools that are suited both to specific stages in the DRA process and to different DRA contexts. It distinguishes between tools for quantitative versus qualitative analyses and clearly identifies those able to be used across multiple DRA stages; this is likely to be particularly useful for those designing a formal DRA from first principles. When several tools are highlighted for use during a particular stage, the matrix highlights their comparative suitability for situations in which data, resources or specialist expertise are in short supply. This should help practitioners to tailor the choice of tool to their specific circumstances.

Once the user has identified a promising tool or group of tools, further information on each, including case studies demonstrating their application and details of how and where they can be accessed, are provided in the Tools Introduction section below.

Tool introductions

This section provides further details about each of the tools listed in the tools matrix, including references to case studies that illustrate their use in real situations. The list is not intended to be exhaustive but rather to provide a representative sample of well-tested tools.

Tool 1: DRAT

K. McInnes

Name: DRAT – Disease Risk Assessment Tool for Wildlife Translocations in New Zealand.

Reference

Department of Conservation, New Zealand.

Source

DRAT will be available from the Department of Conservation, New Zealand website, www.doc.govt.nz/wildlifehealth, from March 2014.

								Suitable for situations with		
Tools	**Qualitative**	**Quantitative**	**PD**	**HI**	**RA**	**RM**	**RC**	**Little technical expertise**	**Few ** financial resources**	**Few data**
1. DRAT										
2. Stella										
3. Vensim										
4. DRA worksheet										
5. Paired ranking										
6. Graphical models										
7. Decision trees										
8. Influence diagrams										
9. Fault trees										Where used qualitatively
10. Scenario trees										Where used qualitatively
11. Cmap										
12. GIS										
13. OIE Handbook										
14. @Risk										
15.OUTBREAK										
16. PopTools										
17. Expert elicitation										
18. Netica										
19. Precision tree										
20. Vortex										
21. RAMAS										
22. Risk communicacion plan template										

PD, problem description; HI, hazard identification; RA, risk assessment; RM, risk management; RC, risk communication
***Indicates tool purchase costs of less than USD 200.00 at time of writing*

Fig. 10
DRA tools matrix

Cost

Free on the web.

Software requirements

None.

Stage(s) of risk analysis when this would be used

DRAT is to be used in the initial planning stage of a translocation where the user wishes to determine if there is a need to undertake a detailed *risk assessment*.

Description of tool use
The user progresses through a flow diagram, answering questions that determine the likelihood and consequences of disease *transmission* arising from *wildlife* translocation. Using geographic and habitat data, the user determines the ecological likelihood of transmitting or contracting disease through the translocation. Where the likelihood is negligible, the user is referred to minimum standards for managing *wildlife* health during the translocation. If the likelihood is not negligible, the user then makes a more detailed assessment based on the potential likelihood of encountering or transmitting novel *pathogen*s and the consequences to the species and release location, using whatever disease *prevalence* information is available. If the risk is considered not negligible, or there are insufficient data to make this assessment, the user is referred to a separate document requiring veterinary or disease ecologist assistance to undertake a more detailed assessment of risk and develop a *risk management* plan.

Experience and expertise required to use the tool

Users require no specific skills or knowledge.

Data requirements

Geographic details of source and release locations and type habitat mapping. Useful, but not essential information includes: presence or absence of diseases in the source and release locations and within the species being translocated.

Strengths and weaknesses, when to use and interpret with caution

DRAT allows anyone to make a general assessment of the risk of any *wildlife* translocation. It is user-friendly and simple to use. The assessment process is logical and transparent. DRAT quickly allows negligible risk translocations to be assessed and processed. It highlights where information gaps affect the assessment and educates the user in the process. It directs the user to more information and further assessment when required. It requires no special knowledge, no software and no training. It is a 'first cut' in the *risk assessment* process for translocations.

Use it for translocations as an initial screening tool to fast-track negligible risk translocations. Decisions made using the flow chart should be documented and reviewed by a neutral party.

It links to a more detailed *risk assessment* process document if the risk is not negligible. This requires veterinary or disease ecologist input and much more detailed disease information.

Case studies

These two case studies present different situations. In the first, birds are being moved locally. In the second, birds are being moved a great distance and there are known disease issues at the source location.

– In case study 1, the conclusion from the DRAT is that the risk of transferring or encountering a new *pathogen* is low, and the transfer can go ahead with some minimum requirements for ensuring individual birds are healthy at transfer.

– In case study 2, the DRAT demonstrates that there are disease issues that need to be examined more closely and mitigated. The user is directed to consult with a veterinarian. This involves some more detailed collection of data and *risk assessment*, and development of a comprehensive risk mitigation protocol.

Case study 1: Flow chart decisions record

Species	**North Island robin/toutouwai (*Petroica longipes*)**	
Source location	**Zealandia – Karori Sanctuary**	
Release location	**Eastbourne Regional Park**	
1. Is the source population captive?	Yes, go to Part B No, continue	No
2. Is the release site or the species listed as high priority by the Department of Conservation?	Yes, go to Part B No, continue	No
3. Are the release site and source site within the same or neighbouring ecological regions?	Yes, go to Q12 No, continue	Yes
4. Is the release site/nearby sites high value?	Yes, go to Q5 No, go to Q9	–
5. Are there diseases of concern in source site/species?	Yes, list them and go to Q6 No, go to Q9	–
6. Are they already present/likely to naturally reach the release site?	Yes for all, go to Q9 No for any, go to Q7	–
7. If they reach are they likely to spread?	Yes for any, go to Part B No for all, go to Q8	–
8. Is there a risk to future translocations?	Yes for any, go to Part B No for all, go to Q9	–
9. Are there novel *pathogens* at the release site?	Yes, go to Q10 No, go to Q12	–
10. Can they infect your animals?	Yes, go to Q11 No, go to Q12	–
11. Can you justify it if it happens?	Yes, go to Q12 No, go to PART B	–
12. Minimum requirements, recommendations and reporting	Compulsory	Yes

Case study 1: Translocation map – ecological regions showing source and release locations (from DOC website http://gis.doc.govt.nz)

The translocation is from one ecological region into an adjoining one.

The species and locations are not listed as high priority. There is no requirement for further disease risk assessment.

Case study 2: Flow chart decisions record

Species	**South Island robin/toutouwai (*Petroica australis australis*)**	
Source location	**Motuara Island, Marlborough Sounds**	
Release location	**Orakanui Restoration Project, Dunedin**	
1. Is the source population captive?	Yes, go to Part B No, continue	No
2. Is the release site or the species listed as high priority by the Department of Conservation?	Yes, go to Part B No, continue	No
3. Are the release site and source site within the same or neighbouring ecological regions?	Yes, go to Q12 No, continue	No
4. Is the release site/nearby sites high value?	Yes, go to Q5 No, go to Q9	Yes
5. Are there diseases of concern in source site/species?	Yes, list them & go to Q6 No, go to Q9	Yes, avian pox, avian malaria, coccidia
6. Are they already present/likely to naturally reach the release site?	Yes for all, go to Q9 No for any, go to Q7	Pox – unknown strain therefore unknown risk Malaria – yes Coccidia – no, species specific
7. If they reach are they likely to spread?	Yes for any, go to Part B No for all, go to Q8	Pox – yes – PART B Malaria – n/a – already present Coccidia – no
8. Is there a risk to future translocations?	Yes for any, go to Part B No for all, go to Q9	Pox – yes – PART B Malaria – no Coccidia – no
9. Are there novel pathogens at the release site?	Yes, go to Q10 No, go to Q12	Unknown
10. Can they infect your animals?	Yes, go to Q11 No, go to Q12	Unknown
11. Can you justify it if it happens?	Yes, go to Q12 No, go to PART B	No
12. Minimum requirements, recommendations and reporting	Compulsory	Yes

Case study 2: Translocation map – ecological regions showing source and release locations (from DOC website http://gis.doc.govt.nz)

In this case:

- the species and locations are not listed as high priority
- the translocation crosses many ecological regions
- there are known disease risks within the source population
- there is a requirement for further disease risk assessment
- the user is referred to Part B.

Part B of the process involves consulting with a *wildlife* veterinarian and reviewing the situation in more detail to determine risks and mitigation measures.

Tools 2 and 3: Visual system-level simulation modelling – Stella and Vensim

P.S. Miller

References

ISEE Systems. An Introduction to Systems Thinking with Stella. Available for electronic or hardcopy purchase at www.iseesystems.com

Vensim Version 5.11 User's Manual. Available online at www.vensim.com

Source

Stella, a dynamic visual simulation modelling environment. See www.iseesystems.com/softwares/Education/StellaSoftware.aspx for detailed descriptions of the software.

Vensim, a graphical system simulation modelling tool. See www.vensim.com/software.html for detailed descriptions of the software.

Cost

A variety of packages are available. See the web links above for more information on pricing.

Software requirements

Stella: Windows: 233 MHz Pentium; Microsoft Windows™ 2000/XP/Vista/7; 128 MB RAM; 90 MB disk space; QuickTime 7.6.5 or earlier.

Macintosh: 120 MHz PowerPC or any Intel-based Mac; Mac OS 10.2.8-10.6.8; 128 MB RAM; 90 MB disk space; QuickTime 7.6.4 or earlier.

Vensim: Vensim runs on Windows XP and Windows 7. Vensim will run on the Macintosh under System X in 'Classic' mode.

Stage(s) of risk analysis when this would be used

Because of the 'systems level' approach to visualising and analysing a given question, these packages can be useful in the problem formulation step. When used in a more traditional modelling capacity, they can also be valuable in the *risk assessment* and *risk management* steps.

Description of tool use

The process of analysing a problem and making decisions on how to act on that problem begins by visualising the problem system. This is done in Stella and Vensim by converting a user's mental *model* into a graphical diagram of the problem system. Reflective thinking about the nature of the system and its components, combined with discussions with colleagues, leads to a refinement in realism and accuracy of the system's visual representation. Mathematical characterisation of the relationships among different elements of the system can be added, allowing the user to investigate the quantitative nature of these relationships and to simulate possible future states of the system under alternative assumptions and scenarios.

When beginning a new *model* in these packages, the user is presented with a blank window, almost like an artist's canvas. This is where the system description takes place. An intuitive icon-based graphical interface simplifies *model* building, with 'stock and flow' diagrams supporting the common language of systems thinking and providing insight into how systems work. A user can create causal loop diagrams to represent overall causal relationships, while model equations are automatically generated and made accessible beneath the model layer. A variety of tools is available to facilitate *model* presentation, including animations, storyboards, and other graphical elements (knobs, sliders, switches, etc.). Simulations 'run' systems over time, and *sensitivity analysis* reveals key system drivers and optimal conditions within the model structure. Simulation results are presented as graphs, tables, animations, QuickTime movies and files.

The emphasis with these software environments is on visualisation and analysis of almost any system imaginable, from complex problems in the physical sciences to art, literature and the process of human communication.

Experience and expertise required to use the tool

When used for purposes of system visualisation in the context of problem formulation, virtually no specific experience or expertise is required to use either Stella or Vensim; project success is limited largely by a user's imagination and creativity. If detailed quantitative analysis is the desired endpoint, the required expertise is similar to that desired for most other simulation modelling exercises. In particular, a thorough understanding of species biology and demography and disease ecology and epidemiology is necessary, and expertise in the statistical manipulation and analysis of model input and output data is essential.

Data requirements

Few specific data are required for visual system representation. For detailed *risk assessment* or *risk management*, specific data on host population demography, disease epidemiology and population-level impacts of disease are necessary.

Strengths and weaknesses, when to use and interpret with caution

The focus on system visualisation as a focus of learning is a major strength of these tools. The open-ended and very flexible approach to model construction and analysis results in a fairly steep learning curve in order to master the software's capabilities. A major strength of Vensim over other similar packages is the very competitive pricing options for the PLE and PLE Plus versions. Treatment of disease can be quite explicit and complex, limited only by the capabilities of the user. As with any modelling package, specific interpretation of simulation output is a direct function of the accuracy and realism of the input parameters.

Case studies

Sgrillo *et al.* 2005; Hannon and Ruth 2009 (a book focusing on the use of Stella for dynamic modelling of disease in a variety of situations).

See also Appendix 8 (p. 125) of this *Manual*.

Tool 4: DRA Worksheet

R.M. Jakob-Hoff

Name: Disease Risk Analysis Worksheet

Reference

Armstrong *et al*. 2003.

Source

Original version available within the above publication downloadable from the Conservation Breeding Specialist Group website at www.cbsg.org/risk/. For current version contact richard@cbsgaustralasia.org

Cost

The tool is freely available from the sources identified above.

Software requirements

Microsoft Word but can also be printed and used as a pencil and paper tool.

Stage(s) of risk analysis when this would be used

This tool guides the user through the entire *disease risk analysis* process and contains prompts for the use of specific analytical and decision-making tools at the relevant stages of the process.

Description of tool use

The Worksheet is designed for use by experienced *wildlife* managers with input from veterinarians and others who have some expertise in diseases of the *wildlife* taxonomic groups under consideration. While this tool can be used by one or two individuals, the best results are obtained when it is used to guide a facilitated discussion involving key stakeholder group representatives. It is of great value to include key decision makers in these discussions from the outset. As much relevant information as possible should be assembled and distributed to participants in advance of a face-to-face discussion.

Experience and expertise required to use the tool

No specialised expertise required. Requires the ability to think logically and communicate clearly.

Data requirements

- The species of concern's geographic distribution, behaviour, ecology and conservation management.
- The disease susceptibilities of relevant species (*wildlife* and domestic) at the geographic site(s) under consideration.

– Disease diagnostic and management options.
– Relevant social (e.g. public health; community cultural practices) and economic issues (e.g. costs of laboratory testing).

Strengths and weaknesses, when to use and interpret with caution

This tool has the flexibility to be applied to situation-specific DRA scenarios. It requires no (or minimal) technical equipment and is written in non-technical language. It provides a structured template for stakeholder discussion and prompts to encourage transparent decision making and consensus building when used with key stakeholder representatives in a workshop setting.

In its current form it is biased towards *wildlife* translocation scenarios and is limited to a *qualitative risk analysis*, although quantitative data generated through other tools can be imported and incorporated. An electronic version is under development but not yet available.

Case studies

Jakob-Hoff 2001; Jakob-Hoff 2009.

Tool 5: Paired ranking for hazard prioritisation

P.S. Miller and R.M. Jakob-Hoff

Name: Paired ranking

Reference

Armstrong *et al*. 2003.

Source

The above publication can be downloaded from the Conservation Breeding Specialist Group website at www.cbsg.org/risk/

Cost

The tool is freely available.

Software requirements

None.

Stage(s) of risk analysis when this would be used

During the hazard prioritisation component of the *hazard identification* stage.

Description of tool use

This is a means of producing a ranked list when it proves difficult to sort listed items into a priority list. It may be useful for an individual or a working group if the disease list is difficult to prioritise.

Experience and expertise required to use the tool

No specialised expertise is required but the process requires someone to facilitate the group discussion.

Data requirements

An initial list of potential hazards.

Strengths and weaknesses, when to use and interpret with caution

This is a tool for a *qualitative risk analysis* that assists groups to rank hazards based on their collective judgement. The process provides *transparency* to the ranking process for those directly involved and helps to build consensus. The limitation is that the ranking will be a reflection of the knowledge and expertise of those present and this needs to be acknowledged.

Case study

The mechanism for carrying out this technique is very simple. As an example here is a limited list of three cat diseases for demonstration purposes:

1. First list the diseases in any order:

Canine distemper
Tuberculosis
Toxascaris

2. Then define the criteria by which you will compare the diseases, such as effect on the individual, potential effect on the wild population, how transmissible the disease is, etc.

3. Then compare the first disease on the list with the second and decide which is more important for the criteria you have defined and place an X to the right of the disease that you feel is more important:

Canine distemper	**X**
Tuberculosis	
Toxascaris	

4. Then compare the first disease on the list with the third and decide which is more important according to your criteria and place an X beside it:

Canine distemper	**XX**
Tuberculosis	
Toxascaris	

5. Then compare the second disease on the list with the third and repeat the exercise, placing an X by the disease you consider more important according to your criteria:

Canine distemper	XX
Tuberculosis	
Toxascaris	**X**

6. Repeat this process until all the diseases on the list have been compared with all the other diseases one at a time. Then add up the number of X's by each disease and rewrite your list so that the disease with the most X's is at the top of the list:

Canine distemper	XX	2
Toxascaris	X	1
Tuberculosis		0

This exercise can be carried out individually or collectively by a working group or can be done individually by all the individuals in a group.

Tool 6: Graphical models

V. Dove

Other name: Epidemiology graphical *models*; conceptual *models*; path diagrams; causal webs

References

Dohoo *et al.* 2003; Murray *et al.* 2004; Thrusfield 2005.

Source

This is a tool that will be developed and constructed by the person or team conducting the DRA.

Cost

Free, if done on a computer using PowerPoint or using a pen and paper. Software such as Miradi is currently available as open source software.

Software requirements

Can be easily constructed in Microsoft PowerPoint or by using a programme such as Miradi (https://miradi.org).

Stage(s) of risk analysis when this would be used

These graphical *models*, which can be used both quantitatively and qualitatively, will identify the various factors involved in the *risk assessment*, and will be a vital resource that can be used in the *hazard identification*, *risk management* and *risk communication* stages of the DRA process.

Description of tool use

A graphical depiction of the steps involved in the DRA process (Fig. 11), together with the biological pathways involved (Figs 12 and 13) provides a useful conceptual framework for visually conveying the range and types of pathways to be considered in a DRA.

As disease is always multifactorial, it may be hard to visualise all the factors at play. A means of conceptualising how these multiple factors combine to cause disease is through a causal web, consisting of direct and indirect causes (Dohoo *et al.* 2003) or through a path diagram (Thrusfield 2005).

Experience and expertise required to use the tool

No specialist expertise is required to use the tool.

Data requirements

A thorough literature review of the relevant hazards that have been identified is required to obtain an understanding of the epidemiology of the disease, including the host factors, the environmental factors and the agent factors. Once all these factors are identified, the causal web can be constructed.

Fig. 11
Conceptual model of the generic disease risk analysis process

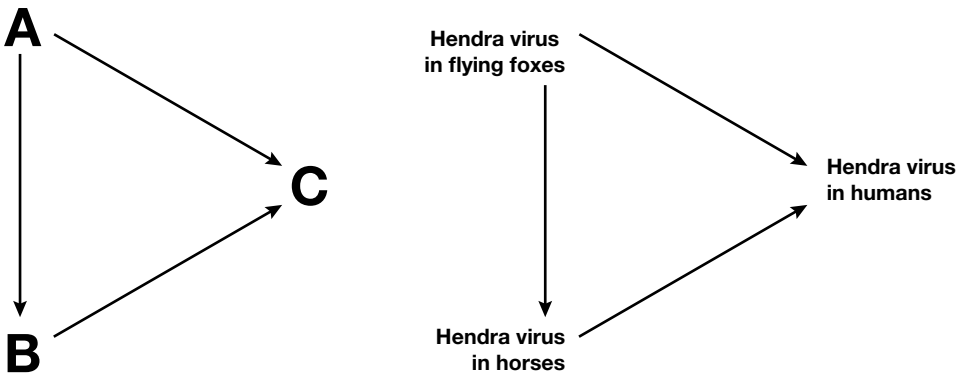


Fig. 12
Path diagram with direct and indirect causal association (A with C)
Adapted from Thrusfield (2005)

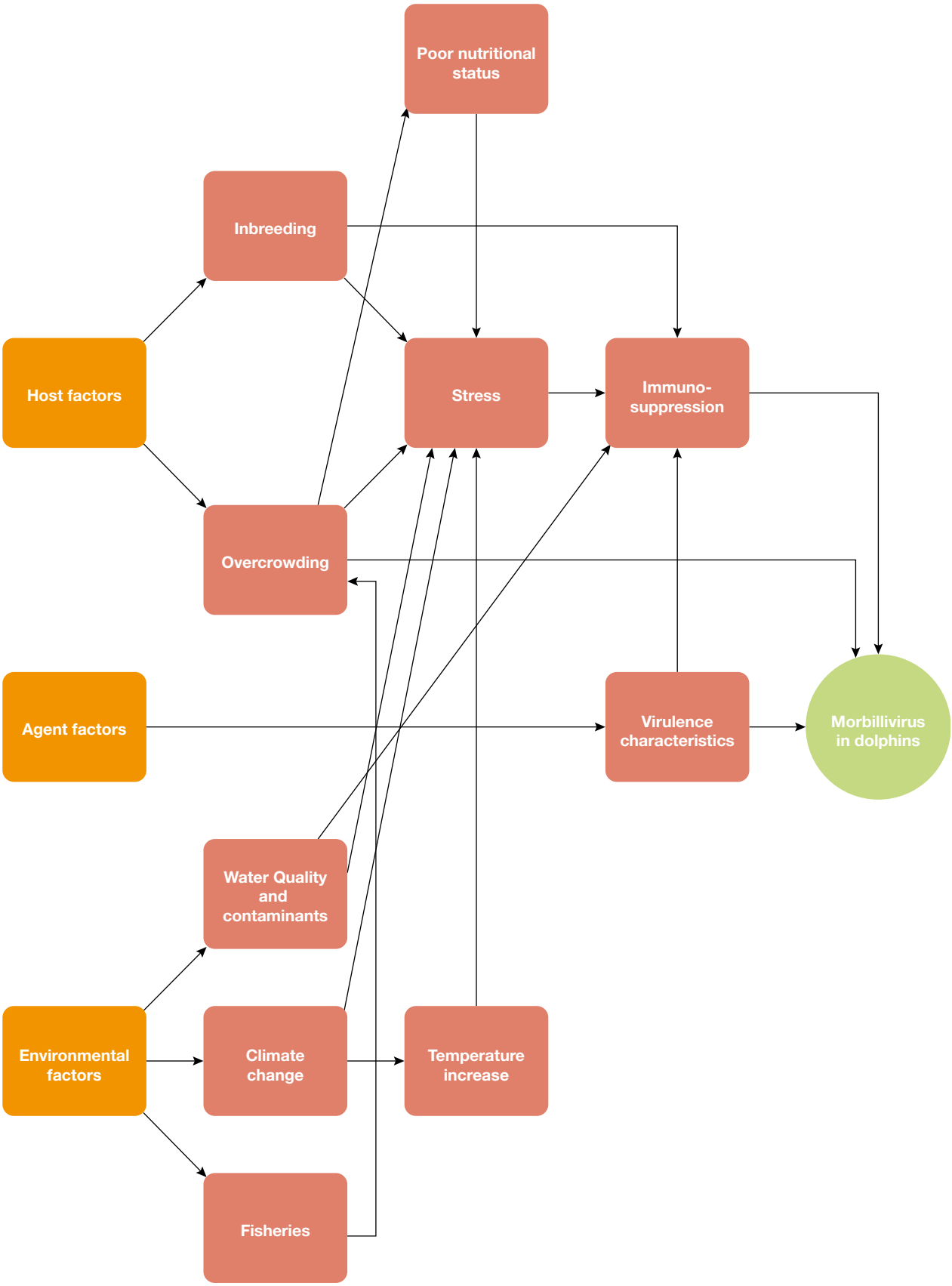


Fig. 13
Causal web model of morbillivirus infection in cetaceans
Figure 13 is a causal web of morbillivirus in dolphins. This was constructed easily using the program Miradi

Strengths and weaknesses, when to use and interpret with caution

Strengths (Murray *et al.* 2004):

- All variables can be identified.
- The relationship between variables can be identified.
- It ensures a logical chain of events.
- It provides a framework for quantification and mathematical modelling.
- It ensures *transparency* and accuracy with *risk estimation* for qualitative analyses.
- It assists with communicating the *model* structure.
- It clarifies ideas and the understanding of the problem.

This process needs to be thoroughly researched in order to be accurate, as the entire DRA process will be based on this information. If variables are ignored or accidentally excluded, this can significantly affect the validity of the DRA process.

Case study

An excellent example of a causal web is given in Thrusfield (2005), fig. 3.6, p. 42.

Tool 7: Decision trees

V. Dove

References

Marsh 1999; Noordhuizen 2001.

Source

This is a tool that will be developed and constructed by the person or team conducting the DRA.

Cost

Free if done manually. There is a software package called DATA that is available to help develop decision trees and simplify the process (see www.treeage.com/). Cost is moderate to high but the producer of the software also offers reduced student rates. Another programme that may be used is Precision Tree (see www.palisade.com/precisiontree/). The cost is high. This programme can also be purchased together with five other risk analysis software programmes, collectively called the Decision Tools Suite, which includes @Risk software. Prices are available through the website: www.palisade.com/decisiontools_suite/save.asp

Software requirements

Can be done manually with pen and paper or in Microsoft Office, including PowerPoint and Excel, but can also use the software programmes mentioned above.

Stage(s) of risk analysis when this would be used

Decision trees can be used both qualitatively and quantitatively, and are most valuable for the *hazard identification*, *risk management* and *risk communication* steps of the *risk analysis* process.

Description of tool use

Decision tree analysis offers a formal, structured, approach to decision making, taking into account the elements of *uncertainty* (Marsh 1999). These analyses allow us to model chance events related to sometimes complex decisions. Graphically these depictions represent the flow of events in a logical, time-related and structured way (Noordhuizen 2001). The first node of a decision tree is always a decision node (rectangular box), each branch of which leads to a terminal node or a chance node. The choice of the preferred course of action is made through a process called folding back, which is done by multiplying the monetary values at each terminal node by the probability at the proceeding chance node (Marsh 1999) The probabilities used can be obtained from the literature, field studies or expert opinion. If *diagnostic test*s are part of the decision process, then additional information such as test sensitivity, specificity and *predictive value*s are required, as these are related to the probabilities of occurrence of events listed on the decision tree (Noordhuizen 2001). In order to build a meaningful decision tree, all the possible courses of action to address the problem need to be identified.

The following four steps can be used as a guide to building a decision tree:

1. Draw the decision tree using squares to represent decisions and circles to represent *uncertainty*.
2. Evaluate the decision tree to make sure all possible outcomes are included.
3. Calculate the tree values working from the right side back to the left.
4. Calculate the values of uncertain outcome nodes by multiplying the value of the outcomes by their probability (i.e. expected values).

An example of a simple hypothetical decision tree is shown in Figure 14.

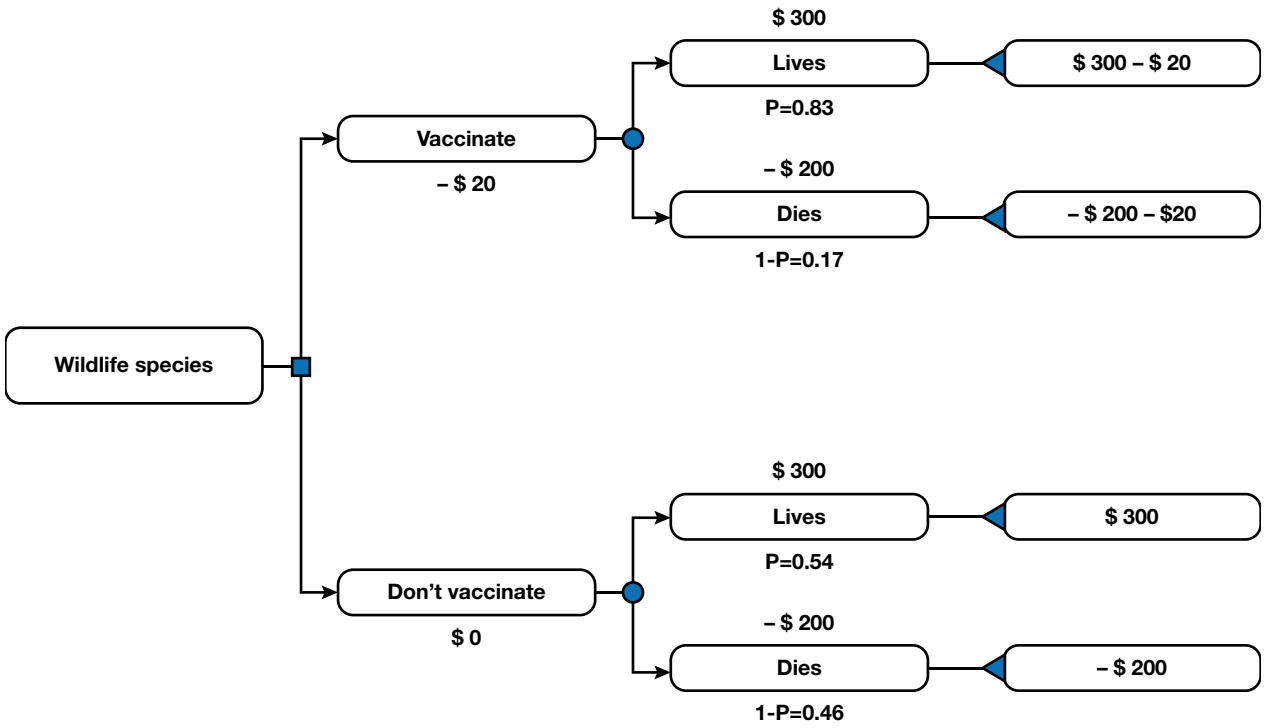


Fig. 14
Decision tree, assessing vaccination as a control strategy

Estimated value (EV)

- EV vaccination lives = 0.83 x (300–20) = $232.40
- EV vaccination dies = 0.17 x (–200–20) = –$37.40
- EV (vaccination) = $195
- EV No vaccination lives = 0.54 x 300 = $162
- EV No vaccination dies = 0.46 x –200 = –$92
- EV (No vaccination) = $70.

The value of the *wildlife* in this hypothetical example was given an arbitrary figure of $300 for the purpose of illustration. This may represent the value of the species in a captive facility, in a breeding programme, to conservation or to eco-tourism, etc. The value of the *wildlife* species that died was also given an arbitrary figure, taking into account necropsies, sample collection, loss to biodiversity, etc.

From this example, *vaccination* has been shown to be more profitable, assuming that the estimated values and probabilities are correct.

Decision trees can be more complex, as illustrated in Figure 15.

For complex decision trees, such as that in Figure 15, it is advisable also to construct an influence diagram, to simplify the decision-making process and aid in the communication of the analysis. For example the corresponding influence diagram would be as in Figure 16.

Influence diagrams are discussed in the following tools template.

Experience and expertise required to use the tool

An understanding of probability is an advantage.

Data requirements

A thorough understanding of the hazard of interest is required, as well as knowledge of all possible event outcomes, so that a meaningful decision tree can be constructed. Good-quality epidemiological data will be required for quantitative decision trees, for example known probabilities for the hazard of interest, test sensitivities and specificities, disease *prevalence*.

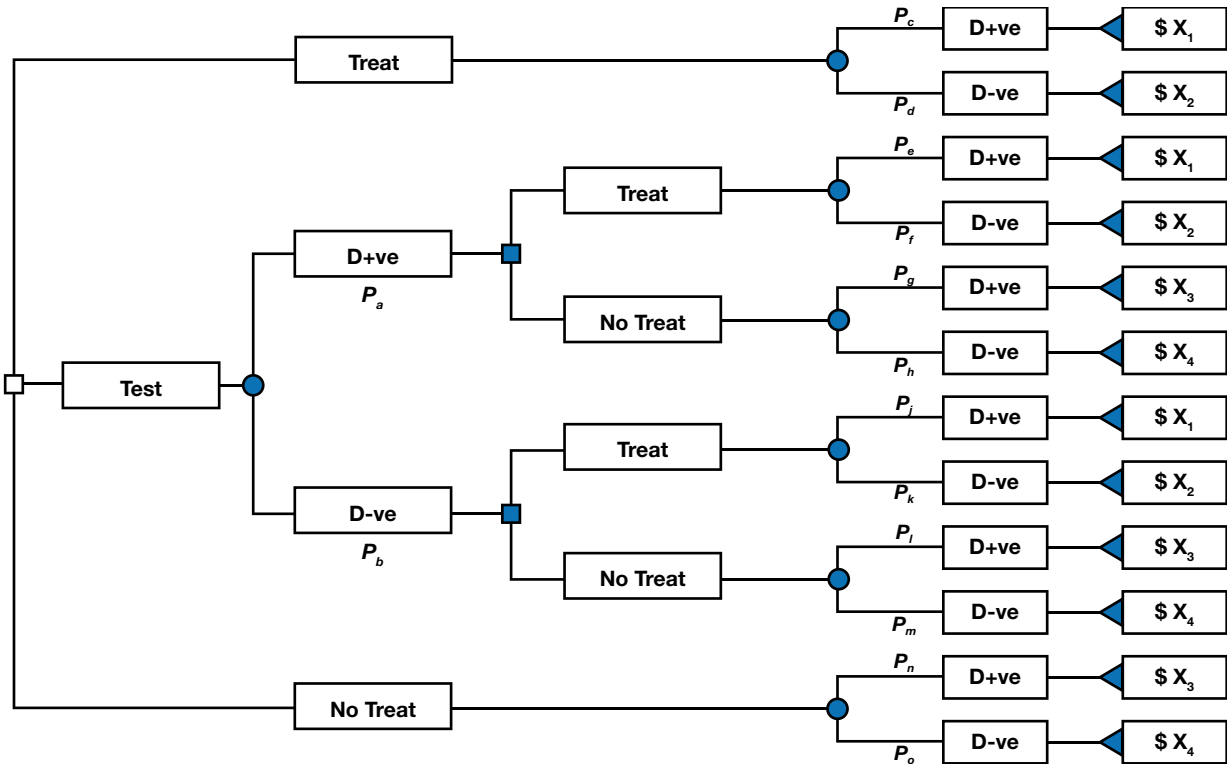


Fig. 15
Example of a more complex decision tree analysis
Where *p*(a–o) = probability; and X = dollar value.

Strengths and weaknesses, when to use and interpret with caution

Decision trees are useful as they:

- clearly demonstrate the various outcomes so that all options can be evaluated
- allow us to analyse fully the possible consequences of a decision
- provide a framework to quantify the values of outcomes and the probabilities of realising them
- help us to make the best decisions on the basis of existing information and expert opinion.

Decision trees have pitfalls in that the branch and node description of sequential decision problems can often become very complicated. Influence diagrams may be used together with decision trees, for added simplicity and *transparency* in the decision-making process. See Influence diagrams tool description.

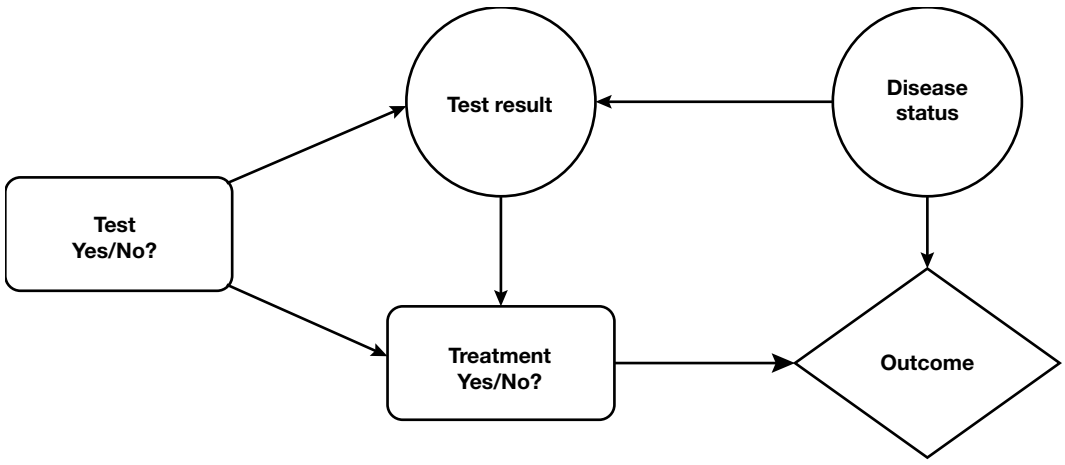


Fig. 16
Influence diagram that complements the decision tree in Fig. 15

Case study

Marsh (1999) offers an excellent example of a decision tree in fig. 1, p. 363.

Tool 8: Influence diagrams

V. Dove

References

Nease and Owens 1997; Murray *et al.* 2004; Ricci 2006.

Source

This is a tool that will be developed and constructed by the person or team doing the DRA. It can be done manually or with the aid of software programmes.

Cost

Free if done manually. Software programmes are available:

- Analytica creates decision models and can be used to build influence diagrams www.lumina.com/software/influencediagrams.html.
- Other programmes include DPL 6.0 www.syncopation.com/monte_60.html.

Software costs can be obtained from the websites.

Software requirements

None if done manually or Microsoft Office applications or the programmes mentioned above can be used.

Stage(s) of risk analysis when this would be used

Influence diagrams may be used in qualitative and *quantitative risk assessment*s and are especially useful at the *hazard identification*, *risk management* and *risk communication* steps.

Description of tool use

Influence diagrams are a conceptual modelling tool for the development of decision *models* and are useful as alternative graphical representations of decision trees, which can often become quite complex. These diagrams compactly and graphically represent the causal relationships among decisions, external factors, uncertainties and outcomes. In essence they demonstrate how different variables interact with one another as well as representing the probabilistic relationships between parameters in the *model*. Influence diagrams are mathematically equivalent to decision trees. However, when used together with decision trees they can be complementary, especially for representing probabilistic relationships among variables in a decision *model* (Nease and Owens 1997). Nease and Owens (1997) present five important principles for structuring a decision as an influence diagram:

1. Start at the value node and work back to the decision nodes.
2. Draw the arcs in the direction that makes the probabilities easiest to assess.
3. Use informational arcs (ending in a decision node) to specify which events will have been observed at the time each decision is made.
4. Ensure that missing arcs reflect intentional assertions about conditional independence and the timing of observations.
5. Ensure that there are no cycles in the influence diagram.

Influence diagrams have four types of nodes and two types of arc:

- *Decision node:* rectangle.
- *Chance node* (variables/*uncertainty*): circle or oval.
- *Deterministic node:* double circle or oval.
- *Value node (results/consequences):* diamond, or rectangle with rounded edges.
- *Influence/conditional arcs:* end on a chance node.
- *Informational arcs:* end in a decision node.

Figure 17 illustrates a simple influence diagram while Figure 18 illustrates a more complex example from a published *risk analysis*. The latter example models the risk of introducing and establishment of infectious bursal disease virus following importation of chicken meat into New Zealand (Ministry of Agriculture and Forestry Regulatory Authority 1999). While it is a useful depiction of a complex series of events, note that this figure does not observe the convention described above for the types of nodes.

Experience and expertise required to use the tool

Understanding of probability.

Data requirements

A good understanding of the hazard of interest is required; an influence diagram should be constructed with available probability data.

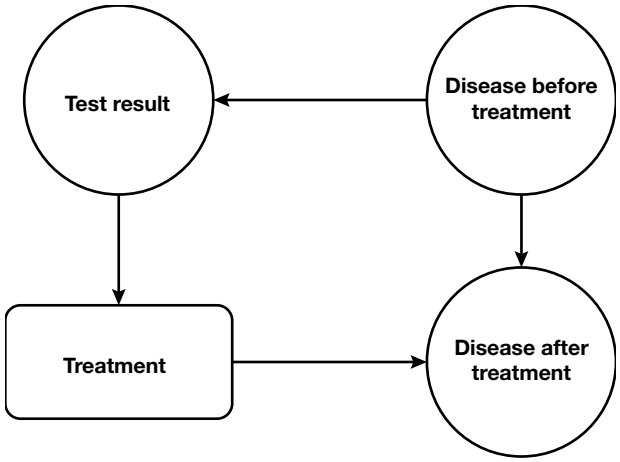


Fig. 17
Simplistic example of an influence diagram
Treatment: decision node
Test result, Disease status: chance nodes
Arrow ending on treatment: informational arc
Arrows ending on chance nodes: conditional arcs

Strengths and weaknesses, when to use and interpret with caution

Influence diagrams offer several strengths for structuring *risk assessment* decisions.

– They allow the *model* to be structured in a fashion that eases the necessary probability assessments, regardless of whether the assessments are based on available evidence or on expert opinion.

– They are useful for:
- facilitating communication among technical experts, decision makers and stakeholders
- integrating knowledge from different sources in decision making
- encouraging disciplined thinking about cause and effect relationships
- being explicit about *uncertainty*, in particular emphasising the existence of competing hypotheses and facilitating informed debate about them
- structuring subsequent quantitative modelling
- documenting the basis for and improving the *transparency* of the *risk assessment*.

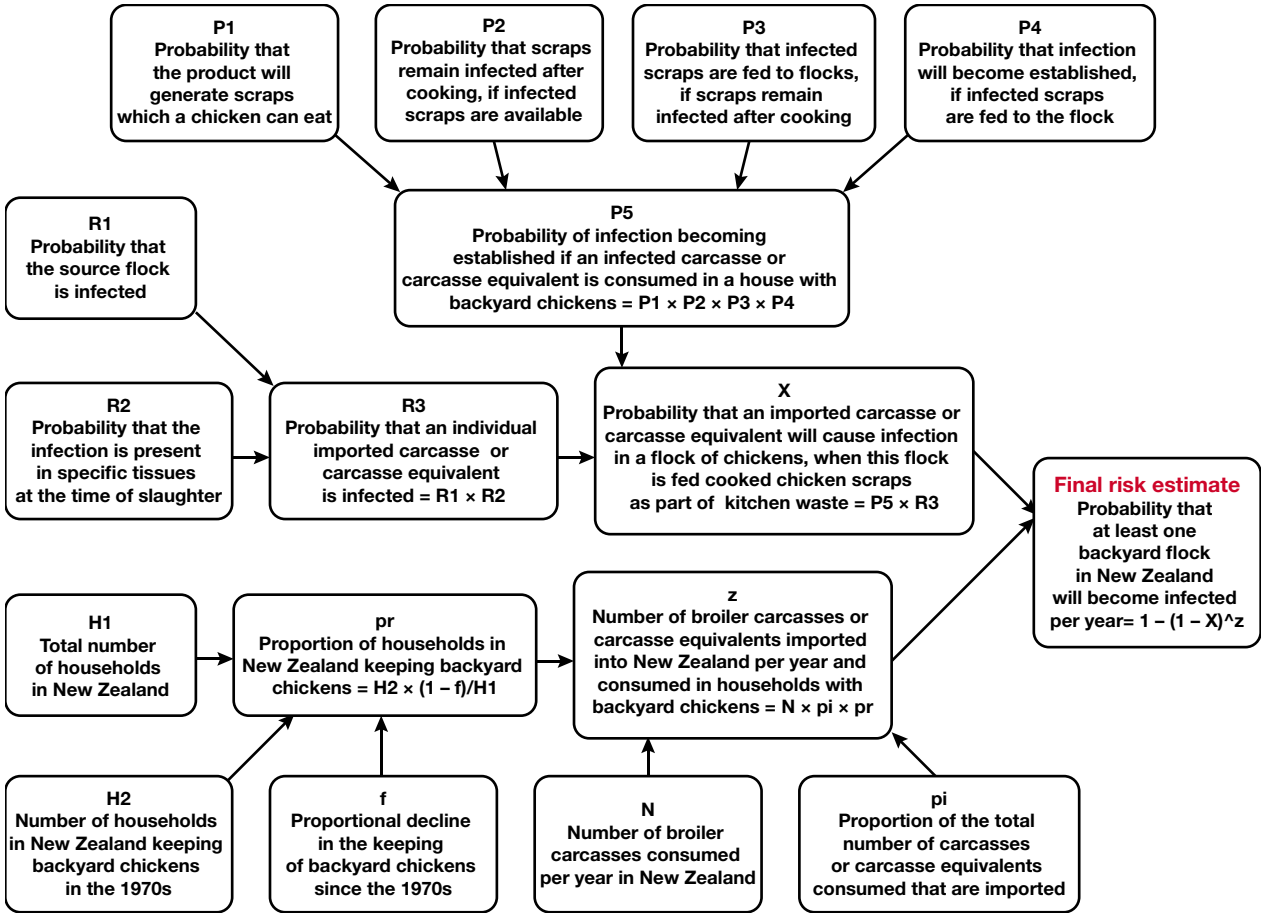


Fig. 18
An example of a complex influence diagram (Ministry of Agriculture and Forestry Regulatory Authority 1999)
From Murray *et al.* (2010). – Handbook on Import Risk Analysis for Animals and Animal Products, Volume 2. Quantitative Risk Analysis, 2nd Ed. World Organisation for Animal Health (OIE), Paris

Some common mistakes when constructing influence diagrams are:

– confusing influence diagrams with flow-charts, which are sequential in nature

– building influence diagrams with many chance nodes pointing to a primary decision node

– inclusion of cycles (circular paths among nodes).

Case studies

Ministry of Agriculture and Forestry (MAF) Regulatory Authority 1999.

Anonymous. – Difference between decision tree and decision table. Available at www.doc.ic.ac.uk/~frk/frank/da/9.Influence%20Diagrams.pdf.

Tool 9: Fault trees

V. Dove

References

Salman *et al*. 2003; Risebro *et al*. 2005.

Veseley W.E., Goldberg F.F., Roberts N.H. & Haasl D.F. (1981). – US Nuclear Regulatory Commission: Fault Tree Handbook. www.nrc.gov/reading-rm/doc-collections/nuregs/staff/sr0492/sr0492.pdf. This reference has a good chapter that clearly explains fault tree logic, and how to use this qualitative model.

Source

To be developed by the DRA team.

Cost

Free.

Software requirements

None, or these trees can be constructed using Microsoft PowerPoint.

Stage(s) of risk analysis when this would be used

Usually in a qualitative *model*, but can also be used in quantitative assessment during the *hazard identification*, *risk management* and *risk communication* steps.

Description of tool use

Fault tree analysis is a method of analysing the ways in which complex systems can fail, and for calculating overall failure rates from the individual component failure rates. Fault trees begin with the occurrence of a hazard (Fig. 19) and from there move backwards to identify and describe the events that must have occurred for the hazard to be present using fault logic gates such as 'AND' or 'OR'. This provides a framework to analyse the likelihood of an event by determining the complete set of underlying conditions or events that allow the given event to occur.

Risebro *et al.* (2005) describe fault tree analysis as a diagrammatical *risk assessment* technique to describe the sequence and inter-relation of possible events leading to an undesirable outcome (in this case, an outbreak). Using a top-down approach, preconditions for the undesirable outcome are determined until the basic causes are identified. All events are joined by a series of branches and gates. An AND gate requires all input events to occur; an OR gate requires one or more input events to occur. Typically the likelihood of each event is determined and probabilities are assigned. When this is done, the qualitative fault tree *model* can be used quantitatively.

Salman *et al.* (2003) provide a good example of a fault tree used in animal disease *surveillance* systems.

Figure 19 is a hypothetical example of a fault tree, where the hazard is 'Disease outbreak' occurring from animals selected for translocation. The events resulting in a disease outbreak include: disease-positive animals must be translocated *AND* the disease agent must infect susceptible naive animals. In the disease-screening process the events that lead to a disease-positive animal being translocated include:

– the first *screening test* fails, *and*

– the second *screening test* fails, *and*

– *quarantine* fails.

Experience and expertise required to use the tool

This tool is used frequently in the engineering field but has been infrequently used in animal risk assessments. However, there are few medical references in which this tool has been used. An understanding of simple logic gates, 'AND' and 'OR' gates, is required to use this tool successfully. Minimal experience is required.

Data requirements

A good understanding of the hazard of interest is required, so that all possible failure scenarios can be incorporated into this *model*. Minimal data are required for qualitative modelling. However, for quantitative *models*, probability data will be required.

Strengths and weaknesses, when to use and interpret with caution

Fault trees have a number of rules for their construction. It is important that the user is aware of the sequence of events for fault tree construction, so that the analysis will be sound. When used correctly these are useful tools. However, if mistakes are made in the construction of the fault tree, this can lead to a faulty analysis.

Case study

Risebro *et al.* 2005.

Tool 10: Scenario trees

V. Dove

Reference

MacDiarmid and Pharo 2003.

Source

This is a tool that will be developed and constructed by the person or team conducting the DRA. Scenario trees are simple to construct, and the user can refer to MacDiarmid and Pharo (2003) in which the various steps in constructing them are clearly outlined.

Cost

Free.

Software requirements

None.

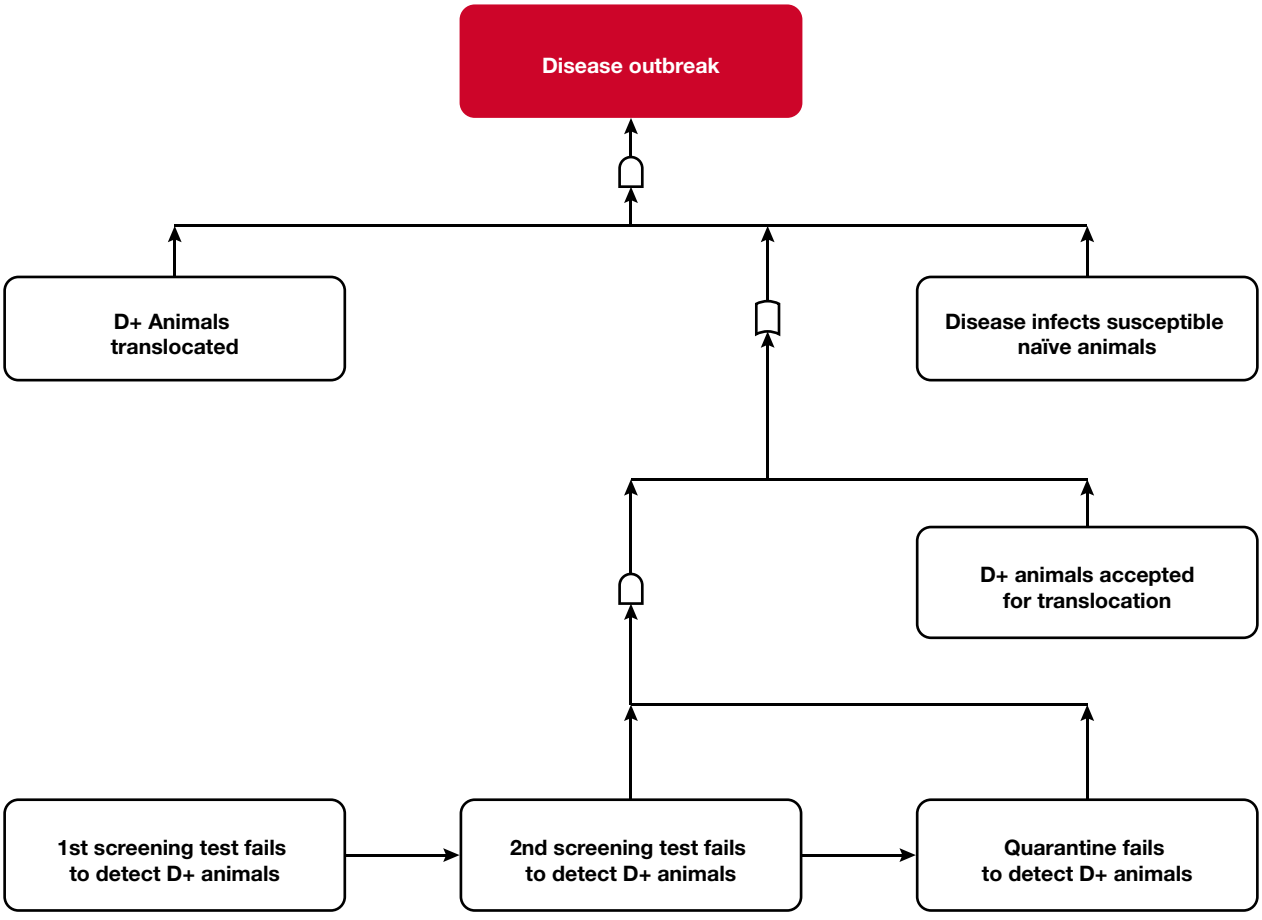


Fig. 19
Fault tree demonstrating the failures needed to result in disease outbreak

Stage(s) of risk analysis when this would be used

These graphical *models* will identify the various factors involved in the *risk assessment* process, and will be a vital resource that guides the *risk assessment* and can be used both qualitatively and quantitatively in the *hazard identification*, *risk management* and *risk communication* steps.

Description of tool use

Scenario trees are graphical depictions that outline the various biological pathways of expected events resulting in the occurrence of a defined outcome. Thus, these visual pictures provide a useful conceptual framework for the *risk assessment*. Scenario trees are useful tools in the *risk assessment* process, as they facilitate *transparency* and aid in communicating the risks to the various stakeholders, in a simple, logical and effective framework.

Scenario trees can be constructed for the following three steps in the *risk assessment* process:

– *release assessment*

– *exposure assessment*

– *consequence assessment.*

Scenario trees start with an initiating event such as:

– selecting a sample of animals to be tested that are potentially infected with the *pathogen* or *hazard* of concern

– disease exposure.

The scenario tree then has branches that outline the various pathways that lead to different outcomes such as:

– accepting animals (e.g. for translocation, export, captive breeding, etc.) that test negative for a particular agent of disease

– pathways that lead to a disease outbreak, or to other defined outcomes.

The following examples of scenario trees (Figs 20 to 25) are provided to give the reader a broad idea of how scenario trees can be used and adapted for different circumstances.

The consequence scenario tree in Figure 25 demonstrates the pathways leading to an outbreak (the consequence of interest) in animals selected for translocation.

Scenario trees can be used in both *qualitative risk assessment*s, as shown above, and *quantitative risk assessment*s. The difference between the scenario trees in the two different types of *risk assessment* is the addition of probability nodes in the quantitative analysis.

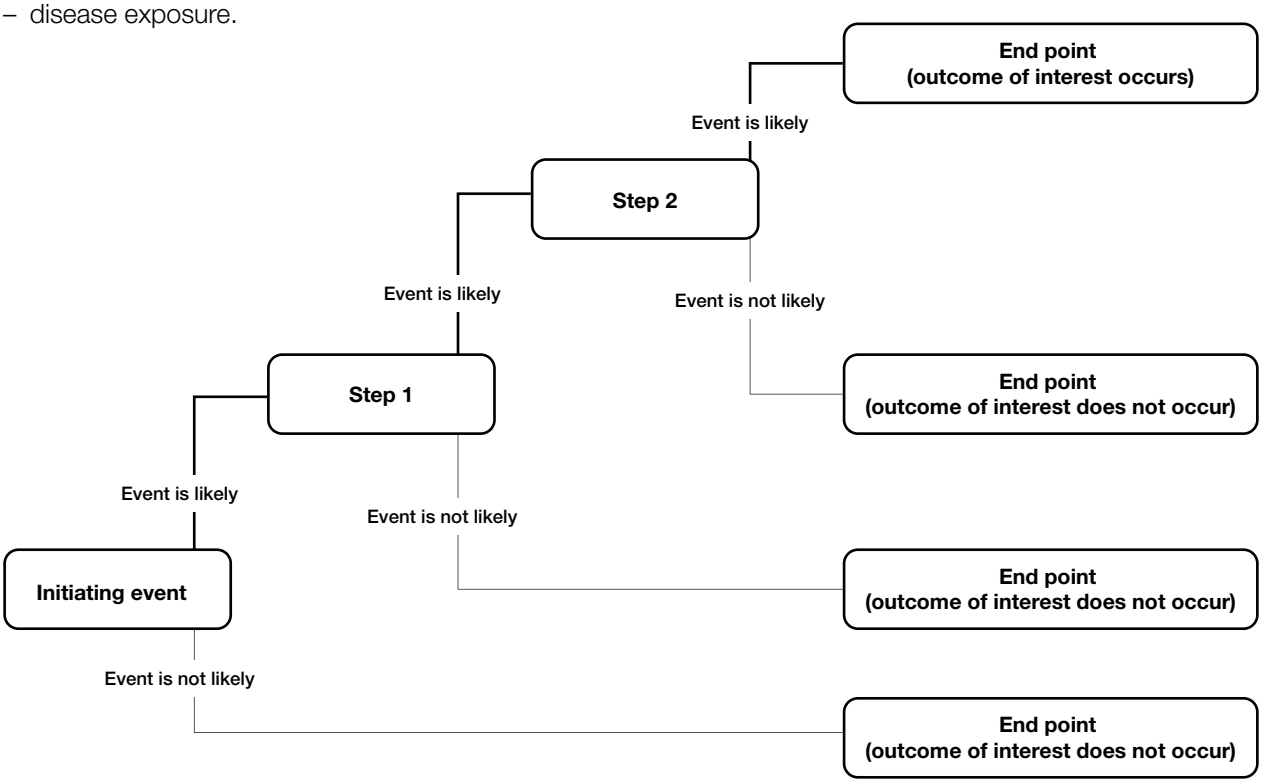


Fig. 20
Example framework for constructing a scenario tree (MacDiarmid and Pharo 2003)

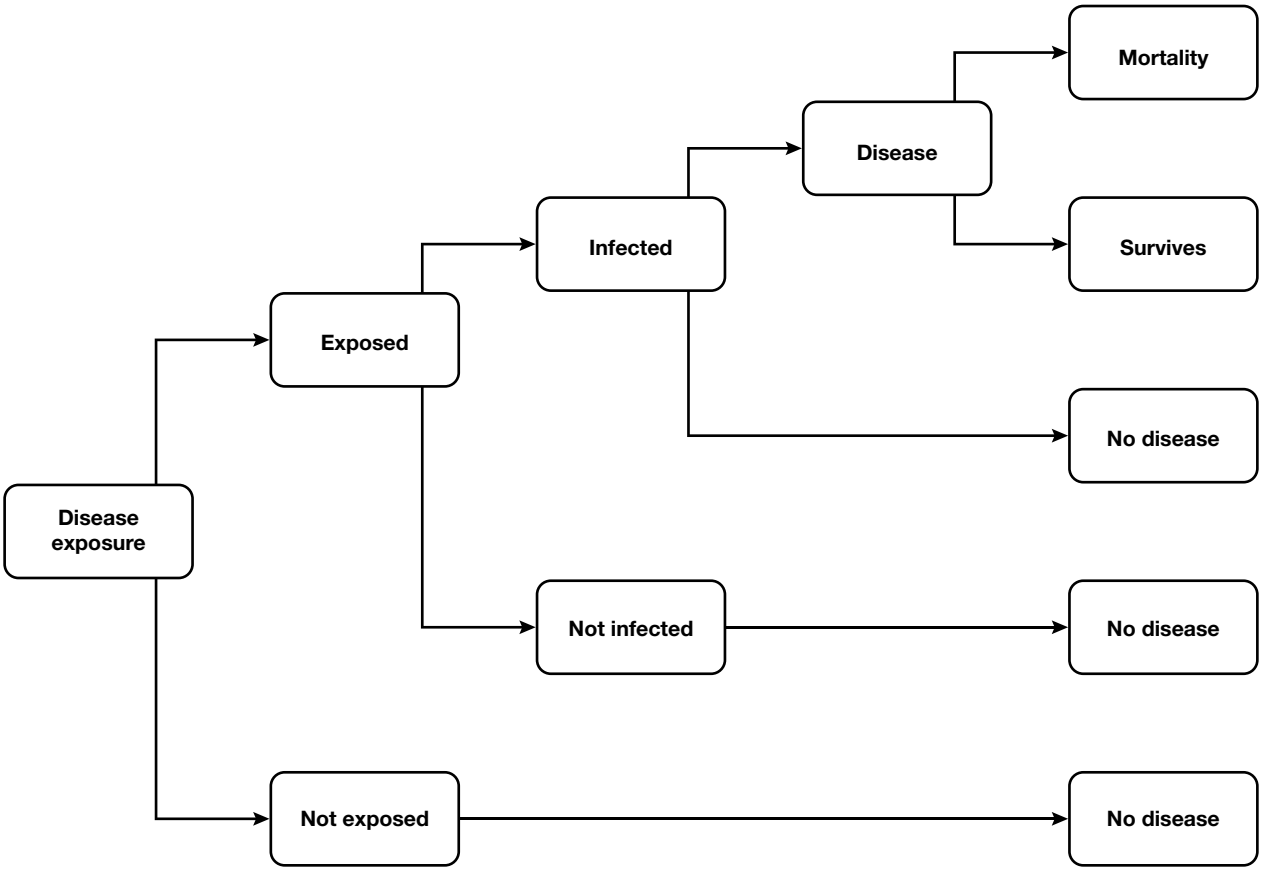


Fig. 21
Scenario tree outlining various events that may result in disease

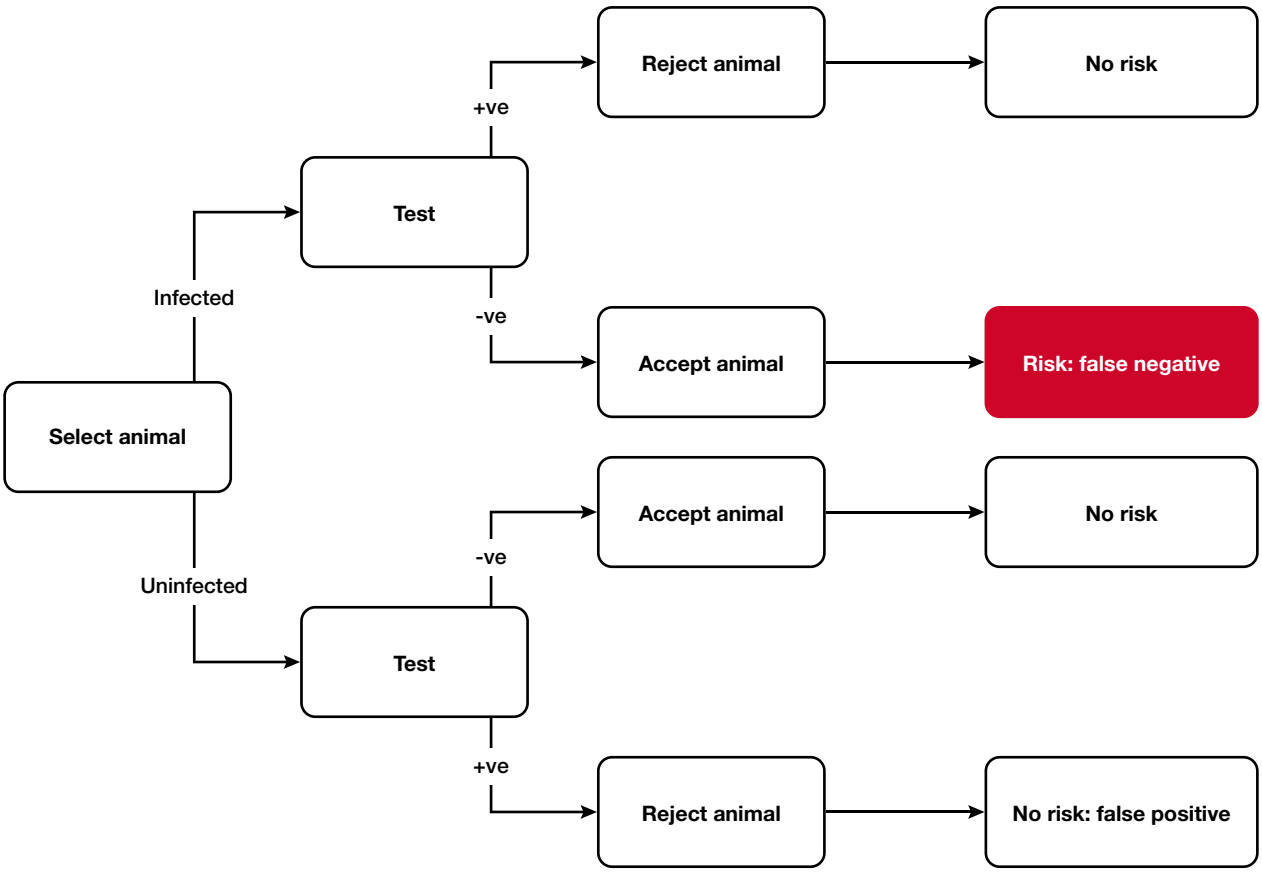


Fig. 22
Scenario tree outlining events that may result in a disease outbreak

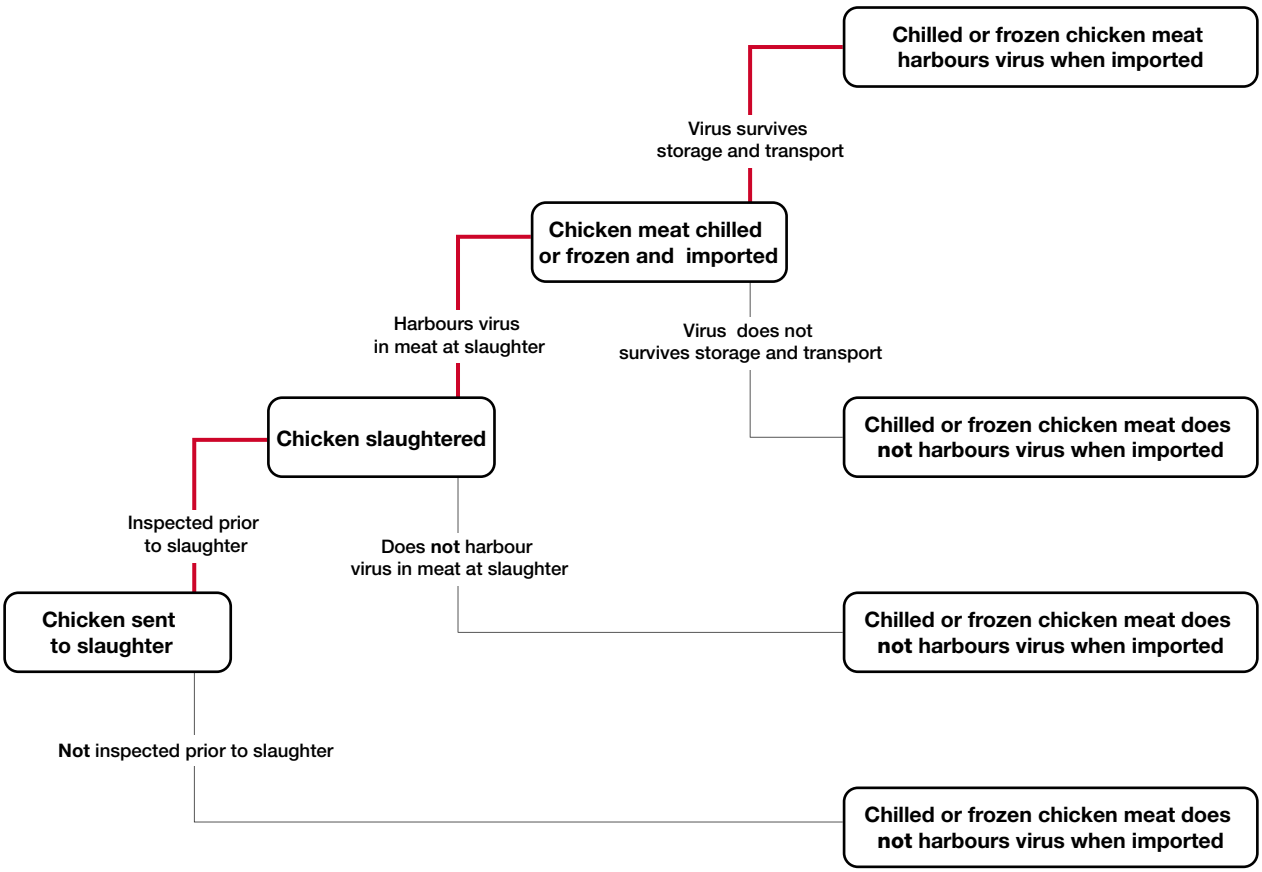


Fig. 23
Scenario tree for release assessment (MacDiarmid and Pharo 2003)

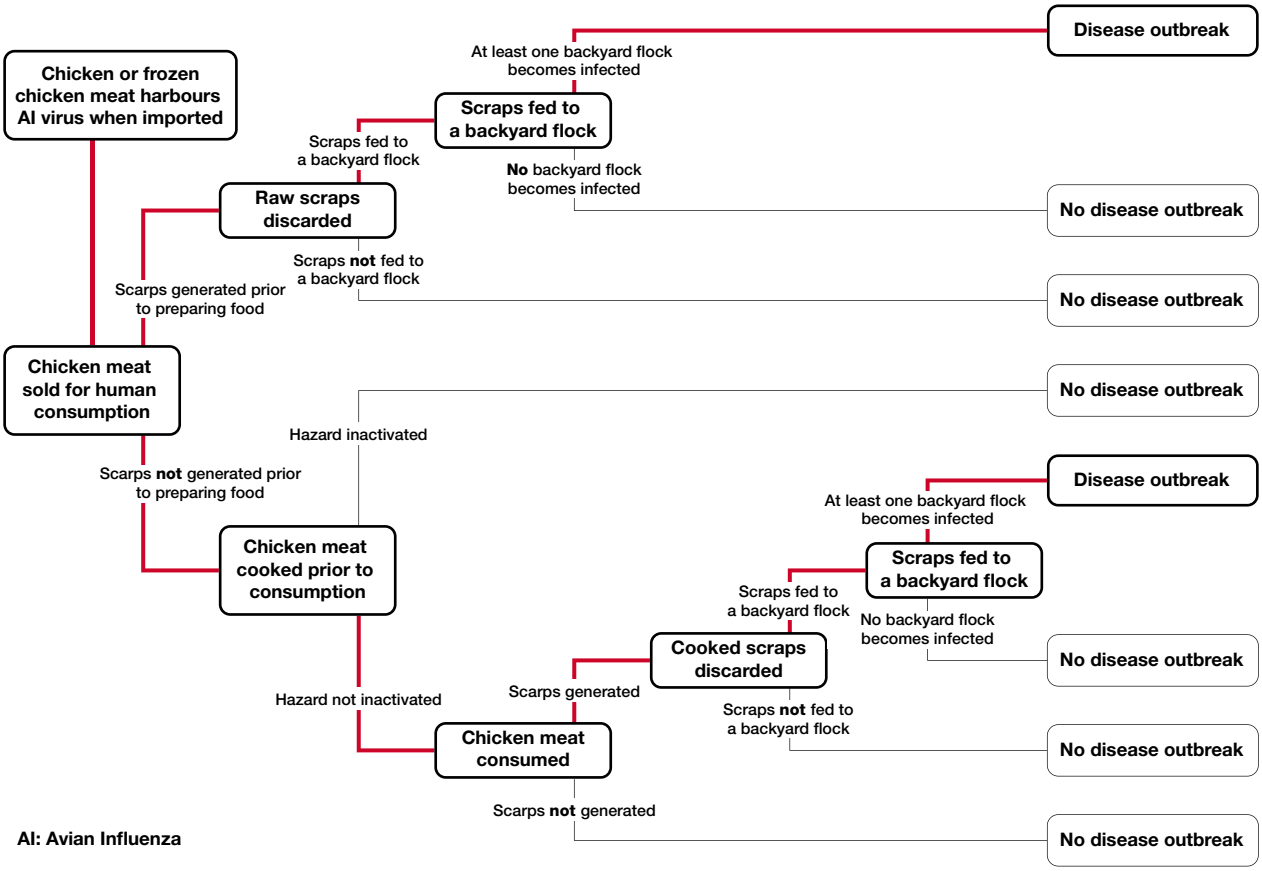


Fig. 24
Scenario tree for an exposure assessment
From MacDiarmid and Pharo (2003), *Rev. sci. tech. Off. int. Epiz.*, 22 (2)

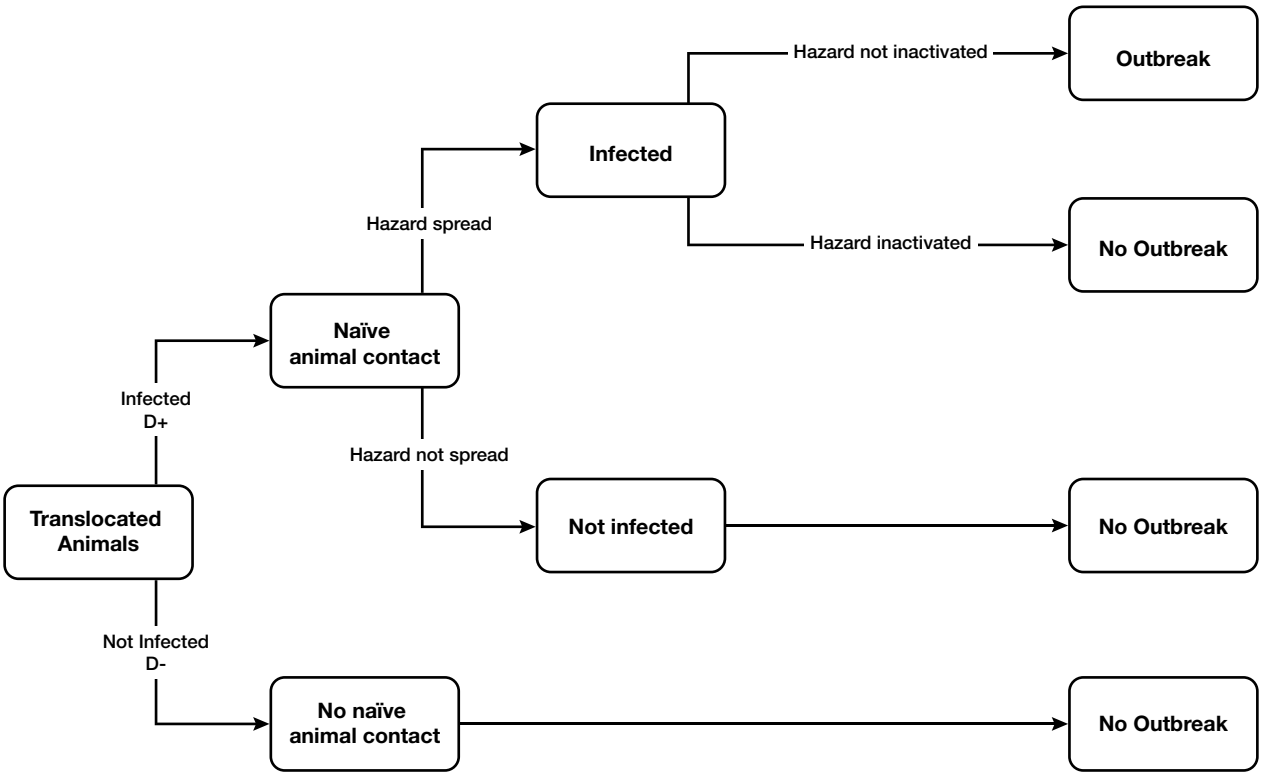
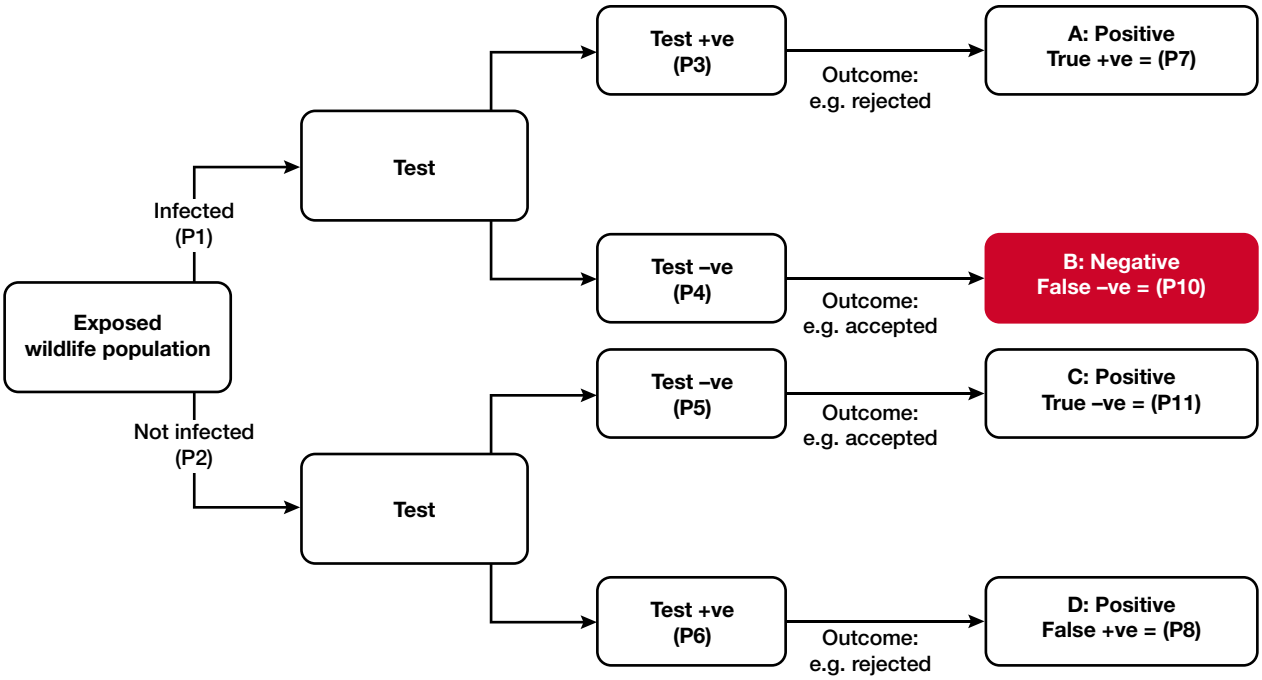


Fig. 25
Scenario tree for a consequence assessment



P1 p = probability of infection
P3 Se = sensitivity
P5 Sp = specificity

P2 1–p
P4 1–Se
P6 1–Sp

P7 p x Se
P8 (1–p) x Se
P10 p x (1–Se)
P11 (1–p) x Sp

Fig. 26
Probability testing scenario tree

Example of a scenario tree (with probability nodes)

The scenario trees used in the qualitative analysis can be used here, with the addition of probabilities included (Fig. 26).

Experience and expertise required to use the tool

No expertise is required to use this tool in qualitative analysis, but a thorough understanding of the identified hazard is required. An understanding of probability is required to use this tool for quantitative analysis.

Data requirements

A good understanding of the hazard of interest is required, so that all possible scenarios can be incorporated into this tool. Minimal data are required for qualitative modelling, whereas probability data will be required for quantitative *models*.

Strengths and weaknesses, when to use and interpret with caution

Scenario trees are useful tools providing all the relevant information has been taken into account and the underlying assumptions clearly stated. Scenario trees can be very simplistic or can incorporate a lot of probability data, allowing for more complicated quantitative assessments to be carried out. They are useful as they can be used in both qualitative and *quantitative risk assessment*s. Owing to the ease with which scenario trees can be evaluated and their *transparency* these *models* have few shortcomings.

Case study

MacDiarmid and Pharo 2003.

Tool 11: Cmap

M. van Andel

Reference

Novak J.D. & Cañas A.J. The theory underlying concept maps and how to construct and use them. Available at: http://cmapskm.ihmc.us/servlet/SBReadResourceServlet?rid=1064009710027_1637638703_27098.

Source

http://cmap.ihmc.us/download/

Cost

Free.

Software requirements

There are two versions available, Cmap and CmapLite. The latter is a version that has been reduced in functionality to allow it to run on machines with less available memory and older machines with a smaller main memory.

Stage(s) of risk analysis when this would be used

Used in the identification of hazards, *risk assessment* and *risk evaluation*. May also have use in the process of eliciting expert opinion. This software is a tool that allows mind maps to be represented and examined by other participants.

Description of tool use

A particular question or problem is identified. This could be in the form of a 'focus question'. Key concepts relating to the focus question in the context of the discussions are identified and entered into Cmap. Concepts can be ranked with the most general concepts at the top of the list and most specific concepts at the end. This list of concepts is called the 'parking lot' and concepts are moved from this area into the concept map and linked to show how different areas of the map relate to each other. Words can be added to the cross-links to show the relationships between the concepts. A review of the map should be performed to make sure that the relationships are clear and well structured. Not all concepts have to be used.

Cmap allows photographs, images, diagrams, graphs and videos to be linked to different concepts in the map. Furthermore, Cmap has servers that allow collaboration via the internet, facilitating review by remote parties of concept maps created in one geographical location.

Experience and expertise required to use the tool

No experience required, simple to use.

Data requirements

None.

Strengths and weaknesses, when to use and interpret with caution

This is a descriptive tool, not one that provides quantitative results. The strength of this tool is that it is a way for participants in the process to share their beliefs about cause and effect in a standardised and clear way with other participants, some of whom may be collaborating remotely.

Case study

Decker *et al.* 2006.

Tool 12: Geographic information systems

V. Dove and N. French

Name: GIS

References

Robinson 2000; Ostfeld *et al.* 2005; Clements and Pfeiffer 2009.

Source

A number of GIS software programmes are available. Below is a list of some of the more commonly used ones:

- EpiMap: a freely available mapping package that can be used as an alternative to ArcView. It does not contain all the features available in ArcView but is nevertheless useful for mapping. www.abdn.ac.uk/immpact/resources/gis/epimap.php
- Quantum GIS (QGIS): also a freely available, user-friendly open source geographic information system licensed under the GNU General Public License. www.qgis.org
- GRASS: free software used for geospatial data management and analysis, image processing, graphics or maps production, spatial modelling, and visualisation. Can be used effectively in combination with QGIS. http://grass.fbk.eu
- gvSIG: another free GIS. www.gvsig.org/web/
- ILWIS: free raster-based software. www.itc.nl/Pub/research_programme/Research_output/ILWIS_-_Remote_Sensing_and_GIS_software.html
- SAGA: another raster-based free GIS. www.saga-gis.org/en/index.html
- ArcView: the entry-level licensing level of ArcGIS Desktop, a GIS software product produced by Esri. Cost can be obtained at this site: www.esri.com/software/arcview/index.html
- Map info: cost reduced in the second year of use. Price available at: www.rockware.com/product/overview. php?id=274&gclid=CKmNy8P3mqsCFZFU7Aod63JjPA
- Maptitude price available at: www.caliper.com/maptovu.htm
- IDRISI: price available at: www.clarklabs.org
- Google Earth www.google.com/earth/index.html: free. Many simple applications are now using Google Earth for displaying spatial and spatiotemporal data for decision making (e.g. used to create kml files for displaying disease data and kmz files for displaying dynamic patterns).

Cost

As noted above many excellent GIS applications are available free.

Software requirements

Depends on the type of software that you determine best fits your need and budget.

Stage(s) of risk analysis when this would be used

During the *hazard identification*, *risk management* and *risk communication* steps.

Description of tool use

Factors affecting the spatial locations of *hazards*, hosts and *vectors*, and their probability of close encounter, are all important to disease dynamics (Ostfeld *et al.* 2005). Spatial epidemiology (the study of the spatial distribution of disease and associated factors) has arisen as the principal scientific discipline devoted to understanding the causes and consequences of spatial heterogeneity in infectious diseases, environmental contaminants, road kills, etc. Risk maps pertaining to specific diseases and climate and weather patterns can be linked to distributions of arthropod *vectors*, vertebrate *reservoirs*, or actual cases of disease in the host (Ostfeld *et al.* 2005). The principal reason for using spatial characteristics of disease and their causal agents is to assist with the decision-making process for disease intervention (Robinson 2000). GIS can then be used to formulate specific plans to manage or control disease, based on the techniques of spatial epidemiology, which can generate recommendations concerning where to

target interventions to prevent the spread of disease (Ostfeld *et al.* 2005), and based on cluster detection and early warning systems, which assist *surveillance* and can also permit timely interventions (Clements and Pfeiffer 2009). That is, GIS allows us to predict the spatial and temporal distribution of disease risk, so that appropriate intervention strategies can be developed (Robinson 2000).

GIS, together with remote sensing (RS), spatial statistics and spatially explicit mathematical *models*, constitute a powerful suite of tools for the study, prevention and control of infectious diseases (Clements and Pfeiffer 2009). However GIS alone is a tool that has been used to aid in decision-making and disease intervention strategies (Robinson 2000) as well as forming an underlying tool for examining landscape epidemiology (Ostfeld *et al.* 2005). It can be used to locate cases of disease and establish the spatiotemporal relationships among the cases and selected environmental features (Ostfeld *et al.* 2005). Mathematical *models* are particularly useful for testing and comparing alternative control strategies, whereas spatial decision-support systems integrate a variety of spatial epidemiological tools to facilitate widespread dissemination and interpretation of disease data (Clements and Pfeiffer 2009). Diseases tend to be limited geographically, with spatial variation arising from underlying variation in the physical or biological conditions that support the *pathogen* and its *vector*s and *reservoirs*. GIS allows these abiotic and biotic conditions to be delimited on maps, so both contemporaneous risk and future change in risk should be predictable (Ostfeld *et al.* 2005).

Ostfeld *et al.* (2005) describe the uses of GIS, which include:

– mapping how the spatial distribution of infectious diseases changes through time (spatiotemporal dynamics), e.g.:
  - retrospective analyses of spatiotemporally dynamic *epidemic*s to understand what factors govern the spatial pattern and rate of spread of diseases
  - characterisation of spatial variation in static ecological risk of infection and potential causes of that variation

– creating static risk maps based on distributions of *vector*s, *reservoirs* and disease incidence

– incorporating explicit landscape elements.

Experience and expertise required to use the tool

GIS is a specialist field, and expertise is required to use the available software tools.

Data requirements

Generally depends on good-quality data but varies with the software package being used.

Strengths and weaknesses, when to use and interpret with caution

One of the main strengths of GIS is their ability to integrate different types of spatial data (Robinson 2000). GIS can also be used with decision trees to implement effective control strategies. A major shortcoming of proprietary GIS programs is their limited but improving analytical capabilities (Robinson 2000). In addition good data are required for GIS analysis.

Case study

Ostfeld *et al*. 2005. Ostfeld and colleagues discuss the use of GIS with the foot and mouth disease outbreak that occurred in the United Kingdom during 2001.

Tool 13: OIE Handbook

V. Dove

Name: OIE Risk Analysis Handbook Volume 1 and Volume 2

Reference

Arrioja 2008; Brückner *et al*. 2010; Murray *et al*. 2010.

Source

Handbook on import risk analysis for animals and animal products. Volume 1: Introduction and qualitative risk analysis. Available at: http://web.oie.int/boutique/index.php?page=ficprod&id_produit=995&lang=en.

Handbook on import risk analysis for animals and animal products. Volume 2: Quantitative risk analysis. Available at: http://web.oie.int/boutique/index.php?page=ficprod&id_produit=45&lang=en.

Cost

These are relatively inexpensive and available through the OIE online bookshop at http://web.oie.int/boutique/index.php?lang=en

Software requirements

None.

Stage(s) of risk analysis when this would be used

These handbooks are an important resource that can be used throughout the entire DRA process. Volume 1 deals with *qualitative risk analysis*, and Volume 2 deals with *quantitative risk analysis*.

Description of tool use

Arrioja (2008) provides a comprehensive review of both volumes of the handbook, which is summarised below:

Volume 1 has three chapters:

- Chapter 1 introduces the concept of *risk analysis* in an international environment and defines terminology.
- Chapter 2 explains how to apply the *risk analysis* framework recommended by the OIE and describes the different components and tasks inherent in conducting a *risk analysis*. One of the components is *risk assessment*, which is a method for evaluating the likelihood and relevance of adverse consequences upon entry or spreading of a pathogenic agent in an importing country.
- Chapter 3 covers *risk communication*.

Volume 2 has eight chapters covering the statistical methods used in *risk analysis*:

- Chapters 1 to 4 introduce the principles of *quantitative risk assessment* and provide an overview of relevant statistical theory, for example probability distributions (binomial, central limit and Bayes's theorems) and binomial and Poisson's probability distributions.
- Chapters 5 to 7 further elaborate on statistical methods applicable to *risk assessment*, for example binomial versus hyper-geometric probability calculations, determining a suitable distribution for a given case, and second-order modelling. Tables of exact binomial confidence limits can be found in Appendix 1 of *Volume 2* of this publication.
- Chapter 8 provides guidelines for developing a *quantitative risk assessment model*.

Experience and expertise required to use the tool

Volume 1 is relatively simple and straight forward to use as a DRA tool. A background in epidemiology would be useful, and a thorough understanding of the hazard of interest and a comprehensive literature review should enable inexperienced persons to carry out a meaningful qualitative *risk analysis*.

Volume 2 is concise and comprehensive. However a background in statistics and statistical methodology is required in order for the user to fully understand and utilise the mathematical formulae.

Data requirements

Risk may be assessed qualitatively, according to the circumstances and data available, and this is a valid approach which is particularly useful when limited data are available. If sufficient data are available, evaluating likelihood in terms of statistical probability contributes to accuracy, provided all assumptions and limitations are clearly stated.

Strengths and weaknesses, when to use and interpret with caution

These volumes are an excellent reference tool that can be used to guide the DRA process, from simple *models* in *Volume 1*, to complex statistical *models* in *Volume 2*. The handbook however is focused on *risk analysis* with regard to importing animals and animal products, so this has to be kept in mind when adapting the situation to *wildlife* disease, and conservation scenarios.

Case studies

Case studies are given throughout the handbook to demonstrate the use of all DRA tools discussed.

An example case study that uses some principles of the handbook is Thrush *et al.* 2011.

MacDiarmid and Pharo (2003) closely follows the application of the DRA tools discussed in the Handbook.

Tool 14: @Risk

S.C. MacDiarmid

Name: @Risk. Risk analysis and simulation add-in for Microsoft Excel.

References

Vose 2000; Murray *et al*. 2004.

Source

Palisade Corporation, 31 Decker Road, Newfield, New York. www.palisade.com/risk/

Cost

Free trial version available for download; purchase price is available on the website.

Software requirements

Microsoft Excel

Stage(s) of risk analysis when this would be used

Throughout the process of a *quantitative risk assessment* step.

Description of tool use

@Risk is an add-in for Microsoft Excel. When constructing a *quantitative risk assessment* spreadsheet, @Risk allows the user to assign probability distributions, rather than single numerical values, to each input variable. Such a *model* is called a stochastic or Monte Carlo model. It allows the risk analyst to calculate the combined impact of variation in each of the model's inputs to determine a probability distribution of the possible outcomes. This is achieved by carrying out a simulation in which random values are automatically sampled from each input distribution and combining these, according to the mathematical logic of the *model*, to produce an output. This is repeated automatically in many iterations the outputs of which are combined to produce a probability distribution of possible model outcomes.

Experience and expertise required to use the tool

An intermediate level of experience and expertise is required to use @Risk, but it is advisable to have an experienced quantitative risk analyst review the appropriateness of the probability distributions applied to each input variable.

Data requirements

The data requirements can be minimal as @Risk lends itself to inputs elicited from expert opinion (see Vose 2000; Murray *et al.* 2004).

Strengths and weaknesses, when to use and interpret with caution

The strengths of @Risk are that it is relatively easy to use for anybody familiar with Microsoft Excel or other spreadsheets. It can be used for simple or complex *models* and can incorporate a range of data inputs ranging from simple uniform or triangular distributions obtained from expert opinion through over 30 other distributions selected on the basis of quantity, quality and type of data. *Sensitivity analysis* of *risk assessment models* is easy and straightforward with @Risk. The quality of outputs is determined by the logic of the *model* and the quality of the data used for the input variables.

Case studies

Paisley 2001; Pharo and MacDiarmid 2001.

Tool 15: OUTBREAK

P.S. Miller

Name: OUTBREAK, a stochastic computer simulation *model* of disease epidemiology in animal populations.

Reference

Verant M. & Miller P.S. (2011). – *OUTBREAK User's Manual*. IUCN/SSC Conservation Breeding Specialist Group, Apple Valley, Minnesota.

Source

OUTBREAK is available from the Conservation Breeding Specialist Group website, www.cbsg.org.

Cost

The software is available at no cost from the CBSG website.

Software requirements

OUTBREAK is a Windows programme and will work under all modern versions of the operating system. While the programme will work with nearly any amount of memory (RAM), analysis of larger populations (e.g. > 5,000 individuals) will be hampered by insufficient memory. At least 1GB of RAM is recommended.

Stage(s) of risk analysis when this would be used

OUTBREAK is designed to be used in the *risk assessment* step, where detailed evaluation of the impacts of disease introduction or *transmission* in animal populations under alternative scenarios is required. Also, it can be used in the *risk management* step where the relative impacts of alternative disease management strategies – including *vaccination* and culling – may be explored.

Description of tool use

Input data on species demography and disease epidemiology, corresponding to a unique model scenario developed by the user, are entered into specific fields located on a set of tabbed input pages (Fig. 27). This set of input data, along with the resultant output, constitutes a modelling project. When model parameterisation is completed, the user specifies the number of iterations to run for that scenario. When the *model* has run through the designated number of iterations, the user interacts with a series of pages that depict the demographic and epidemiological structure of the population. Graphical output (Fig. 28) can be copied to a separate project report page where graphs and text can be combined to create a written description of the *model* results.

Experience and expertise required to use the tool

Users should be experienced in the use of computer simulation *models*, including the appropriate analysis of demographic and epidemiological data. While the software is rather simple to use at a basic level, expertise in the relevant biological and statistical fields is strongly recommended for proper use of the tool.

Data requirements

Simple demographic data (fecundity and survival rates) are required to characterise the growth potential of the population. In addition, detailed data on the epidemiology of a specific disease is necessary, such as contact rate, *transmission* probability, latent period, duration of *infectious period*, disease-based mortality rate, probability of recovery, etc.

Strengths and weaknesses, when to use and interpret with caution

OUTBREAK provides an outstanding platform to explore the epidemiological dynamics of infectious disease in animal (production and *wildlife*) populations, and the impact of the disease on population demographic structure and future viability.

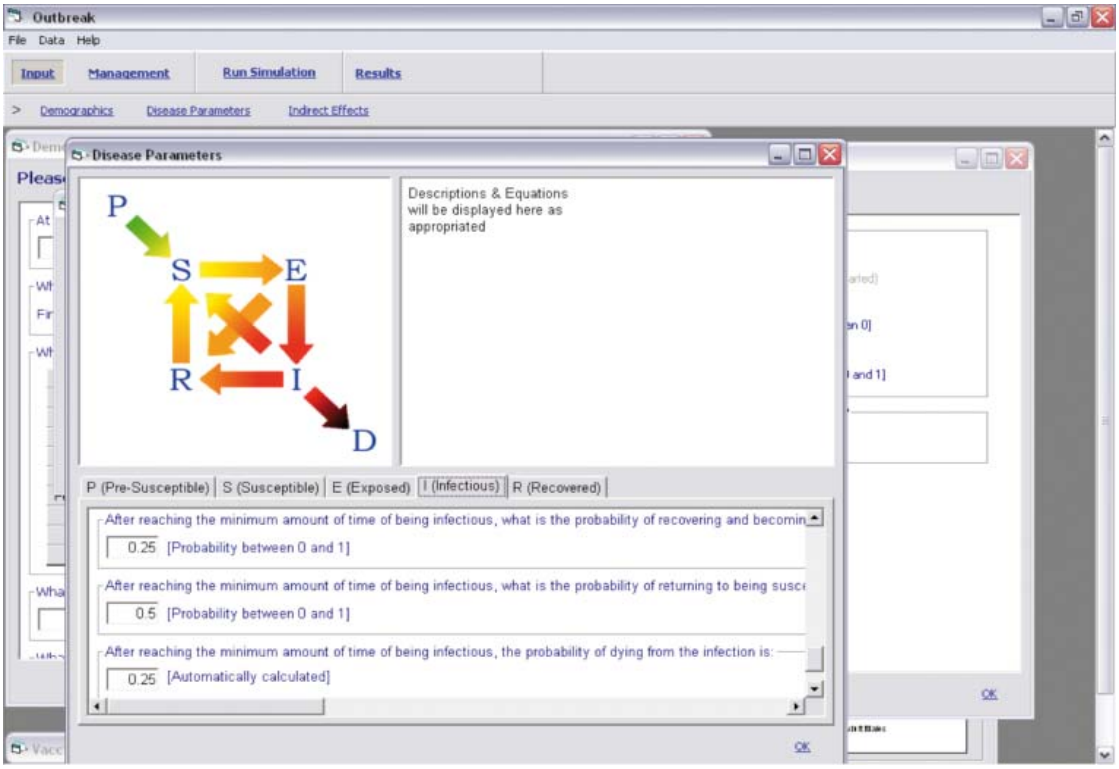


Fig. 27
Graphical interface for the OUTBREAK simulation software

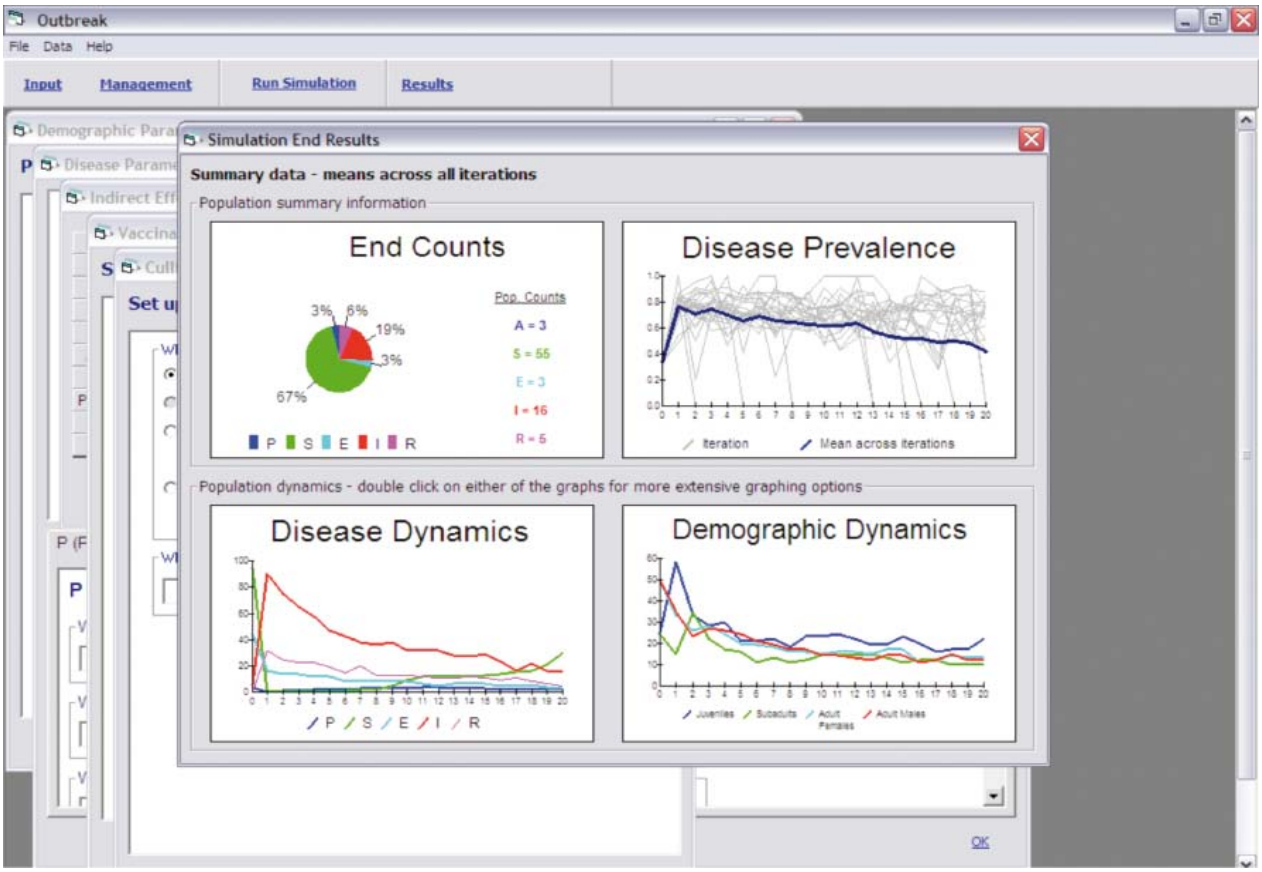


Fig. 28
Sample output from a simulation using OUTBREAK

The software is flexible and adaptable to a variety of infectious disease types, and can be tailored to a variety of species (mostly mammals, birds and reptiles). The software can also be linked to other demographic *models* such as Vortex (written by R.C. Lacy and available at www.vortex9.org) through a process known as metamodelling, thereby greatly increasing the *model's* realism and utility. (Contact pmiller@cbsg.org for more information on this capability). However, as the *model* counts each individual, there is a limit to the size of the population under consideration – typically in the order of 10,000 individuals. The *model* will run significantly more slowly when populations are large (e.g. >5,000) or when computer hardware is inadequate. In addition, as this is a relatively advanced quantitative tool for disease risk assessment, a rather high level of expertise in the relevant fields of study is strongly recommended for proper use of the tool.

Case studies

Keet *et al*. 2009; Bradshaw *et al.* 2012.

Tool 16: PopTools

M. van Andel & V. Dove

References

www.poptools.org/

CSIRO (The Commonwealth Scientific and Industrial Research Organisation). Once installed PopTools has an extensive 'Help' file that describes each function.

Hood G.M. (2011). – PopTools version 3.2.5. Available on the internet. URL www.poptools.org; e-mail: poptools@csiro.au

Source

www.poptools.org/download/

Cost

Free.

Software requirements

Microsoft Excel (PopTools is an Excel add-in).

Stage(s) of risk analysis when this would be used

PopTools can be used at the *risk assessment* step once an appropriate probability distribution has been selected to model the available data using a Monte Carlo simulation (e.g. binomial, Poisson, hypergeometric, exponential, gamma, beta, pert, triangular, uniform, normal, log-normal distribution, etc.). A good understanding of probability distributions can be obtained in Murray *et al.* (2004)

Description of tool use

PopTools is an add-in for Microsoft Excel. PopTools helps with the analysis of matrix population *models* and the simulation of stochastic (random) processes. It adds more than 100 new worksheet functions to Excel, including the ability to generate random variables in different distributions without knowledge of programming. PopTools has four main functions:

1. Matrix tools: used for the analysis of population dynamics and life-history strategies.

2. Tools for stochastic processes, including generation of random variables in a variety of distributions. It includes statistics for random (stochastic) processes.

3. Simulation: models can be constructed to represent both random and predetermined (deterministic) processes.

4. Statistical and graphical processes.

Experience and expertise required to use the tool

PopTools requires no knowledge of programming and is easy to use. However, the results of the analyses and the selection of appropriate statistical analyses require some existing knowledge of probability and statistics.

Data requirements

Depends on the probability distribution you have selected, and what question you want answered (see example in Table XI).

Example of using binomial distributions in PopTools

If we have five animals (n = 5), with a 10% *prevalence* (p = 0.1) of disease *y*, calculate the number of test positives (x) you are likely to get.

This is a simple scenario that will demonstrate how PopTools in Microsoft Excel can be used to generate an answer.

Strengths and weaknesses, when to use and interpret with caution

PopTools is a powerful tool and a great resource for those who cannot afford the program @Risk. Unfortunately, few resources exist to assist with learning how the programme works, and so becoming a competent user can take some initial trial and error, though familiarity with other modelling programmes such as MARK (http://warnercnr.colostate.edu/~gwhite/mark/mark.htm) will speed the learning process. Occasionally, when running simulations, PopTools can be slow, particularly when running on a Windows-based PC with a slow processor.

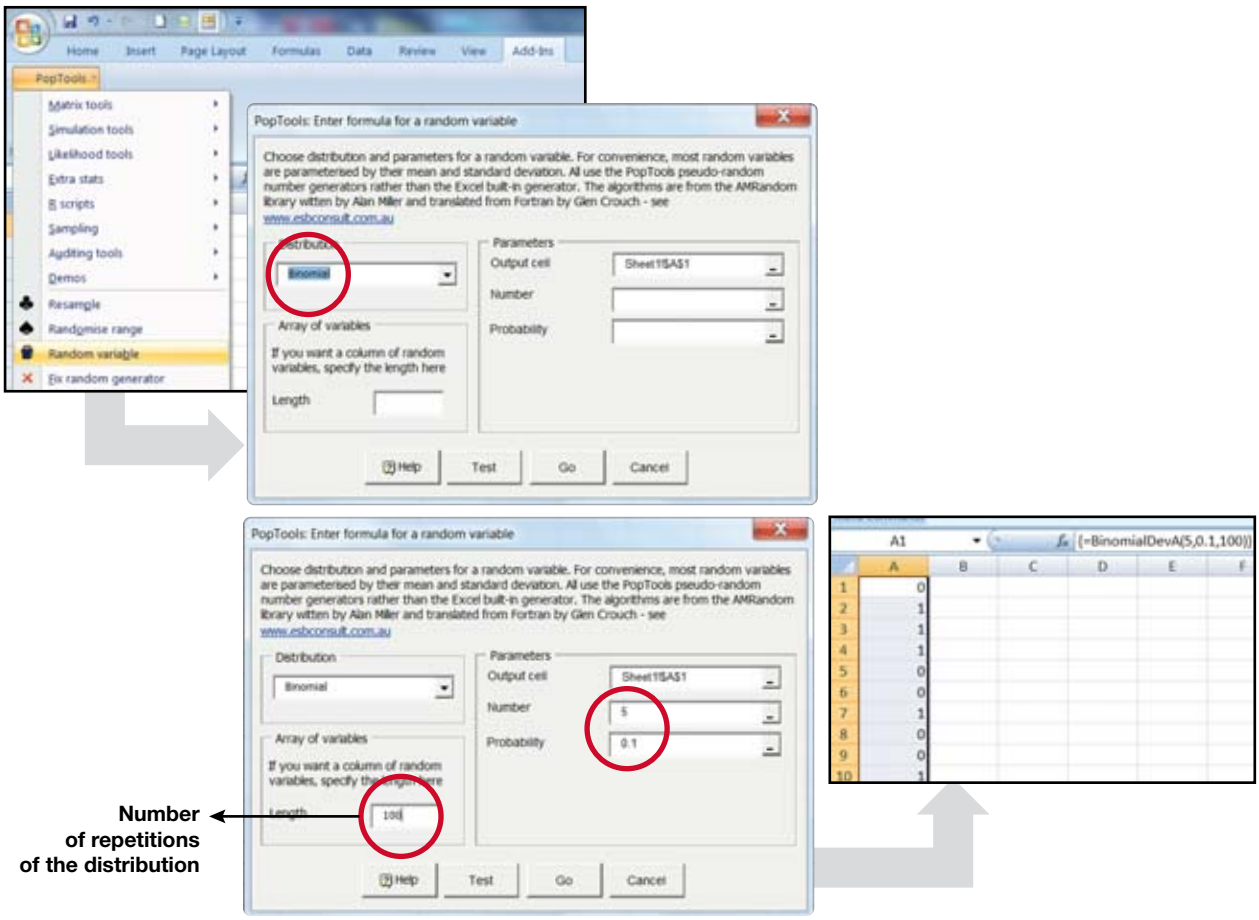
Case studies

More than 600 peer-reviewed references are listed at www.poptools.org/papers_all/, for example: Vose 2000; Murata *et al.* 2003; Murray *et al.* 2004; Budke *et al.* 2005; Di Stefano *et al.* 2007; Davis 2008; Hood *et al.* 2009.

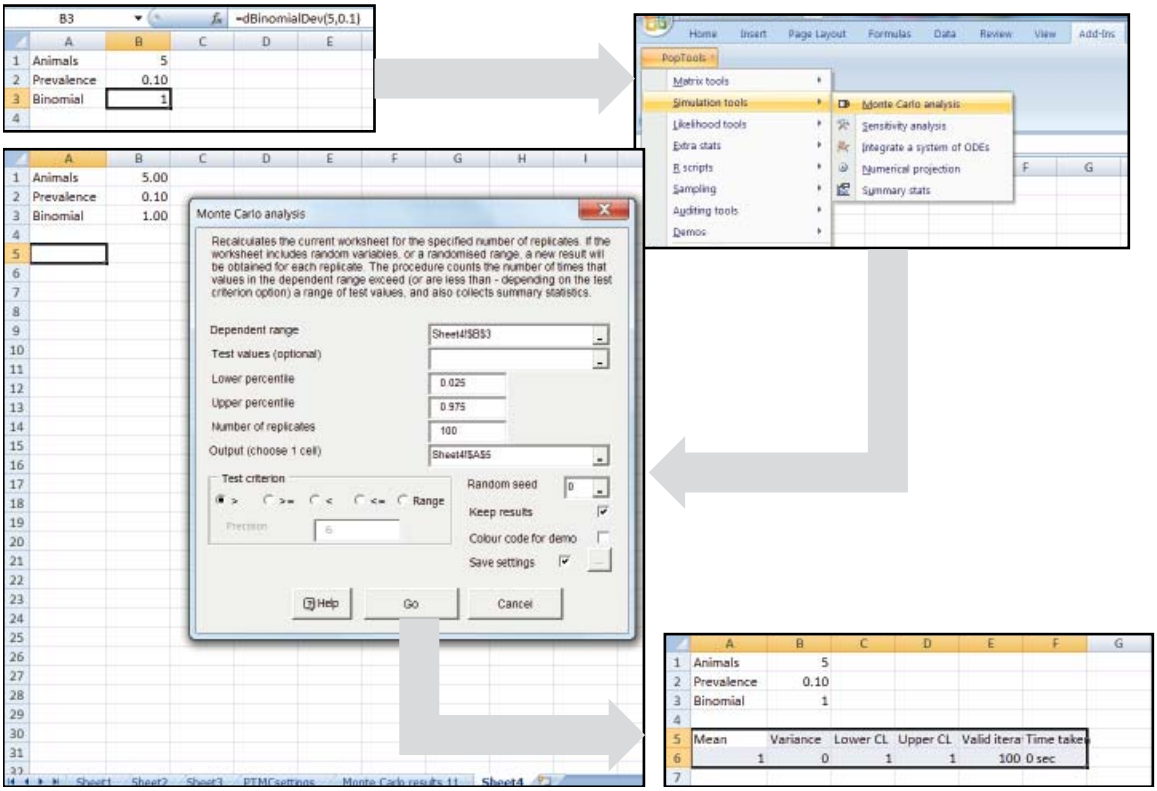
Table XI
Summary of probability distributions selected for modelling data

Probability distribution	Models for	Data required	Examples
Binomial	Successes (x)	n p	x = Binomial (n,p)
Beta	Probability of success (p)	n x	p = Beta (x + 1, n – x + 1)
Negative binomial	No. of trials (n)	x p	n = x + Negative binomial (x,p)

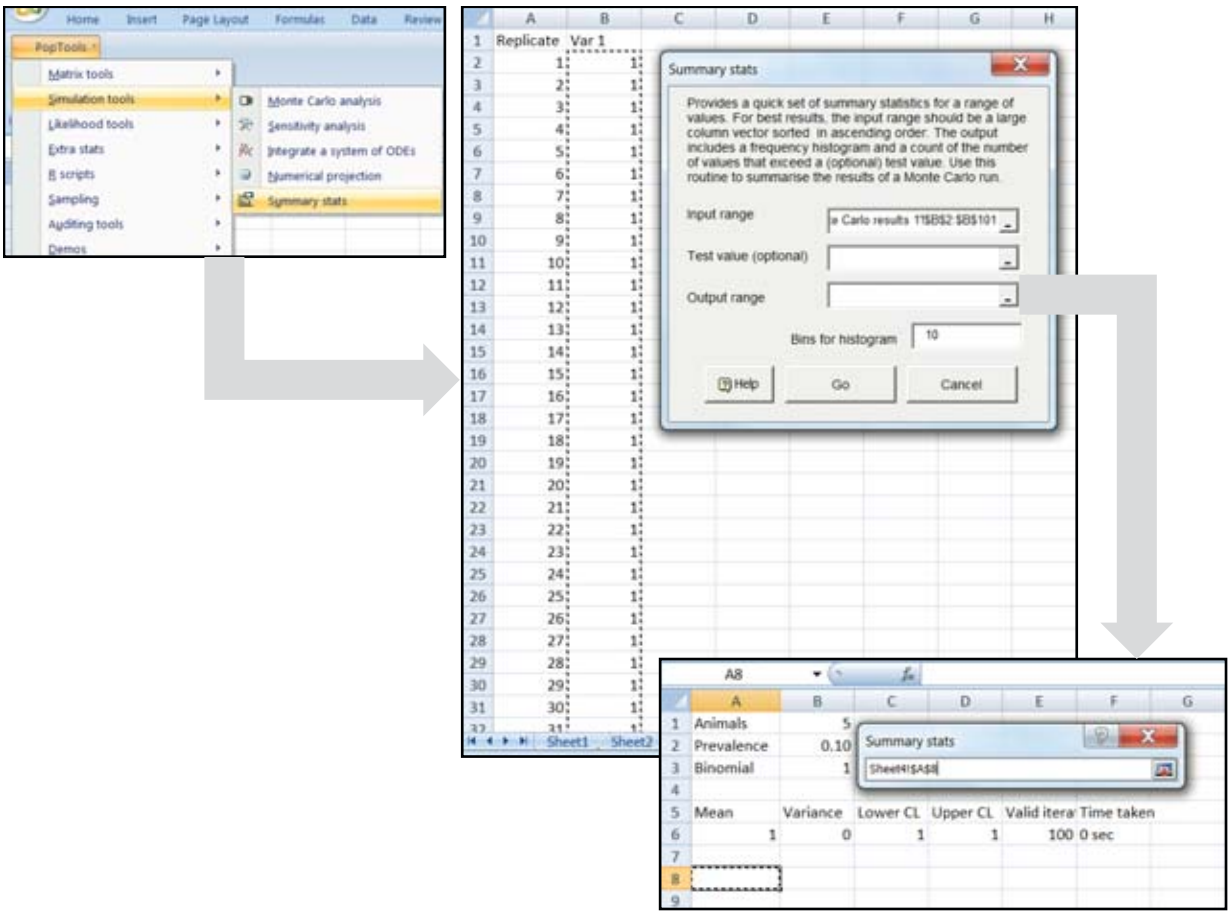
n= No. of trials; p= Probability of success; x = Successes



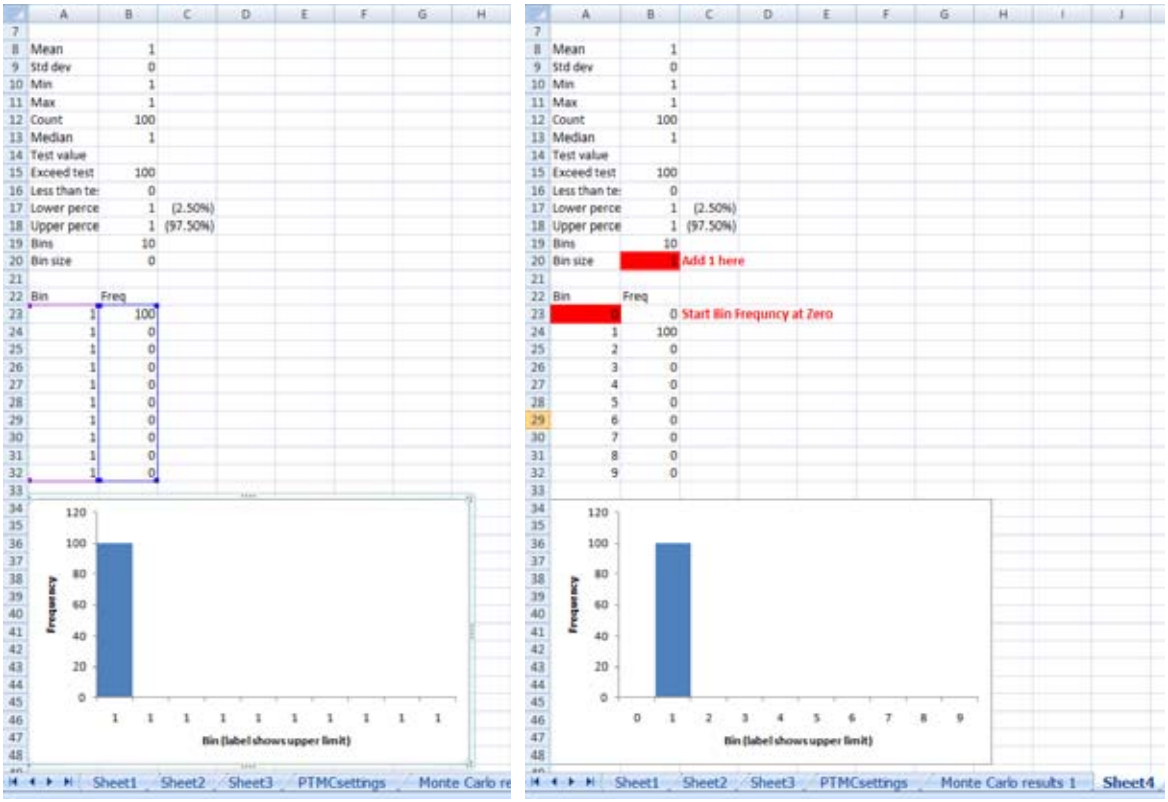
Binomial distribution in PopTools



Monte Carlo simulation with binomial distribution in PopTools



Monte Carlo simulation with binomial distribution in PopTools



Summary statistics of Monte Carlo simulation with binomial distribution in PopTools

Tool 17: Formal elicitation of expert opinion

S.C. MacDiarmid

In the *wildlife* conservation arena, expert opinion is most often sought on an informal basis. However there are times when a more formal approach is warranted. The following was developed for the Food and Agriculture Organization of the United nations (FAO) as a tool for eliciting the best expert judgements for numerical inputs. It avoids the process being dominated by a particular point of view and allows the combination of different experts' opinions into one probability distribution.

References

Vose 2000; Murray *et al.* 2004.

Source

Murray *et al.* (2004) and Vose (2000) provide instruction on the process of developing probability distributions through the elicitation and combination of expert opinion.

Cost

Completely dependent on circumstance and likely to be high.

Software requirements

In situations in which expert opinion is used to derive quantitative inputs, @Risk (Palisade Corporation) and Excel (Microsoft) are required (Gallagher *et al.* 2002).

Stage(s) of risk analysis when this would be used

In situations in which there is a paucity or absence of data, a subjective approach utilising expert opinion is appropriate in determining the probability distributions to be used as inputs into a *risk assessment*. The probabilities derived from elicitation of expert opinion may be quantitative (for example as in Gallagher *et al.* 2002) or qualitative (as in Gale *et al.* 2010).

Description of tool use

Elicitation and combination of expert opinion to generate inputs for a *risk assessment* are best conducted through a workshop approach using a modified Delphi process (Murray *et al.* 2004).

Murray and colleagues (2004) consider that 20 is the maximum number of experts that can be managed appropriately in a workshop. The choice of experts is crucial and each should be selected impartially through a consultative process based on their knowledge of the given subject. Experts should be selected from a variety of disciplines appropriate to the subject under consideration. It may be useful, however, to include subsidiary experts who do not necessarily have quite the same degree of expertise as the core group. Subsidiary experts may provide extreme values in their estimates, which can be used to generate discussion and provide evidence of overconfidence, overestimation or underestimation. Discussion of these extreme values can be used to reduce biases and obtain more accurate estimates from the second questionnaire (see below). It may be considered that it is not appropriate to include the estimates of subsidiary experts in the final analysis; such a decision should be made prior to the workshop.

The workshop method is conducted as follows[6]:

Introduction

- Explain the background to the project and aims of the workshop.
- Briefly introduce the discipline of *risk analysis* and the use of expert opinion and probability theory.
- Explain the questions to be asked, the definitions used in the questions and the assumptions made.

Conditioning the experts

- Explain the importance of accurate estimates, emphasising that this is an elicitation of opinion, not a test of knowledge.
- Provide in an easily understood format any data that may be available that is associated with the question(s) being asked.

Questionnaire 1

- Prior to the workshop, conduct a pilot questionnaire with a different group of individuals to ensure that each question is clear and to gauge how long it will take to answer.
- Ensure that the questionnaire is clear, easy to understand and not too long. Where possible, break the questions down into parts.
- Allow the questionnaire to be answered individually and anonymously.
- Ask the experts to provide estimates for the maximum and minimum values followed by a most likely value for each question. Asking for estimates in this order reduces anchoring bias.
- Ask the experts to provide percentage estimates rather than probabilities because percentages are conceptually easier to estimate.

6 Adapted with permission of the World Organisation for Animal Health (OIE) from Murray N., MacDiarmid S.C., Wooldridge M., Gummow B., Morley R.S., Weber S.E., Giovannini A. & Wilson D. (2004). – Handbook on import risk analysis for animal and animal products, Volume 2. Quantitative risk assessment. World Organisation for Animal Health (OIE), Paris. 126 pp.

– Provide aids such as computer software, graph paper or pie charts to help experts visualise percentages.
– Allow enough time during the workshop to complete the questionnaire.

Analysis 1

– Produce PERT (Beta-PERT) distributions (See Appendix 4, p. 103: Monte Carol modelling) to describe each expert's *uncertainty* around each question using the minimum, most likely and maximum values elicited.
– Combine the distributions from each expert regarding a particular question using a discrete distribution, appropriately weighted (if necessary) for each expert.

Results 1 and discussion

– Use a facilitator to ensure that all experts are included equally in the discussion so as to allow a free exchange of information between them.
– Discuss the combined distribution for each question in turn.

Questionnaire 2

Present the questionnaire to the experts again, ideally the next day, to allow them to amend their previous answers, if they consider it appropriate.

Analysis 2

– Analyse the answers to Questionnaire 2 as described for Questionnaire 1.
– Depending on what was decided before the start of the workshop, answers from subsidiary experts may or may not be included.

Results 2

– Provide the experts with preliminary results as soon as possible after the workshop and send out a validation questionnaire to ensure that results are reproducible.
– Provide the experts with the final results as soon as possible.
– Invite feedback on the usefulness of the results and the process itself.

Experience and expertise required to use the tool

A high degree of expertise is required in the formal elicitation of expert opinion. When quantitative inputs are derived from expert opinion, experience in their appropriate use and interpretation of probability distributions is essential.

Data requirements

Elicitation of expert opinion is used where there is a paucity or absence of data (Vose 2000).

Strengths and weaknesses, when to use and interpret with caution

Potential sources of bias and dealing with disagreement among experts need to be considered carefully (Murray *et al.* 2004).

Bias

A person's estimate of a distribution's parameters may be biased by a number of factors. People tend to:

– weight information that comes readily to mind
– be strongly influenced by small, unrepresentative sets of data with which they are familiar.

They may:

– be overconfident and estimate *uncertainty* too narrowly
– resist changing their mind in the face of new information
– try to influence decisions and outcomes by casting their beliefs in a particular direction
– state their beliefs in a way that favours their own performance or status
– knowingly suppress *uncertainty* in order to appear knowledgeable
– persist in stating weakening views simply to remain consistent over time.

Expert disagreement

In cases of expert disagreement, it is usually best to explore the implications of the judgements of different experts separately to determine whether substantially different conclusions are likely. If the conclusions are not significantly affected, one can conclude that the results are *robust* despite the disagreement among experts. In some cases, experts may not disagree about the body of knowledge; rather, they may draw different inferences from an agreed body of knowledge. In such cases one needs to make a judgement about which expert is more authoritative for the problem under scrutiny.

Choice of probability distribution

The PERT (Beta-PERT) distribution is used most commonly when eliciting quantitative estimates from experts (see Gallagher *et al.* 2002) although other distributions such as the uniform, general, cumulative or discrete may sometimes be used (Vose 2000; Murray *et al.* 2004). The uniform distribution is used in situations where experts are unable to propose a 'most likely' value but will propose a minimum and a maximum value. However, the uniform distribution is a very poor modeller of expert opinion and should be avoided if possible. It is very unlikely that an expert will be able to define a maximum and minimum value but have no opinion on a most likely value (Vose 2000). Individual PERT (Beta-PERT) distributions elicited from each expert are combined in a discrete distribution to produce the input value for each variable in the *risk assessment model* (Vose 2000; Gallagher *et al.* 2002).

Case studies

Gallagher 2002; Gale *et al.* 2010.

Tool 18: Netica

M. van Andel

References

Dambacher *et al.* 2007; Walshe and Burgman 2009.

Source

www.norsys.com/download.html.

Cost

A limited version that can handle up to 15 decision points can be downloaded free of charge. For a version that can handle a network of larger than 15 decision points the costs are listed here: www.norsys.com/netica.html.

Software requirements

No specific requirement; Netica is a small programme that runs easily in a Windows environment.

Stage(s) of risk analysis when this would be used

Used in the *risk assessment* step and more specifically in the *risk evaluation* step.

Description of tool use

Bayesian belief nets (BBNs) describe our understanding of cause and effect. BBNs are being used more frequently in *risk assessment* with applications in public and environmental health. Like a conceptual map (see Cmap tool description), BBNs provide a graphical representation of beliefs and are based on concepts of cause and effect. BBNs can be used to describe links between actions and outcomes. In this way a series of conditional relationships can be represented.

An example of conditional probability is *diagnostic test* performance. The probability that an animal will test positive relies on the disease status of the animal. The probability that an infected animal will test positive is called the test sensitivity, and the probability that an animal that is not infected will test positive is one minus the test specificity.

A BBN consists of three elements:

– nodes representing key variables

– links that represent the cause and effect relationship between the nodes

– the probability that a node will be in a given state, given the state of the connected nodes.

Variables can be categorical (example of categorical data 0–5 deaths, 5–15 deaths above 15 deaths) or discrete (12 deaths).

Experience and expertise required to use the tool

Once the network is created elements can easily be updated and manipulated as information is received. Creation of the initial network is simple. Users of the tool do need to have an understanding of the relationships between different steps of the diagram to be able to interpret the results.

Data requirements

The probabilities of different events need to be known.

Strengths and weaknesses, when to use and interpret with caution

Incorrect probabilities entered into the programme will yield incorrect results at the end of the process. It is advisable that input values are consulted on by experts and agreed on.

BBNs cannot represent feedback loops. An example of what this means in an infectious disease setting is that the presence of *wildlife* infected with rabies may increase the *prevalence* of rabies in domestic animals and this may have the effect of increasing

the *prevalence* of rabies in the *wildlife* population. This cannot be represented as a BBN. However the increase in *prevalence* in the domestic population due to the *wildlife* population can be represented as a BBN.

Case study

Pollino Carmel *et al.* 2007.

Tool 19: Precision Tree

P.S. Miller

Name: Precision Tree, a decision analysis software package for spreadsheets from Palisade, Inc.

Reference

Clemen and Reilly 2001.

Source

The software can be purchased and downloaded from Palisade's website at www.palisade.com/precisiontree/

Cost

Can be purchased as a stand-alone application or as part of Palisade's larger Decision Tools Suite. Prices can be obtained through the website.

Software requirements

Precision Tree requires a Pentium PC or higher processor, Microsoft Excel 2000 or higher, and Microsoft Windows 2000-SP4 or higher.

Stage(s) of risk analysis when this would be used

Precision Tree can be used in the *risk assessment* and *risk management* steps, where current and potential risks of disease introduction and *transmission* are evaluated across specific scenarios.

Description of tool use

Decision analysis provides a systematic method for describing problems. Taking into account the decision maker's preferences and beliefs regarding *uncertainty*, it is the process of modelling a problem situation in order to identify the decision that should be made. Decision trees, as opposed to influence diagrams, show all possible decision options and chance events with a branching structure. They proceed chronologically, left to right, showing events and decisions as they occur in time. All options, outcomes and pay-offs, along with the values and probabilities associated with them, are shown directly in the tree. There is very little ambiguity as to the possible outcomes and decisions the tree represents.

Precision Tree is an add-in to Microsoft Excel that allows the user to create influence diagrams and decision trees directly within a spreadsheet. A variety of diagram and tree nodes are available during construction, and values and probabilities are placed directly in spreadsheet cells, allowing the user to easily enter and edit decision *model* definition. Model results are used as pay-offs for each path through the decision tree, with calculation of payoffs occurring in real time as node values are edited. Model output reports provide information on statistical *model* summaries, risk profiles and policy suggestions. One- and two-way sensitivity analyses are easily created, with graphical results displayed within the spreadsheet. Another component of Palisade's Decision Tools Suite, @Risk, can be linked to any decision tree to quantify the *uncertainty* throughout the *model* using probability distribution functions. Monte Carlo simulation (Appendix 4, p. 103) is then used to evaluate the range of possible outcomes associated with a given decision.

Experience and expertise required to use the tool

Users should be familiar with the use of computer simulation *models* and the basics of decision analysis theory. While the software is rather simple to use at a basic level, expertise in the relevant biological and statistical fields is strongly recommended for proper use of the tool.

Data requirements

This is highly specific to the question being asked as part of the *risk assessment*. For a proper decision analysis, data on both the biological characteristics of the problem, as well as auxiliary factors that define the larger system (e.g. economic cost, impacts on other species, etc.) must be available in order to properly define and calculate pay-offs for each candidate decision.

Strengths and weaknesses, when to use and interpret with caution

Decision trees are designed to show a given decision problem in great detail, whereas influence diagrams are simplified depictions of the problem. This is both a strength and a weakness of the decision tree approach, as complex problems with many alternative decision pathways can very rapidly become difficult to view and properly interpret. As

with any type of modelling tool, the accuracy of any specific outcome (decision) is greatly influenced by the detail of the information used as model input. However, if the overall decision analysis structure is *robust*, the relative value of a given decision is usually quite reliable.

Case study

Murayama *et al*. 2006.

Tool 20: Vortex

P.S. Miller

Name: Vortex, a stochastic simulation of the *wildlife* population extinction process.

Reference

Lacy R.C., Borbat M. & Pollak J.P. (2005). – Vortex: A Stochastic Simulation of the Extinction Process. Version 9.50. Chicago Zoological Society, Brookfield, Illinois.

Source

See www.vortex9.org for full details on the software, and to download an installation package.

Cost

Vortex is available to download at no cost from www.vortex9.org

Software requirements

Personal computer running Microsoft Windows 95, 98, 2000, NT 4.0 or XP, with at least 128MB of RAM.

Stage(s) of risk analysis when this would be used

Vortex can be used in the *risk assessment* and *risk management* steps, where current and potential risks of disease introduction and *transmission* are evaluated across specific scenarios.

Description of tool use

Vortex is an individual-based simulation model for population viability analysis (see Fig. 29 for an example data input interface and Fig. 30 for an example output screen). The package models population dynamics as discrete, sequential events (e.g. births, deaths, catastrophes, etc.) that occur according to defined probabilities. The probabilities of events are modelled as constants or as random variables that follow specified distributions. Vortex simulates a population by stepping through a series of events that describe the typical life cycle of sexually reproducing, diploid organisms.

The programme was written originally to model mammalian and avian populations, but its capabilities have improved so that it can now be used for modelling some reptiles and amphibians and perhaps could be used for fish, invertebrates or even plants, if they have relatively low fecundity or could be modelled as if they do.

In addition to single-population analysis, Vortex has the capacity to analyse complex metapopulation dynamics with dispersal among subpopulations. In addition, Vortex models loss of genetic variation in populations by simulating the *transmission* of alleles from parents to offspring at a hypothetical genetic locus. In this way, the demographic impacts of inbreeding depression can be included where appropriate. Density dependence in reproduction or mortality can be explicitly modelled, and management actions in the form of harvest, supplementation and translocation are included as well. Demographic parameters can be specified with greater complexity and specificity through the use of a built-in flexible mathematical function editor.

Multiple scenarios can be created within a single modelling project, allowing the user to quickly and easily create and review alternative *models* representing different management strategies, etc. Tabular and graphical output is available for a wide variety of model results, including population extinction risk, population abundance, mean or median time to extinction, mean inbreeding coefficient, population gene diversity (heterozygosity) and final population size. All input and output information for a set of analyses is stored within a project file, simplifying the process of scenario organisation.

As with other generic demographic modelling packages, disease is treated rather simply in Vortex, i.e. as a catastrophic event that is either totally absent or present and significantly affecting the population. The program's function capability allows for somewhat greater realism in modelling disease, but *epidemics* are not simulated as emergent events based on the underlying epidemiology of the disease. For greater realism in modelling disease dynamics, Vortex can now be physically linked to a disease dynamics *model* such as *OUTBREAK* (see p. 78) to create a metamodel, offering considerably greater realism.

Experience and expertise required to use the tool

Responsible Vortex users should have a thorough understanding of population demography and statistical methods for data analysis. The data input process is highly explicit, simplifying somewhat the process of analysing field data for use in the *model*.

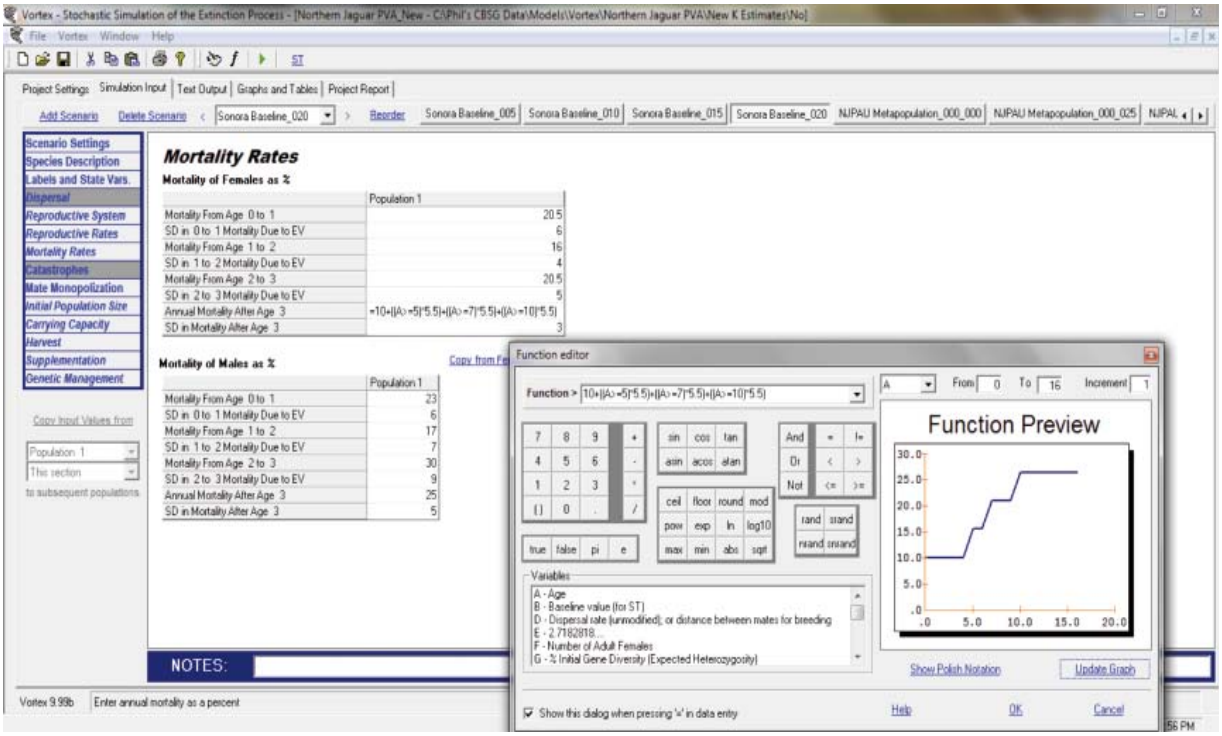


Fig. 29
Sample input screen in the Vortex simulation package, showing use of function editor interface

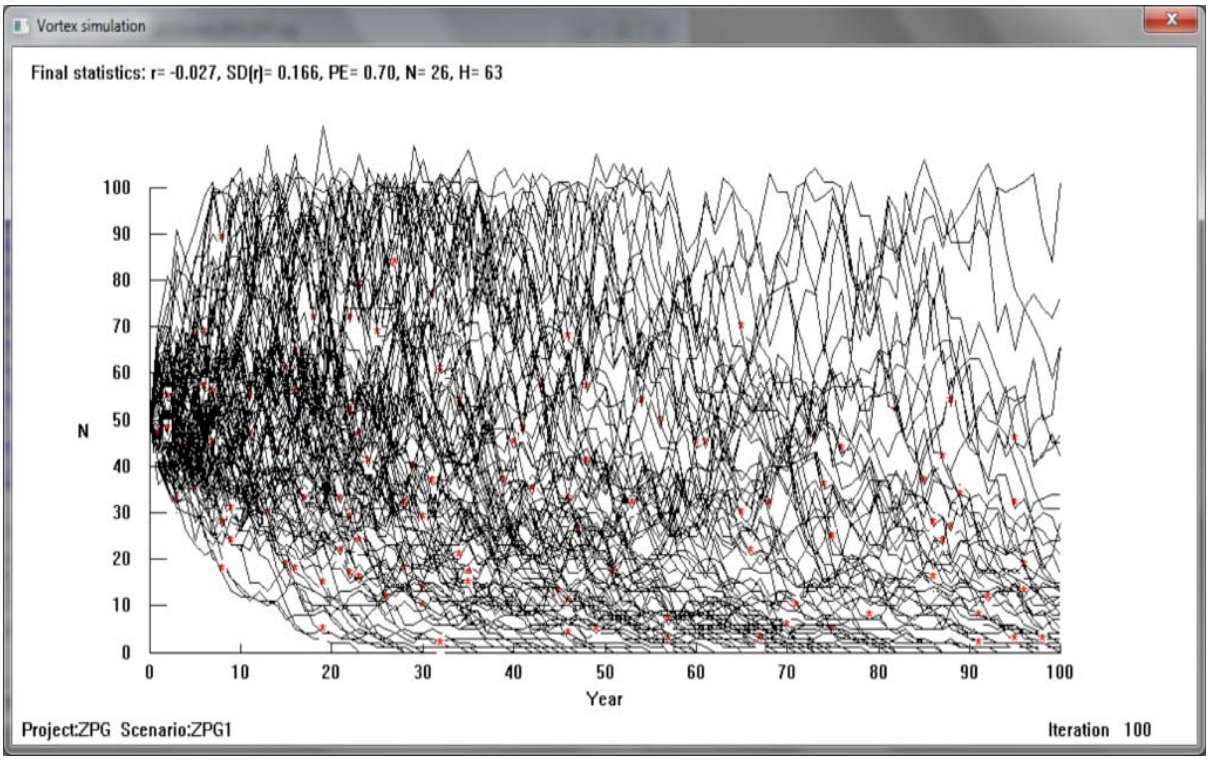


Fig. 30
Sample output from a simulation using Vortex

Nevertheless, careful attention to model structure and input is critical to developing a realistic and useful *model* for management decision making.

Data requirements

Realistic *models* of population demographic dynamics require considerable knowledge of population demographic rates (both mean and variance over time), and the ecological factors that affect them.

Strengths and weaknesses, when to use and interpret with caution

Since Vortex is an individual-based *model*, it is very useful for understanding and predicting the demographic dynamics of small populations that are subject to random fluctuations in birth and death rates brought about by environmental *variability*, etc. In the same way, the software can be very helpful for studying disease dynamics in *wildlife* populations, especially in a metapopulation context and when linked to an explicit disease *model* such as OUTBREAK. This same characteristic makes it unsuitable for studying large populations of *wildlife* (e.g. more than 30,000 individuals). As with any modelling package, specific interpretation of simulation output is a direct function of the accuracy and realism of the input parameters.

Case study

Bradshaw *et al*. 2012.

Tool 21: RAMAS

P.S. Miller

Name: RAMAS, viability analysis for stage-structured metapopulations

Reference

Akçakaya H.R. (2005). – RAMAS Metapop: Viability Analysis for Stage-Structured Metapopulations. Version 5. Applied Biomathematics, Setauket, New York.

Source

See www.ramas.com/ramas.htm for detailed descriptions of the software. The programme can be ordered from Applied Biomathematics, 100 North Country Road, Setauket, New York.

Cost

RAMAS Metapop – reduced student prices are offered for this and the RAMAS GIS application. See the website above for current prices and licence conditions.

Software requirements

IBM-compatible personal computer, running Microsoft Windows 95, 98, 2000, NT 4.0 or XP, with 30 megabytes of free hard disk space.

Stage(s) of risk analysis when this would be used

RAMAS can be used in the *risk assessment* and *risk management* steps, where current and potential risks of disease introduction and *transmission* are evaluated across specific scenarios.

Description of tool use

RAMAS Metapop is an interactive programme that allows the user to build matrix-based population demographic *models* for species that live in multiple patches. It incorporates the spatial aspects of metapopulation dynamics, such as the configuration of the populations, dispersal and recolonisation among patches and similarity of environmental patterns experienced by the populations. The programme can be used to predict extinction risks and explore management options such as reserve design, translocations and reintroductions, and to assess the impact of humans on fragmented populations. Features of RAMAS Metapop include age or stage structure for each population, random variation and temporal trend in vital rates (survivorships, fecundities) and carrying capacities of populations, several types of density dependence, age- or stage-specific dispersal rates and catastrophes. The programme produces a variety of output metrics for each *model*, including risk of population extinction or decline, median time to extinction, expected minimum abundance, metapopulation occupancy through time, and histograms of abundance at each time step for each life-history stage that is part of the *model*.

RAMAS GIS is designed to link a GIS with a metapopulation *model* for population viability analysis and extinction *risk assessment*. The software imports spatial data on ecological requirements of a species and creates a habitat suitability map with a user-defined functional *model*. The software then uses the habitat suitability map to find suitable habitat patches on the landscape and then combines the spatial information on the metapopulation with user-defined ecological parameters of the species to create a functional metapopulation *model* that is evaluated using the built-in RAMAS Metapop package.

As is typical for most generic population viability analysis packages, disease in animal populations is treated rather abstractly in RAMAS, usually as a catastrophic event that has a significant impact on the population(s) of interest when present but

is otherwise absent from the environment. If a metapopulation structure is part of the model, RAMAS has a 'spreading catastrophe' feature that could simulate movement of the disease from one subpopulation to another via dispersing individuals.

Experience and expertise required to use the tool

Because of its flexible approach to model definition and construction, RAMAS users must be well versed in the fields of demographic data analysis, age- and stage-based population growth matrix theory, and statistical interpretation of population data. Navigation through the software is intuitive, but input and output data file management can be a bit cumbersome.

Data requirements

Realistic *models* of population demographic dynamics require considerable knowledge of population demographic rates (both mean and variance over time), and the ecological factors that affect them.

Strengths and weaknesses, when to use and interpret with caution

RAMAS is a very flexible package for analysing the viability of populations, suitable for animals, plants or insects. It is a population-based *model*, allowing the user to study very large populations without computational limitations. On the other hand, its flexible matrix-based approach requires the user to have a more advanced knowledge of population demographic processes and data analysis than with some other population viability analysis software packages. Its treatment of disease is comparatively implicit, but with expertise and care RAMAS can provide useful insights into the impacts of disease processes on animal populations (with its application to plants less well defined). As with any modelling package, specific interpretation of simulation output is a direct function of the accuracy and realism of the input parameters.

Case study

Akçakaya and Atwood 1997. (Does not include disease, but demonstrates the general use of RAMAS in population viability modelling.)

Tool 22: Risk communication plan template

R.M. Jakob-Hoff

Name: Risk communication plan template.

Reference

Modified from Armstrong *et al.* 2003.

Source

As above.

Cost

Free – reproduced as Table XII, below.

Software requirements

Can be used with pen and paper or with Microsoft Word or Microsoft Excel.

Stage(s) of risk analysis when this would be used

Risk communication.

Description of tool use

The information captured within this template (Table XII, p. 92) should be gathered at the beginning of the DRA process and reviewed frequently as the DRA progresses. The template is designed to capture essential information on the stakeholders, experts and decision makers for a specific *wildlife* DRA. This tool is designed to be used in consultation with these individuals to establish their information needs and preferred methods and frequency of communication. The template can readily be modified to include full names and contact details of each person listed and to accommodate additional or alternative communication needs.

Experience and expertise required to use the tool

No specialised expertise required

Data requirements

Names and contact details of DRA participants and contributors, their information needs and preferred methods and frequency of communication.

Table XII
Risk communication plan template

Group	Stakeholder name	Information needs	Communication method(s)	Frequency	Contact details
Stakeholders					
Experts					
Decision makers					

Strengths and weaknesses, when to use and interpret with caution

This is a simple and easily modified template. Its main value is in prompting for the capture of the most basic information needed to enable effective communication among DRA stakeholders, experts and decision makers. An individual must be assigned responsibility to capture this information and to maintain and frequently review the communication plan to ensure that it remains current.

Case studies

See the example in Table III in the 'Risk communication' section of this *Manual*.

Appendices

Appendix 1
Sources of information for wildlife disease risk analysis[7]

R.M. Jakob-Hoff and S.C. MacDiarmid

Information to assist in identifying hazards, assessing likelihoods of release, exposure and consequences and exploring options to manage risk can be found in a variety of sources including scientific journals, textbooks and websites devoted to diseases of *wildlife* and zoo animals, aquatic animals and livestock. Specific examples are:

Key textbooks

Friend M. (2006). – Disease emergence and resurgence: the wildlife–human connection. Circular 1285, US Department of the Interior and US Geological Survey, Washington, District of Columbia.

Hudson P.J., Rizzoli A., Grenfell B.T., Heesterbeek H. & Dobson P. (eds) (2006). – The ecology of wildlife diseases. Oxford University Press, Oxford, United Kingdom.

Kaner S., Lind L., Toldi C., Fisk S. & Berger D. (2007). – Facilitator's guide to participatory decision making. 2nd Ed. Jossey-Bass, San Francisco, California.

Ostfield R.S., Keesing F. & Eviner V.T. (eds) (2008). – Infectious disease ecology: effects of ecosystems on disease and of disease on ecosystems, Princeton University Press, Princeton, New Jersey.

Salman M.D (ed.) (2003). – Animal disease surveillance and survey systems Methods and applications. Iowa State Press, Ames, Iowa.

Thrusfield M. (2007). – Veterinary epidemiology, 3rd Ed. Blackwell Publishing, Oxford, United Kingdom.

Vose A. (2008). – Risk analysis, a quantitative guide, 3rd Ed. John Wiley and Sons, Chichester, United Kingdom.

Wobeser G.A. (2006). – Essentials of disease in wild animals. Blackwell Publishing, Oxford, United Kingdom.

Wobeser G.A. (2007). – Disease in wild animals: investigation and management, 2nd Ed. Springer, Berlin.

Key journals

Journal of Zoo and Wildlife Medicine (http://zoowildlifejournal.com/)

Journal of Wildlife Diseases (www.jwildlifedis.org)

EcoHealth (www.ecohealth.net/aboutus.php)

Wildlife websites

Avian reintroduction and translocation database – Lincoln Park Zoo (www.lpzoo.org/conservation-science/projects/avian-reintroduction-and-translocation-database)

FAO Scientific Taskforce on Wildlife and Ecosystem Health (http://wildlifeandecosystemhealth.org/)

IUCN SSC Conservation Breeding Specialist Group wildlife disease risk analysis (DRA) tools (www.cbsg.org/cbsg/risk/)

IUCN SSC Invasive Species Specialist Group database (www.issg.org/database/welcome/)

IUCN SSC Reintroduction Specialist Group (www.iucnsscrsg.org)

IUCN SSC Wildlife Health Specialist Group (www.iucn-whsg.org)

OIE Working Group on Wildlife Disease (http://web.oie.int/wildlife/eng/en_wildlife.htm)

Health Risk Analysis in Wildlife Translocations (www.ccwhc.ca/wildlife_health_topics/risk_analysis/rskguidintro.php)

7 Section based on Brückner *et al.* 2010

Wildpro, the electronic encyclopaedia and library for wildlife (http://wildpro.twycrosszoo.org)

Wildlife data integration network (www.wdin.org)

Data from disease *surveillance* and *monitoring* and investigations of outbreaks (see below)

OIE website (www.oie.int/):

– official country disease status

– animal disease information sheets

– *Terrestrial Animal Health Code* (www.oie.int/international-standard-setting/terrestrial-code/)

– *Manual of Diagnostic Tests and Vaccines for Terrestrial Animals*

– *Aquatic Animal Health Code*

– *Manual of Diagnostic Tests for Aquatic Animals*

– publications and documentation including the *Scientific and Technical Review*, *World Animal Health* and the *Bulletin*

– World Animal Health Information Database (WAHID) (http://web.oie.int/wahis/public.php?page=home)

FAO/WHO Health Standards – Codex Alimentarius (www.codexalimentarius.net/web/index_en.jsp)

FAO EMPRESS (www.fao.org/ag/AGAinfo/programmes/en/empres/home.asp)

The joint FAO/OIE/WHO global early warning system for major animal diseases including *zoonosis* (GLEWS) (www.glews.net)

Emslie R.H., Amin A. and Kock R. (eds) (2009). – Guidelines for the in situ reintroduction and translocation of African and Asian rhinoceros. IUCN Species Survival Commission African Rhino Specialist Group and Asian Rhino Specialist Group and Wildlife Health Specialist Group (www.rhinoresourcecenter.com/pdf_files/123/1236876187.pdf)

IUCN/SSC African Elephant Specialist Group. Guidelines for the in situ translocation of the African elephant for conservation purposes (www.african-elephant.org/tools/trnsgden.html)

Conservation and Development Interventions at the Wildlife/Livestock Interface – Implications for Wildlife, Livestock and Human Health. To download this IUCN/SSC Occasional Paper from the Animal and Human Health for the Environment and Development (AHEAD) Program go to: www.wcs-ahead.org/wpc_launch.html.

Published wildlife disease risk analyses

One should ascertain whether or not these have been adequately peer reviewed; more weight can be given to a peer-reviewed analysis. Care must be taken to ensure that the circumstances pertaining in one situation are relevant in another.

Assistance and advice

Assistance and advice can also be sought from a variety of specialists including other *wildlife* specialists, ecologists, entomologists, climatologists, epidemiologists, veterinary pathologists, virologists, microbiologists, parasitologists, laboratory diagnosticians, livestock industry specialists, agricultural economists and field veterinarians. If it is decided to undertake a *quantitative risk analysis*, advice should probably also be sought from mathematical modellers and statisticians.

In situations in which information is scarce or lacking, a subjective approach utilising *expert opinion* is appropriate for release, exposure and *consequence assessment*s. However, care must be taken when eliciting expert opinion to avoid bias and to deal with disagreement among experts. Appropriate methods for eliciting and combining expert opinion have been described (Vose 2000; Murray *et al.* 2004). Psychological research has shown that it is hard to elicit good subjective probability judgements; bias may be introduced both by the methods used to elicit the judgements and by the means by which these are modelled. Murray and colleagues (2004) outline a modified Delphi technique that has proven useful in many situations.

Appendix 2
Surveillance, monitoring and outbreak investigations as a source of information

S.C. MacDiarmid

In general, *surveillance* is aimed at demonstrating the absence of disease or infection, determining the *prevalence* or distribution of disease or infection, or detecting new or emerging diseases as soon as possible (OIE 2010).

Surveillance is the systematic ongoing collection, collation and analysis of information related to animal health and the timely dissemination of information to those who need to know so that action can be taken. *Monitoring*, on the other hand, is the intermittent performance and analysis of routine measurements and observations, aimed at detecting changes in the environment or health status of a population. Both are valuable sources of information for *hazard identification* and *risk assessment*.

Surveillance may be carried out for a number of reasons (Thrusfield 2007; OIE 2010). Specific examples include:

- early detection of disease outbreaks
- assessment of the health status of a defined animal population
- identification of new and emerging diseases
- identification of priorities for disease control and prevention
- evaluation of disease control programmes
- confirmation of the absence of a specific disease
- gathering information on disease occurrence for research or *risk analysis* purposes.

Domestic animals and *wildlife* may be susceptible to the same diseases, but infection in one does not necessarily mean that it also present in the other. It is intrinsically more difficult to monitor diseases in *wildlife* than in domestic animals and *surveillance* for diseases in *wildlife* presents challenges that may differ significantly from those encountered in *surveillance* in domestic animals (Mörner *et al.* 2002; OIE 2010).

Disease *surveillance* may be based on many different data sources and can be classified in a number of ways (OIE 2010). For example:

- the means by which the data are collected ('active' versus 'passive' *surveillance*)
- the disease focus (*pathogen*-specific versus general *surveillance*)
- the manner in which units for observation are selected (structured surveys versus non-random data sources).

Passive *surveillance* is that based on reports of laboratory diagnosis, results of routine slaughterhouse or game packhouse inspection, statutory notification of disease, etc. The data obtained from passive *surveillance* are often biased, because they are dependent on voluntary submission of samples to laboratories, and they usually lack denominator values. Passive *surveillance* thus cannot give unbiased estimates of disease *prevalence*. However, it can be carried out at a lower cost than active *surveillance* and has the advantage that it is the first stage in identifying new and emerging diseases, which active *surveillance* cannot do, as one cannot target *surveillance* at a disease not yet identified (Thrusfield 2007).

Active, or targeted, *surveillance* collects specific information about a particular disease so that its *prevalence* in a defined animal population can be measured or its absence demonstrated. It is often planned using appropriate statistical sampling theory and commonly focuses on populations that are at increased risk of being affected by the disease under consideration, thus increasing the efficiency of detection (Thrusfield 2007; OIE 2011). However, for certain diseases likely to be present at very low *prevalence*, statistical sampling may be inappropriate because of the very large numbers that would be required to be sampled. Hugh-Jones and colleagues (2000) observed that 'Beyond a certain very small *prevalence* or risk, one must abjure statistics and use epidemiological common sense. At this point, one employs disease 'traps'. When one is poaching rabbits, one does not spread snares all over the countryside but only in those few places where the most rabbits are most likely to be running. Similarly, when one has a disease *surveillance* system that has actively watched these sites and found nothing over a reasonable period of time, the disease does not exist'.

Serological *surveillance*, or sero-*surveillance*, is the identification of patterns of current and past infection using serological (antibody) tests (Thrusfield 2007).

Surveillance may be aimed at an entire animal population in a defined area or country. However, an alternative approach may be sentinel *surveillance* in which attention is restricted to certain species that act as 'sentinels' for a much broader population. For example, eastern equine encephalitis is a mosquito-borne virus disease of horses and other vertebrates,

including humans, the *reservoir* of which is wild birds. A *surveillance* programme for eastern equine encephalitis may, therefore, include the regular serological testing of sentinel chickens which are kept inside but to which mosquitoes have access (Thrusfield 2007).

Specimens for disease *surveillance* in *wildlife* may be obtained from sources such as hunters and trappers, road kill, wild animal meat markets, sanitary inspection of hunted animals and game packhouses, morbidity and mortality observations by the general public, *wildlife* rehabilitation centres, *wildlife* biologists and government *wildlife* agency field personnel, farmers and other landholders, naturalists and conservationists. It may seem that a disease case collected by such passive *surveillance* represents merely a record in a laboratory database. However, such acquisitions may provide insights into the occurrence of important disease processes in wild animal populations (Mörner *et al.* 2002; OIE 2010).

Investigations into outbreaks of disease or mortalities in *wildlife* can provide useful *surveillance* data. In a discussion on *surveillance* for *wildlife* diseases, Mörner and colleagues (2002) point out that while many factors should be taken into consideration during a disease investigation, they consider it 'impossible' to prepare a comprehensive list of all the factors that should be investigated. Nevertheless, Bengis and colleagues (2002) list several techniques that can maximise the *surveillance* information gained from the investigation of disease outbreaks. Examples listed include:

– active investigation of any reports of abnormal *clinical signs*, mortalities or a sustained increase in vulture activity in a given area

– necropsies on all carcasses that become available on an *ad hoc* basis; collection of road kills or examination of hunters' kills can substantially increase the number of carcases examined

– veterinary inspections at all *wildlife*-culling operations

– veterinary supervision of protected area systems for disease *monitoring*

– veterinary examination of all animals captured for any reason including translocation, clinical assistance, fitting radio transmitters or removal of problem animals

– veterinary supervision at all wild animal holding facilities and game sales

– dedicated serological surveys.

Bengis and colleagues (2002) emphasise that in all these situations, sample collection, including body fluids, tissues and excretions should be maximised and serum samples should be banked for possible future retrospective studies.

Additional indirect *surveillance* techniques may include:

– rodent trapping for serological surveys, such as for arboviruses and cardioviruses, or for *pathogen* isolation

– *vector* trapping for distribution studies (for example, for *Glossina* spp. and *Culicoides* spp.) or virus isolation (for example, for orbiviruses and phleboviruses) and xenodiagnosis.

Appendix 3
Screening tests: selection, interpretation, and sample size calculator

B.A. Rideout

The use of screening tests to identify the presence or absence of *pathogens* is an important feature of the *disease risk analysis* process described in this volume, and a valuable tool for some of the *surveillance* techniques described in the previous appendix. There are a number of pitfalls and challenges associated with any screening effort and in a large, multidisciplinary DRA it may be useful for all contributors to have a basic knowledge of these. This appendix provides an introduction to three important areas:

– test selection

– test interpretation and use in decision making

– calculating sample sizes for pathogen screening.

Note that while the text here is intended for use by non-specialists, consultation with veterinary experts is recommended for the design, implementation and interpretation of any pathogen screening effort.

Screening test selection

In most cases, the goal of screening will be to rule out the presence of a disease agent of concern (identified in the *hazard identification* step), so that appropriately healthy animals can be selected for movement. If it has been determined that screening for the *pathogen* of concern is warranted, an appropriate test needs to be selected. Factors that determine test selection include the host species, the estimated *prevalence* of the agent in the population, the sensitivity and specificity of the test, the number of individuals to be tested, the nature of the agent, whether it causes acute or chronic disease, whether the goal is detecting exposure or active infection, the cost and availability of the test, the volume and nature of the samples needed, and the sample handling requirements (See 'Explanation of factors influencing test selection' on page 98). Table XIII lists the characteristics of the most widely available tests for animal diseases.

Before deciding on the optimum testing method, it is important to consider the host species being tested and whether the test has been validated for that species. Test validation is an important but often overlooked subject. Validation of a test ensures its accuracy (that the test will reliably identify the agent if present, will only identify that agent and will not identify the agent if it is absent). It also ensures that the test results are reproducible (the same result is produced each time a particular sample is tested) and responsive (that the positive result goes away if the agent goes away).

Unfortunately, very few tests have been validated for use in any *wildlife* species. In spite of this, the pitfalls of using an unvalidated test can be minimised by avoiding tests that are species specific. For example, many enzyme-linked immunosorbent assays (e.g. indirect antibody ELISAs) require labelled antibodies that recognise the antibodies of a specific domesticated animal species. It should *not* be assumed that such tests will work on a *wildlife* species (i.e. bind its antibodies with the same affinity and avidity) simply because it is of the same taxonomic group as the domesticated animal for which the test was developed. Some tests, such as those that directly detect the agent, do not rely on species-specific reagents and would therefore be better choices. Although conventional polymerase chain reaction (PCR) is one such test, most commercial laboratories use these tests in a species-specific way by interpreting a band of appropriate molecular weight on a gel as being a positive test result. When using conventional PCR tests in *wildlife*, it is important to confirm any positives by DNA sequencing or Southern blots of these bands. False-positive test results are common. Non-species-specific tests are listed in Table XIII, and should be preferred options.

Table XIII
Intrinsic (analytical) characteristics of tests

Serological (antibody) tests	Usefulness in wildlife	Sensitivity
Competitive inhibition ELISA	High	High
Protein A or G ELISA	High	Moderate
Virus neutralisation	High	Moderate
Haemagglutination inhibition	High	Moderate
Complement fixation	High	Moderate
Agar gel immunodiffusion	High	Low
Direct immunofluorescence	High	Moderate
Indirect antibody ELISA	Low	High
Indirect immunofluorescence	Low	High
Western blot	Low	Moderate
Agent or antigen detection tests		
TaqMan/real-time PCR	High	High
Bacterial or fungal culture	High	Moderate
Virus isolation	High	Moderate
Necropsy/biopsy/cytology	High	Variable
Conventional PCR for agent DNA	High*	High
Conventional PCR for agent RNA	High*	High
Direct antigen capture ELISA	Moderate	High

*If positive results confirmed

The sensitivity of a test refers to its ability to correctly identify the agent when it is present. Since the goal in most cases will be ruling out the presence of a disease agent of concern, choosing a test with the highest possible sensitivity is important. However, since the test sensitivity is seldom available, a practical alternative is to choose a testing method with a high intrinsic (or potential) sensitivity, such as PCR or a non-species-specific ELISA. Running two different tests in parallel will also increase the sensitivity.

It is also important to choose a laboratory with appropriate experience with the testing methods and the species being tested. Ideally, the laboratory staff should have experience in developing and validating tests, understand the pitfalls of applying tests to new species and settings, and have a willingness to work collaboratively to maximise the value of the testing.

Screening test selection can be viewed as a multi-step process:

1. Based on the nature of the agent of concern, determine whether it is best detected directly (e.g. by PCR or culture) or indirectly by measuring the host's immunological response to the agent (e.g. an antibody test for an agent that causes life-long infections).

2. Based on the number of animals to be tested and the sample handling requirements, identify the most sensitive, logistically feasible and cost-effective test available. If little is known of the sensitivity of the specific test, choose a method with high intrinsic sensitivity and consider running two different tests in parallel to maximise sensitivity.

3. Based on the host species to be tested, identify the most appropriate validated test, or one that is not species specific.

4. See 'Test interpretation and using test results for decision making' on p. 99.

Case study

A group of three juvenile California condors (*Gymnogyps californianus*) was scheduled to be transferred from a breeding facility in southern California, United States, to a release site in Baja California, Mexico. The birds were required to be test negative for highly pathogenic H5 and H7 avian influenza within 30 days of transfer. We were asked to test the birds for antibodies to H5 and H7 avian influenza types by agar gel immunodiffusion (AGID).

At the time of the testing request, the United States was declared free from highly pathogenic avian influenza, so *pathogen prevalence* was expected to be zero. Based on the nature of the agent and host, we would expect any *subclinical infection*s to have been cleared within 2–3 weeks but for antibody titres to persist for an unknown but potentially lengthy period. Because of this, the best choice of test would be one that detects only active infection, has the highest possible specificity (to minimise false positives), and is not species specific.

Although AGID is a non-species-specific test, it is a poor choice in this situation because it is an antibody test with the potential to detect past exposure to a low *pathogenicity* H5 or H7 avian influenza strain, resulting in a positive test and an erroneous interpretation that the bird has an active infection with a high *pathogenicity* avian influenza strain. Because of this concern, we were allowed to use a real-time PCR assay specific for highly pathogenic H5 and H7 avian influenza strains instead. Real-time PCR is also a non-species-specific test and has the advantages of only detecting active infection and being more sensitive and specific than AGID. Although real-time PCR assays are expensive, this test method was still the most cost-effective available because the number of birds involved was small and the consequences of a false positive were significant. The plan called for confirmation of any positive tests by virus isolation. All birds were test negative for H5 and H7 by real-time PCR and were transferred successfully.

Explanation of factors influencing test selection

Host species
If the host species is a domesticated animal, a validated species-appropriate test should be selected. If the host is a *wildlife* species, there are very few validated tests available, so a test with low species specificity should be selected (see Table XIII). If the host species is CITES[8] listed or sample movements are otherwise regulated, tests that are readily available in country might be preferred.

Agent prevalence
If the *prevalence* of the agent is expected to be low in the population, the most sensitive test available should be selected to increase the probability of detection. However, when *prevalence* is low, the probability of false-positive test results increases dramatically. As a result, any positive tests should be followed with a confirmation test that has the highest possible specificity (and is therefore different from the *screening test*). When agent *prevalence* is high in a population, a test with the highest possible specificity should be chosen to increase the probability of correctly identifying the uninfected individuals. However, when *prevalence* is high, the probability of false negatives increases dramatically (see, for example, case scenario 2 in the test interpretation tool). As a result,

8 Convention on International Trade in Endangered Species of Wild Fauna and Flora.

long *quarantine* periods and repeated testing might be required to ensure that an individual is free of the agent. See the test interpretation tool for additional discussion of this topic.

Sensitivity and specificity
Sensitivity refers to the ability of a test to correctly identify the presence of the agent, while specificity refers to the ability to correctly identify the absence of the agent. When sensitivity is high, there will be fewer false negatives. When specificity is high, there will be fewer false positives. While these test characteristics are important, they are seldom available for any given test. Because the goal of screening in most cases will be to rule out the presence of the agent, we will generally want to maximise sensitivity (thereby minimising the possibility of a false negative). Even if the sensitivity of the available tests is unknown, certain test types have higher intrinsic sensitivity (see Table XIII), which will make them preferred choices for screening purposes. In addition, the available sensitivity for any testing scenario can be maximised by running two different tests simultaneously.

Number of individuals to be tested
If the population is large and the agent *prevalence* is expected to be low, a large number of individuals will need to be tested to ensure the absence of the agent. In this situation, the cost and sample handling requirements become increasingly important. See the sample size calculation tool for additional discussion of this topic.

The nature of the agent
Agents that are present in very low numbers in the host or have the capability of causing latent or slowly progressive infections are inherently more difficult to detect and therefore require more complex screening strategies. Certain agents may be difficult to detect because they are labile (e.g. RNA viruses can be rapidly degraded by RNases if samples are not carefully handled using RNA preservation protocols), or because they are difficult to isolate. Tests need to be chosen carefully based on the agent characteristics in order to optimise the chances of detection. Consultation with professionals in the chosen laboratory, or other experts, is recommended.

Detecting exposure versus active infection
In cases where the agent of concern causes latent or chronic infections, detecting exposure might be a practical alternative to detecting infection (because exposure is nearly synonymous with infection). In most other situations (e.g. agents causing acute infections with relatively short *incubation periods*), the goal will be to detect active infection. Test selection will obviously differ in these two scenarios.

Cost and availability of the tests
Cost and availability of tests become obvious matters of concern with increasing sample numbers and more remote geographic locations.

Samples and handling
The size and nature of the host species might limit the availability of certain types of samples (e.g. blood samples), and the geographic location or skill of the operators may limit the complexity of sample handling that can be accommodated. Table XIII can aid with test selection in these situations.

Note
Analytical sensitivity reflects the potential performance of a test in ideal circumstances and may not necessarily reflect the actual diagnostic sensitivity in real-world scenarios. Table XIII can be a starting point for test selection, but consultation with experts is highly recommended.

Test interpretation and using test results for decision making

Diagnostic or *screening test*s should be used in *risk assessment*s only if the results will contribute to decision making. Testing for the sake of curiosity only causes confusion and *uncertainty* in the *risk assessment* process. Any decisions that will be based on test results should be determined in advance through careful planning, with an understanding of how tests perform in real-world situations. When it comes to test performance, there is a widespread misperception that laboratory test results are always reliable, particularly when they provide a concrete answer such as ‘positive’ or ‘negative’. In order to properly interpret a test result and use it for decision making, we need to understand some basic principles of test performance.

Test refers to the ability of a test to correctly identify the presence of a disease agent, while **specificity** refers to the ability to confirm the absence of an agent. As important as these test parameters sound, they have little practical value when it comes to interpreting test results or using results for decision making. We seldom know the sensitivity or specificity of a test, and, if we did, those values would only be relevant to the extent that our test population exactly matches the study population on which those values were originally calculated. More importantly, sensitivity and specificity are essentially fixed characteristics of a test and do not help us understand variations in test performance. The more practical parameter is the *predictive value* of a test, which tells us the probability that a result is correct. In most real-world situations, when we

receive a test result what we really need to know is whether or not the result is true, because we will be making important decisions based on that result. The positive *predictive value* gives us the probability that a positive test result is true, while the negative *predictive value* gives us the probability of a negative result being true.

Unfortunately, calculating the actual *predictive value* requires not only knowledge of the sensitivity and specificity of the test but knowledge of the *prevalence* of the agent in the population as well (see Example 1 below for a *predictive value* calculation). Although we will seldom have the data needed to calculate the *predictive value*, we can use some basic principles of test performance to generate simple rules for estimating *predictive value*. The estimated *predictive value*s can then be used as a guide for interpreting test results and making decisions.

The simple rules we are about to develop are based on a qualitative estimate of the *prevalence* of an agent in the population being tested (low, medium or high *prevalence*). Even with a highly sensitive and specific test, when agent *prevalence* is low the positive *predictive value* will also be low. This means that any positive test result will have a high probability of being a false positive. Because of that, when *prevalence* is low we need to be suspicious of any positive test results and have a plan in place to confirm them. The confirmatory test should be different from the *screening test* (repeating the *screening test* would probably only generate another false positive and create more confusion). Although the positive *predictive value* is low in this situation, the negative *predictive value* will be correspondingly high. This means that we can generally trust a negative test result when the *prevalence* is low.

As agent *prevalence* increases, these relationships reverse: the positive *predictive value* increases (so we can trust a positive result), while the negative *predictive value* decreases (we can no longer trust a negative result because there will be a high probability of false negatives). Confirming negative test results is more difficult and could require extended *quarantine* and repeated testing over time.

Example 1: a low-prevalence situation

In this hypothetical scenario, the plan is to translocate 1,000 frogs from one area to another. The chytrid fungus (*Batrachochytrium dendrobatidis*) has been identified as a concern during the *hazard identification* process. The source population has been monitored and is thought to have a very low *prevalence* (2%). The goal is to create a chytrid-free cohort of frogs from the source population that can be used for this translocation. Let us assume that our *screening test* is very good and has a sensitivity of 95% and a specificity of 90%. If the actual *prevalence* is 2% in the population we would expect 20 individuals to be truly positive. Given our test sensitivity and specificity, we can expect the following results after testing 1,000 frogs:

Test result	**Agent present**	
	Yes	No
Positive	19	98
Negative	1	882

Presenting our results in this 2 x 2 table enables us to see that our test has correctly identified 19 of the 20 truly infected individuals, which is very good and reflects the high sensitivity of the test. However, the test has also incorrectly identified 98 frogs as being test positive when in fact they did not have the agent. If we calculate the positive *predictive value* it turns out to be the following:

Positive *predictive value* =
19/(19 + 98) = 0.16 = 16%.

What this means is that any positive test result from this population has only a 16% chance of being correct. If our predetermined plan was to euthanise any test positive frogs, we would have a high probability of unnecessarily euthanising healthy frogs because of these false-positive test results. That is why it is important to have a plan in place to confirm any positive results, using a test of a type different from the original *screening test*. If we use the same data to calculate the negative *predictive value*, we find that it is extremely good:

Negative predictive value =
882/(882 + 1) = 0.999 = 99.9%

This demonstrates that in a low-*prevalence* situation, positive results should be viewed with suspicion and confirmed by follow-up testing using a different test, while negative results can generally be trusted.

Example 2: a high-prevalence situation

In this hypothetical scenario, the plan is to rescue 1,000 frogs from a wild population that is suffering a chytridiomycosis outbreak. The goal is to identify the chytrid-negative frogs so that we can establish a chytrid-free reserve population for breeding and eventual release back into the wild. We are using the same test, with a sensitivity of 95% and a specificity of 90%, only now the *prevalence* is very high (90%). With this *prevalence*, we would expect 900 frogs

out of 1,000 to be infected and 100 to be free of the agent. If we again put our test results in a 2 x 2 table, we get the following:

Test result	Agent present	
	Yes	No
Positive	855	10
Negative	45	90

Our test has correctly identified 90 of the 100 uninfected frogs, which reflects the high specificity of the test. But our test has also incorrectly identified 45 frogs as being test negative when in fact they had the agent. If we calculate the negative *predictive value* we get the following:

Negative predictive value = 90/(90 + 45) = 0.67 = 67%

What this means is that, for any negative test result, we have only a 67% probability that the result is correct. In other words, 33% of the frogs we are using to establish our chytrid-free colony are actually infected, so our effort will inevitably fail. However, in the same situation our positive *predictive value* would be very good:

Positive predictive value = 855/(855 + 5) = 0.99 = 99%

This example demonstrates that in a high-*prevalence* situation, we cannot trust a negative test result and would need to have a plan for extended *quarantine* and repeated testing, but a positive test result can generally be trusted.

Caution

Test interpretation is a complicated subject and is influenced by many more variables than we have presented here, such as stage of infection, the presence of concurrent diseases, the immunological competence of the individual, the experience of those performing the test, sample handling requirements, and the cut-off values used to establish a positive test. It is always preferable to consult appropriate individuals with expertise in diagnostic test interpretation when carrying out surveillance testing and interpreting results.

Sample size calculator for pathogen surveys

When conducting *pathogen* surveys on small target populations (100 or fewer individuals), sampling 100% of the animals is the preferred option because it provides the greatest population-level *pathogen* detection sensitivity, and with appropriate confirmation testing allows decisions to be made at the individual animal level.

However, when the target population is large or resources are limited, it will be necessary to select a subset of animals for testing. In this situation it is important to choose an appropriate number of animals from the target population for testing so that acceptable levels of risk (or confidence limits) can be maintained, as determined by the *risk evaluation* process. When only a subset of animals is being tested, it is essential to make resulting decisions at the population level. The goal is to detect the presence of the *pathogen* in the population so that a decision can be made about whether the entire population is eligible or ineligible for movement or other management action.

Alternatively, if the *pathogen* of concern is detected in the population, an individual animal testing strategy could then be developed and implemented to allow decision making at the individual animal level.

In order to calculate the appropriate number of animals to test we need to know:

- the total population size
- the sensitivity of the test
- the minimum *prevalence* level we want to be able to detect, and
- our desired probability of detecting infection if the true *prevalence* meets or exceeds our minimum *prevalence*.

In the simplest scenarios we assume 100% specificity of the test, which although unrealistic makes the calculations much simpler. Decision makers sometimes expect *pathogen* surveys to provide proof of freedom from disease (i.e. 100% probability of detecting the *pathogen* if present), but it is important to clearly convey throughout the *risk communication* process that this is an unattainable goal. It would at minimum require testing 100% of the animals no matter how large the population and the use of a test with consistently perfect sensitivity and specificity.

In the simplest scenarios we also assume that any infected animals would be randomly distributed throughout the population so that randomly selecting individuals for testing will have the best chance of detecting the agent if it is present. Truly random selection of the individuals to be tested requires the use of a random number generator or a table of random numbers (such as the table of random numbers, p. 432, in Thrusfield 2007). In some situations it might only be possible to approximate truly random sample selection, but it is important to avoid bias in the selection process.

It is also important to ensure that this random distribution assumption is valid for the agent and population under consideration. In some situations, disease agents might be spatially segregated within a population (creating clusters of infected individuals) or could be stratified by age class. If the assumption of random distribution of infected individuals is likely to be violated, it is worth consulting an epidemiologist or other specialist in *pathogen* survey design, as the calculations can become quite complicated.

Example scenario

A translocation of 200 wild frogs is being planned to repopulate an area from which they have been extirpated. The disease risk assessment has determined that testing for the chytrid fungus (*B. dendrobatidis*) is warranted and that our level of risk tolerance requires that we be 95% confident that we can detect the agent even if the *prevalence* is as low as 5%. Our test has an expected sensitivity of 95%, we assume 100% specificity, and we have previous survey data suggesting that the agent, if present, would be randomly distributed in the population. If we enter these numbers into the sample size calculator on the 'Epitools' section of the Ausvet.com.au website (http://epitools.ausvet.com.au/content.php?page=FreedomFinitePop), we find that we would need to test 55 of the 200 animals if we want to be 95% confident of detecting the agent if the true *prevalence* is 5% or greater. If we have a much lower risk tolerance and desire 99% confidence that we can detect the agent even if the *prevalence* is as low as 2%, our sample size requirement increases to 144, which reveals how dramatically the sample size requirement increases as our risk tolerance decreases.

If the online sample size calculator is not available, the following formula can be used:

$$n = [1 - (1 - p)^{1/d}] [N - d/2] + 1$$

where n is the required sample size, p is the probability of finding at least one infected animal in the sample, N is the population size, and d is the minimum number of infected animals expected in the population (derived from the minimum *prevalence* we want to be able to detect).

So in the above case scenario where our minimum *prevalence* is 5%, we would expect at least ten animals in the population of 200 to be infected. We have set our desired probability of detecting at least one infected animal at 95% (or 0.95), so our calculation becomes:

$$n = [1 - (1 - 0.95)^{1/10}] [200 - 10/2] + 1$$

$$n = [1 - 0.74] [195] + 1$$

$$n = 52$$

This value closely approximates the sample size derived from the online calculator.

Strengths and weaknesses, when to use and interpret with caution

Screening animal populations for diseases of low *prevalence*, which is the most common scenario, is a complex task. Test selection, design of survey protocols, and interpretation of test results must be approached with caution. Consult with experts whenever possible.

References

Thrusfield (2007).
See also: http://epitools.ausvet.com.au/content.php?page=home

Appendix 4
Monte Carlo modelling for risk assessment

N. Murray

1. The use of Monte Carlo simulation in a risk assessment

As discussed by Murray *et al.* (2004), while a *qualitative risk assessment* is suitable for the majority of *risk assessment*s, there may be some situations in which it can be useful to adopt a quantitative approach to gain further insights, identify critical steps, assess the impact of *uncertainty* in more detail or compare risk mitigation strategies. Quantification involves the development of a mathematical *model* that links the various steps in the risk pathway. In its simplest form a deterministic or point estimate approach is undertaken whereby each of the inputs, such as disease *prevalence* and test sensitivity or specificity, is represented by a single value such as the 'best guess', 'least likely' or 'worst case'. These values, in turn, may have been derived from a statistical table where the 'best guess' is the average or expected value and the 'least likely' and 'worst case' are associated with the lower and upper confidence limits.

For very simple *models* with only a few inputs, a deterministic approach may be reasonable as there will be only a limited number of possible scenarios to explore. However, as more inputs are added there will be a rapid escalation in the number of potential combinations or 'what if' scenarios. For example, if we had just four inputs, each with a mean and upper and lower 95% confidence limits, we would have 34 or 81 possible scenarios. Such an approach obviously has significant drawbacks. It can rapidly become impractical to interpret the results meaningfully as there is no relative weighting for each combination of values. Fortunately, we can overcome these limitations by undertaking what is commonly referred to as a Monte Carlo simulation.

If we have information about the range of values and the likelihood of each value, we can assign a probability distribution to each input. They can now be described as random variables as they can take on a different value as a result of a random process. The resulting *model* is called a stochastic *model*, and we can calculate the combined impact of the variation in each of the *model's* input distributions to determine a probability distribution of the possible model outcomes. The simplest way to do this is to perform a simulation using computing software such as @Risk (Palisade Corporation, Newfield, New York – see Tool 14, p. 78). This involves randomly sampling values from each distribution and combining the values generated, according to the mathematical logic of the *model*, to produce a result for a particular scenario. This process is repeated many times and the results from each scenario, which are also known as iterations, trials or realisations, are combined to produce a probability distribution of possible model outcomes.

Sampling values from probability distributions is most commonly undertaken by Monte Carlo sampling, a technique first used by scientists working on the atomic bomb. It was named after the resort town of Monte Carlo in Monaco, renowned for its casinos. The Monte Carlo method is based on simple random sampling from the entire distribution, which represents the sampling frame for each iteration. It is essentially sampling with replacement, as it is possible for the same values to be selected more than once.

Latin hypercube sampling is an alternative method that involves stratified sampling without replacement. The range of the distribution is divided up into a number of intervals, equal to the number of iterations to be performed and a simple random sample is then chosen from within each interval. Since each interval is selected only once during a simulation, Latin hypercube sampling ensures that values from the entire range of the distribution will be sampled proportionally to the probability density of the distribution. Fewer samples are usually required to reproduce the probability distribution so it is more efficient than Monte Carlo sampling for the same number of iterations. It is generally the preferred method of numerical simulation since fewer iterations are required for a particular level of accuracy.

Although Latin hypercube sampling may be the default sampling method in software products such as @Risk, the overall stochastic process is referred to as Monte Carlo simulation. This is an extremely useful modelling technique and underpins many *quantitative risk assessment*s.

2. Differentiating variability and uncertainty

Before turning our attention to some examples of the types of distributions commonly used to model biological processes it is important to distinguish between *uncertainty* and *variability* as these terms have often been used interchangeably, leading to a degree of confusion.

Uncertainty reflects a lack of understanding or incompleteness of one's knowledge or information about a particular thing. *Variability*, on the other hand, reflects the heterogeneity or variation that exists naturally within any biological system, whether we have a good understanding of that system or not. So, while *uncertainty* is reduced as knowledge increases, *variability* remains the same. In most, if

not all, situations, it is likely that the varying degrees of *uncertainty* that exist at different points in the risk pathway will be of more concern than *variability*. How then can we determine the impact of these uncertainties on the final risk estimate? Fortunately, *risk analysis* provides us with a technique that enables the inevitable uncertainties to be considered in context. For example, it could turn out that, while considerable *uncertainty* exists at one point in the risk pathway, its overall contribution to the final risk estimate is inconsequential. In such circumstances, it is important not to overemphasise the *uncertainty* that exists but to provide appropriate perspective.

3. Defining a distribution

There are basically two families of distributions, discrete and continuous, which are defined by the characteristics of their respective random variables. Discrete variables can take on only a limited number of values, whereas continuous variables can take on any value within a given range. Distributions can be further specified as either parametric or non-parametric. In the statistical sense, a parameter refers to a numerical descriptive measure that characterises a population, such as the mean and standard deviation, as well as the minimum, maximum or most likely values. As far as distributions are concerned, parameters are values that define their shape and range, either in combination with a mathematical function, in the case of a parametric distribution, or directly for non-parametric distributions. Examples of parametric distributions include the normal, binomial, Poisson and beta distributions while non-parametric distributions include the uniform, triangular, discrete and general distributions.

4. Guidelines for developing a simulation model

Before turning attention to some specific examples of distributions used to model biological processes in a *quantitative risk assessment*, it is worthwhile emphasising that a number of important steps must be worked through in a systematic manner when developing a simulation *model*. These steps include:

- ensuring that the scope of the assessment is adequately characterised by identifying the population of interest and clearly and explicitly stating the question to be answered

- providing a graphical outline of the biological pathways considered in the *model* to identify the variables, their relationships and information requirements as well as ensuring that there is a logical chain of events in space and time leading to the appropriate estimate being calculated

- keeping the *model* as simple as possible to represent as accurately as necessary the system of interest

- documenting the assumptions, evidence, data and uncertainties for each variable to ensure that an appropriate distribution is chosen

- verifying that each iteration of the *model* is biologically plausible and that unexpected or counter-intuitive results are not ignored.

For further elaboration of these and a number of other important guidelines the reader is referred to Murray *et al.* (2004).

5. Some examples of distributions used to model biological processes

As discussed by Murray *et al.* (2004) there are essentially two sources of information from which a distribution can be developed to represent a variable in a *risk assessment model*; empirical data and expert opinion. While a large number of probability distributions is available to the risk analyst, caution is warranted. Unless careful consideration is given to the theoretical basis and underlying assumptions, particularly for parametric distributions, an inappropriate choice may be made that could lead to significant flaws in the assessment. It is important to ensure the distribution selected is biologically plausible and not just simply selected arbitrarily or because it provides a 'good fit' to the data. Several techniques, which are beyond the scope of this book, are available to assist in developing an appropriate distribution. They include fitting empirical data to a distribution using either parametric or non-parametric techniques, a purely subjective approach using expert opinion, and, a combined approach that incorporates empirical data and expert opinion using Bayesian inference. For further details the reader is referred to other texts, including those of Murray *et al.* (2004) and Vose (2008).

Rather than simply listing the various distributions and their characteristics, the following sections focus on the amount and type of information available followed by the distribution relevant under those circumstances. Throughout this text, probability distributions will be described in terms of functions used in the *risk assessment* computing software @Risk, for example, Binomial, Beta, and Uniform.

5.1 Distributions used to model expert opinion or to convert a set of data into a distribution

Non-parametric distributions provide a convenient means of modelling either expert opinion or converting a set of data into an empirical distribution as their parameters are intuitive and simple to use.

Depending on the circumstances either a continuous or a discrete distribution can be developed.

5.1.1 Minimum, maximum

For the most basic situation the amount of information available may simply cover a range of possible values without any relative weighting of one value over another. In such cases a uniform distribution defined by two parameters, a minimum and maximum value, would be appropriate as all possible values within the range have an equal probability of occurrence:

Uniform (minimum, maximum).

This distribution, which is a simple, continuous distribution, is commonly used to model expert opinion as well as those situations in which the available data are restricted to defining a range. It has a wide variety of applications from defining a distribution of disease *prevalence*, test sensitivity and specificity, *incubation period*, duration of viraemia, etc. Figure 31 provides an example of a uniform distribution, which is also known as a rectangular distribution. While it is the most maximally uninformed distribution of all, it is nevertheless useful in some circumstances.

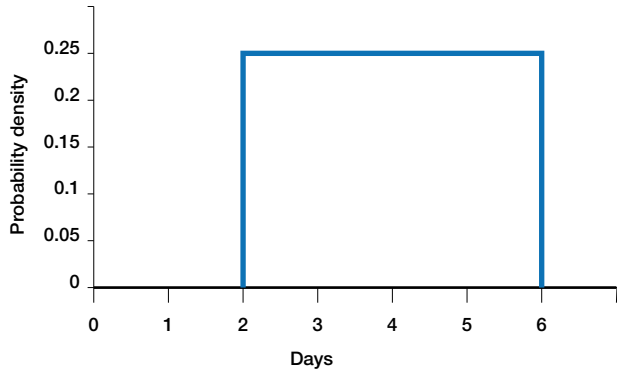


Fig. 31
A uniform distribution of the duration of viraemia where the range has been estimated to be from two to six days

5.1.2 Minimum, most likely, maximum

In addition to defining a range of possible values there may by some information or opinion that enables an estimate of the most likely value within the range to be obtained. The appropriate distribution to use here is either the pert or the triangular, which are both continuous distributions:

Pert (minimum, most likely, maximum)
Triangular (minimum, most likely, maximum).

The pert distribution is actually a modification of a specific type of parametric distribution, the beta distribution (discussed below). It provides a more 'natural' shape than the corresponding triangular distribution (Fig. 32). It is not as influenced by the extreme (minimum and maximum) values, particularly when the distribution is skewed. The main drawback of the triangular distribution is its unnatural shape, which rarely, if ever, provides a reasonable description of a biological process. As can be seen from Figure 32 it tends to overemphasise the tails and underestimate the shoulders relative to the pert distribution. Both the pert and triangular distributions have found widespread application for many biological processes.

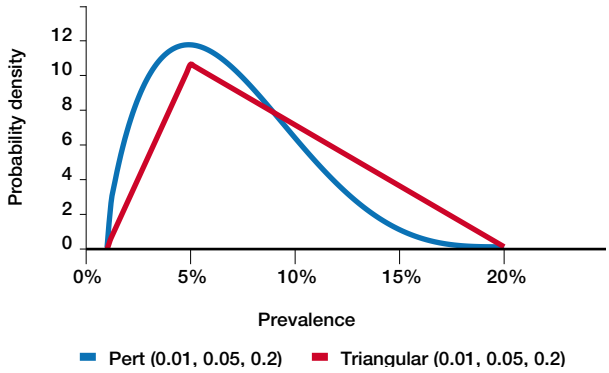


Fig. 32
Comparing a pert and a triangular distribution

The pert distribution can be easily and conveniently manipulated by applying a weighting factor to the mean of the distribution, enabling various shapes to be generated for the same values of the minimum, most likely and maximum. This can be particularly useful in refining the shape of the distribution when eliciting expert opinion, as shown in Figure 33. In this example, adapted from an import *risk analysis* on chicken meat undertaken by the Ministry of Agriculture in New Zealand, the age at which chickens are likely to become infected with infectious bursal disease (IBD) virus prior to being slaughtered at 49 days of age is depicted. Initially there was a great deal of *uncertainty*, so a uniform distribution, Uniform (1, 49) was used. Later some information became available indicating that they were most likely to become infected around 3 weeks of age. This was modelled as a Pert (1, 21, 49). After further enquiries the estimate was refined to 'most chickens become infected between 14 and 28 days of age'. This was interpreted as 90% of chickens being likely to become infected during this period. A modified pert with a corresponding weighting factor was used to model this new information. The same estimates for the minimum, most likely and maximum values were used as in the original pert distribution. For further details on this technique refer to Murray *et al.* (2004) and Vose (2008).

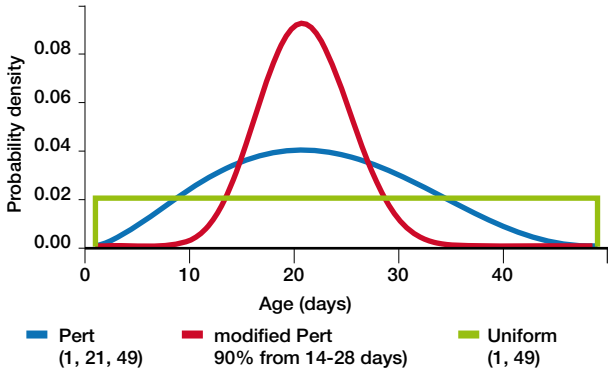


Fig. 33
A comparison of a uniform distribution, a standard pert distribution and a modified pert distribution of the age when a chicken is likely to become infected with IBD virus prior to slaughter at 49 days of age
From Murray *et al.* (2004)

5.1.3 Minimum, maximum with a specified number of equal length classes, each with a probability pi of occurring

The histogram distribution can be used to model a set of continuous data that is grouped into equal-length non-overlapping classes bounded by a minimum and a maximum class interval whereby each class has a certain probability *p*i of occurring. It is useful for replicating the shape of a set of data as shown in Figure 34.

*Histogram (minimum, maximum, {*p*i}).*

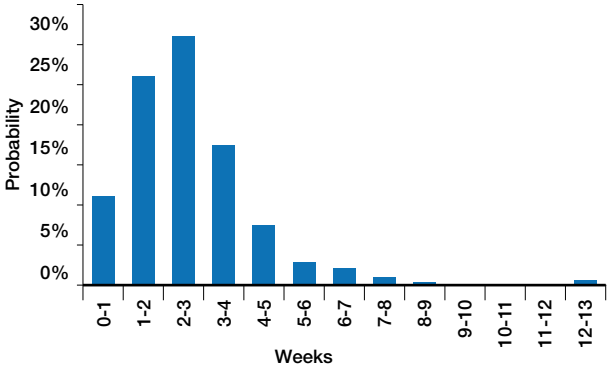


Fig. 34
A histogram probability distribution of the duration of viraemia in cattle naturally infected with bluetongue virus
From Murray *et al.* (2004)

5.1.4 Data grouped in specified (x_i, p_i) pairs

There are a number of situations when it may be convenient to group data into specific (x_i, p_i) pairs where each pair has a value x and a weight p which specifies the value's relative probability of occurrence. The underlying data may be discrete or continuous.

Two distributions are available to model discrete data; the discrete and discrete uniform (duniform):

Discrete ({x_i*}, {*p_i*})*
Duniform ({x_i*}).*

The discrete uniform distribution is a special form of the discrete distribution that can have one of several discrete values (x_i) each with an equal probability of occurrence.

These distributions can be used to define an empirical distribution directly from a data set that is organised into (x_i, p_i) pairs, particularly where there is an abundant amount of representative data. The discrete distribution can also be used to model a posterior distribution in a Bayesian inference calculation. The discrete uniform distribution can be usefully employed in a non-parametric bootstrap simulation to determine a sampling distribution for an uncertain parameter where there are few representative data. It is used to resample from the original data set. For further information on Bayesian inference and bootstrap simulation refer to Murray *et al.* (2004) and Vose (2008).

An important application of these discrete distributions is in modelling expert opinion where there are divergent views, in which case each expert's opinion would be captured by the x_i value with a corresponding weighting of p_i. In those situations where each expert's opinion is considered to be equally valid, the discrete uniform distribution would be appropriate.

For continuous data, two distributions are available: the general and cumulative distributions. The range of each distribution is defined by a minimum and a maximum value.

General (minimum, maximum, {x_i*}, {*p_i*})*
Cumul (minimum, maximum, {x_i*}, {*p_i*}).*

They can both be used to convert a set of data into an empirical distribution provided the data are continuous and cover a reasonable range. In the case of the cumulative distribution, the probability values (p_i) are the corresponding ascending cumulative probabilities (Fig. 35). While both distributions may be used to model expert opinion, special care should be taken when using the cumulative distribution, as small changes in a cumulative plot can lead to significant distortions in its corresponding relative frequency plot. The general distribution can be used to model a posterior distribution in a Bayesian inference calculation where the parameter being estimated is continuous.

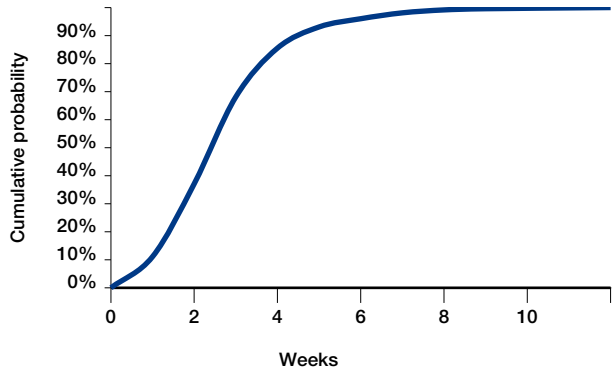


Fig. 35
A cumulative probability distribution of the duration of viraemia in cattle naturally infected with bluetongue virus
From Murray *et al.* (2004)

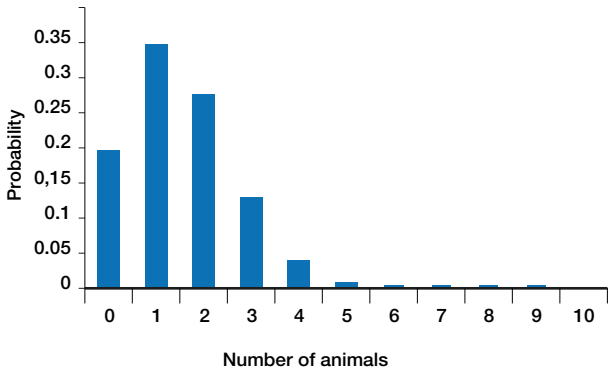


Fig. 36
A binomial distribution of the variation in the number of infected animals (x) likely to be in a sample (n = 10) drawn from a population with a disease prevalence (p = 0.15)
From Murray *et al.* (2004)

5.2 Distributions used to model a binary response

The outcome of interest in many *risk assessment*s is a binary response. That is, there are only two possible outcomes. For example: an animal is infected or it is not; when tested it is positive or it is not; a disease outbreak occurs or it does not. Such binary responses can be conveniently modelled as a binomial process, provided we can reasonably satisfy its underlying assumptions.

A binomial process consists of *n* identical trials each with the same probability of success (*p*). The variation in the number of successes (*x*) is modelled by the binomial distribution:

$$x = Binomial\ (n, p).$$

Since the probability of success remains constant, a binomial process is effectively sampling from an infinite population with replacement. While this would obviously not be the case in practice, for example where a sample of animals is drawn from a particular population harbouring a certain disease, provided the size of the population relative to the sample size is large, it is reasonable to assume that the probability of sampling an infected animal remains constant. As a guide, if the size of the population is at least ten times the sample size, such an assumption is appropriate. In those situations where it is not reasonable to assume that probability remains constant, a hypergeometric process, discussed below, is applicable. Figure 36 provides an example of a binomial distribution modelling the number of infected animals (*x*) in a sample (*n*) drawn from a population with a disease *prevalence* (*p*).

In some situations we might be interested in estimating the number of animals that we would need to select before we included a certain number with a trait of interest (diseased, pregnant, etc.) in the sample. Since the negative binomial distribution *models* the number of failures likely to arise before *x* successes are observed, the variation in the number of animals that would need to be selected (*n*) before *x* successes is determined by:

$$n = Negbin\ (x, p) = failures.$$

If the level of interest is in estimating the number (*n*) that would need to be selected to include (*x*) successes in the sample, then:

$$n = x + Negbin\ (x, p) = successes + failures.$$

As an example, in planning a survey and estimating costs it could be informative to determine the variation in the number of animals from an infected population that would need to be tested before identifying an infected individual; that is, the number of 'failures'. Figure 37 provides an example of the variation in the number of uninfected animals that are likely to be selected before an infected animal is included in a sample.

Under an empirical definition of probability, the number of events of interest (*x*) that occur in a number of identical and repeatable trials (*n*) is expressed as a ratio (fraction or proportion) of the total number of events that occurred. As a result, probability is a measurable property of the physical world and can never actually be observed.

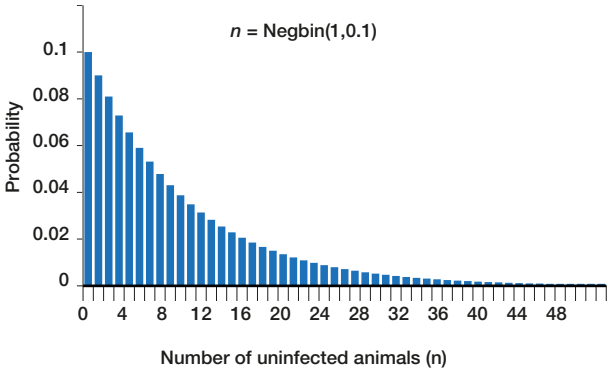


Fig. 37
A negative binomial distribution of the number of uninfected animals likely to be selected from a population with a disease prevalence of 10% before including an infected animal in the group

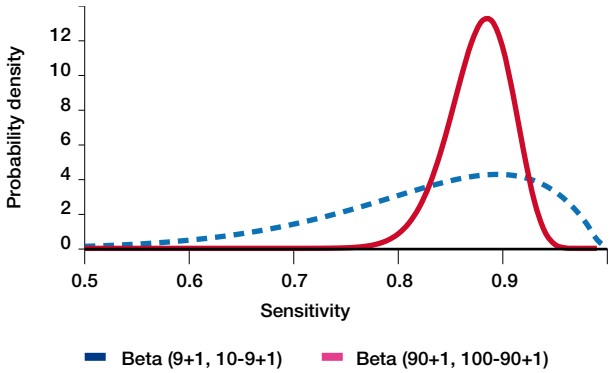


Fig. 38
Using the beta distribution function to model an uncertain parameter p, of a binomial distribution. In this case p represents test sensitivity

As *n* approaches infinity it is the limit of the ratio:

$$\lim_{n \longrightarrow \infty} \frac{x}{n}.$$

In other words, we can be increasingly certain of its true value as more and more trials are undertaken. The level of confidence we have in an estimate of probability (*p*) after having observed *x* successes in *n* trials is embodied in the beta distribution, which provides a convenient way of modelling *uncertainty* about *p*:

p = *Beta* (x + 1, n – x + 1).

This particular formulation of the beta distribution is actually the posterior distribution that arises from using the beta distribution as a non-informative conjugate prior to a binomial likelihood function in a Bayesian inference (for further details refer to Murray *et al.* 2004 and Vose 2008).

Figure 38 provides an example of a beta distribution used to model test sensitivity. In this example, if nine out of ten animals known to be infected with a particular disease were positive to a serological test, the point estimate of the test's sensitivity would be 90%, that is, the probability that the test is positive given that an animal is infected. But, how confident can we be that this is a reasonable estimate, particularly considering that there were only ten animals in the trial? By inserting the appropriate values into the beta distribution function $p = Beta(x + 1, n - x + 1) = Beta(9 + 1, 1 - 9 + 1)$ and plotting the results we can readily assess the impact of *uncertainty*. As more information is gathered by testing more animals we would be increasingly confident of the test's 'true' sensitivity. In the end there is always a trade-off between obtaining a reasonable level of confidence and the cost and effort needed to acquire additional information.

5.3 Sampling from finite populations: the hypergeometric process

As discussed earlier, since probability remains constant and the results from succeeding trials are independent under a binomial process, the binomial distribution is effectively modelling sampling with replacement from a very large (essentially infinite) population. However, in most, if not all, practical situations when modelling biological processes, sampling would be undertaken without replacement from finite populations. For example, in a group of 100 animals ($M = 100$) where there are five with a trait of interest ($D = 5$), the initial probability that an animal has the trait would be 0.05. If the first animal selected has the trait, then the probability that the next animal selected would also have the trait would be $4 \div 99 = 0.04$, whereas, if it does not, the probability would be $5 \div 99 = 0.051$. As a result the probability, measured by $D \div M$, changes depending on whether the previous animal had the trait or not. That is, the probability of success is no longer independent of the outcome of the previous trial.

Provided the population size is at least ten times the sample size, the probability of success remains more or less constant. However, as the ratio of population size to sample size diminishes, proper account needs to be taken of fluctuations in probability through the application of a hypergeometric process. The corresponding hypergeometric distribution *models* the number of successes (*x*) in a sample of size *n* from a population of size *M* where there are *D* individuals with the characteristic of interest:

x = *Hypergeo* (n, D, M).

Since the probability of success changes each time an individual is selected and removed from the population, the hypergeometric distribution is modelling sampling without replacement. As can be seen from Figure 39 it is not really until the population

size in relation to the sample size (*M:n*) falls below about ten that important differences begin to emerge between the results generated from a binomial distribution and the hypergeometric distribution.

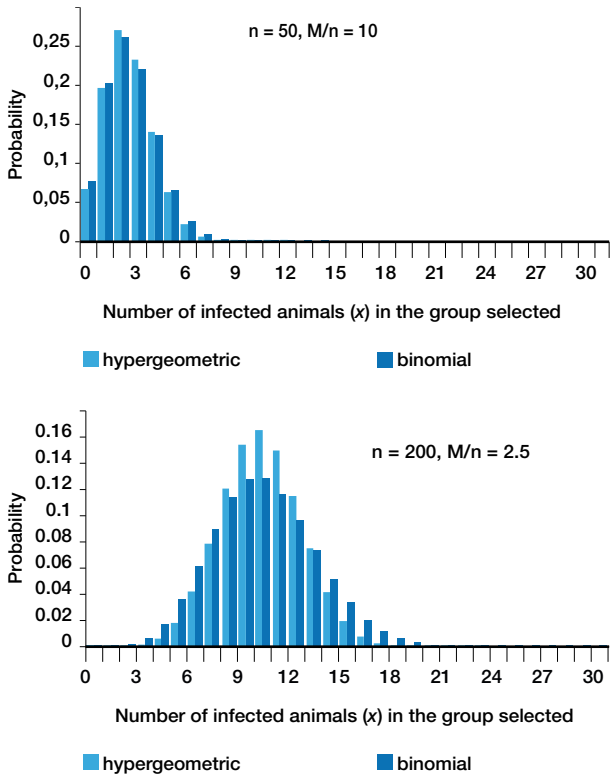


Fig. 39
A comparison of the hypergeometric and binomial distribution
For the number of infected animals (*x*) in a group *(n)* selected from a population (*M = 500*) with a number of infected animals (*D = 25*). For the hypergeometric distribution, *x = Hypergeo (n, D, M)*, while for the binomial distribution prevalence is calculated as *D/M* and *x = Binomial (n, D/M)*

5.4 Distributions used to model variables that are normally or log normally distributed

Many naturally occurring variables such as weight, height, viral titre in tissues, physiological characteristics, pH of tissues and fluids, and milk and egg production are normally distributed. Others are normally distributed following some sort of transformation of the data; for example, taking the logarithm of a set of data on the *incubation period* of a disease. The normal distribution has an extensive variety of applications ranging from statistical theory, where it is widely used in statistical inference and hypothesis testing, to the central limit theorem. This theorem establishes a relationship between the average of each of a set of samples drawn from any population, regardless of the shape of its underlying distribution, and the normal distribution. Since the averages are approximately normally distributed, there are a number of useful applications, including, for example, ensuring that proper account is taken of heterogeneity in a population (for further details refer to Murray *et al.*, 2004, Vose 2008).

The normal distribution is characterised by two parameters, the mean ( ) and standard deviation (σ):

Normal (, σ).

It is an unbounded continuous distribution that extends from minus infinity to plus infinity and has a bell-shaped curve. Since it is unbounded, we may need to impose a restriction on its limits if we are to avoid implausible values. This is done by truncating it using the Tnormal (,σ, *minimum, maximum*) function where *minimum* and *maximum* define the minimum and maximum of the plausible range of values.

The log normal distribution often provides a good representation for data that extend from zero and are positively skewed, that is, data that have a longer right hand tail, such as herd size and disease *incubation periods*. In addition, the outputs from computer simulations involving the multiplication of two or more distributions are often distributed log normally.

The log normal distribution is characterised by two parameters, the mean ( ) and standard deviation (σ):

Lognorm (, σ).

It is an unbounded, continuous distribution extending from zero to plus infinity that is used to model a variable (*x*) the natural log of which (ln(*x*)) is normally distributed. The parameters μ and σ are the actual mean and standard deviation of the log normal distribution. Alternatively, the log normal distribution may be specified by the mean and standard deviation of the normal distribution of ln(*x*).

Since the log normal distribution extends from zero to plus infinity we may need to truncate it to avoid implausible values:

Tlognorm (, σ, *minimum, maximum*).

5.5 Distributions used to model events in space or time

The Poisson, gamma and exponential distributions can be used to model events in space or time provided we can satisfy the underlying assumptions of a Poisson process that there is a constant, continuous probability of an event occurring in a particular interval (*t*). It is essentially a memory-less system, as the number of events occurring in any one interval is independent of the number in any other interval, regardless of whether an event has only just been observed or there has been a considerable amount of space or time between them.

The Poisson process is characterised by one parameter lambda (λ), the average number of events per unit interval (t) of space or time. The interval t is measured in either space (per litre, per kilogram, per kilometre, etc.) or time (per second, per hour, per day, per year, etc.). The reciprocal of (λ) is the mean interval between events (β) so that

$$\lambda = \frac{1}{\beta}.$$

5.5.1 The number of events in an interval

The Poisson distribution is used to model the *variability* in the number of events (x), in an interval (t):

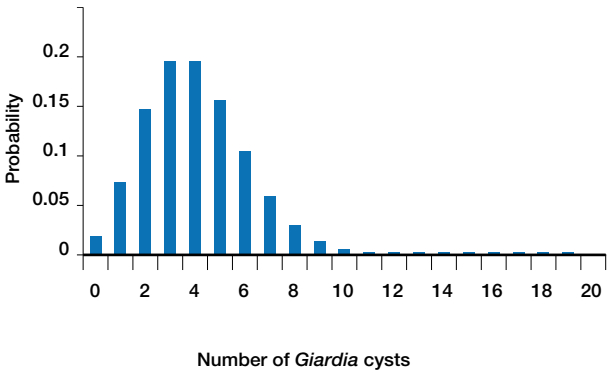
$x = Poisson(\lambda \times t)$, *or in terms of* ($\beta$),

$$x = Poisson\left(\frac{t}{\beta}\right).$$

It is worth noting that in @Risk the Poisson function is expressed as Poisson (lambda), where lambda actually equals either

$$\lambda \times t \quad \text{or} \quad \frac{t}{\beta}$$

not just simply λ, unless, of course, t equals one. Although, theoretically, there can be any value between zero and an infinite number of events in a specific interval, in practice this is almost never a restriction. For example, if there are four *Giardia* cysts per litre of contaminated drinking water on average, Figure 40 demonstrates that the probability of more than 20 cysts is vanishingly small.



where λ = 4/litre, t = 1 litre

Fig. 40
A Poisson probability distribution of the number of *Giardia* cysts per litre of water

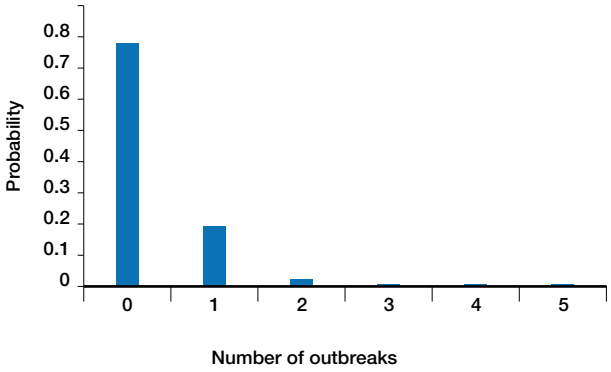


Fig. 41
A Poisson probability distribution of the number of disease outbreaks expected during the next time interval t,
where t = 6 months and the mean interval between events (β) is 24 months.

Provided we can satisfy the assumption that there is a constant and continuous probability of a disease outbreak over a certain period, we could estimate the number of outbreaks expected during, say, the next 6 months, given that historical information indicates an outbreak occurs on average every 24 months. In this situation the mean interval between events (β), would be 24 months so that λ is 1/24 outbreaks per month. The number of outbreaks in the next six months could then be modelled as Poisson (6/24) as presented in Figure 41. Of course, given that *risk factor*s may change over time through varying levels of exposure as well as the result of intervention strategies on population immunity, etc., it might not be reasonable to assume that a Poisson process applies.

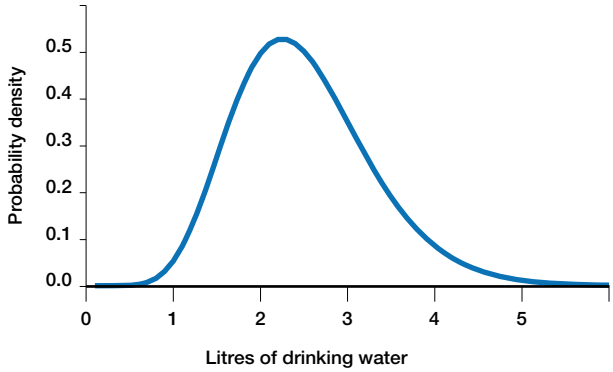
5.5.2 Estimating the amount of space or time until the next (x) events have occurred

The gamma distribution can be used to model the variation in the space or time until the next (x) events have occurred:

$$t_x = Gamma\left(x, \frac{1}{\lambda}\right)$$

or in terms of β, $t_x = Gamma(x, \beta)$.

If it has been determined that an infectious dose for *Giardia* is ten cysts, we can estimate the amount of contaminated drinking water with an average of four cysts per litre that would need to be ingested before becoming ill. Figure 42 plots a distribution of the volume of water that would need to be ingested in order to be exposed to ten cysts.



t_{10} = Gamma (10, 1/4)

Fig. 42
The amount of contaminated drinking water that would need to be ingested in order to consume ten *Giardia* cysts

5.5.3 Estimating the average number of events per unit interval λ

The gamma distribution can be used to model *uncertainty* about λ as we can never actually be sure of its true value unless our observations extend over an infinite interval. However, we can be increasingly confident of its true value by collecting more data.

$$\lambda = Gamma\left(x, \frac{1}{t}\right).$$

For example, if we tested a one litre sample of contaminated drinking water and found four *Giardia* cysts we could estimate that the average number is two per litre. But how confident can we be that this is a reasonable estimate? We can use the gamma distribution to model the uncertainty surrounding λ as shown in Figure 43. If we sampled a larger volume of water and found 400 cysts in 100 litres we would be increasingly confident that the *true* value of λ is four cysts per litre (Fig. 43).

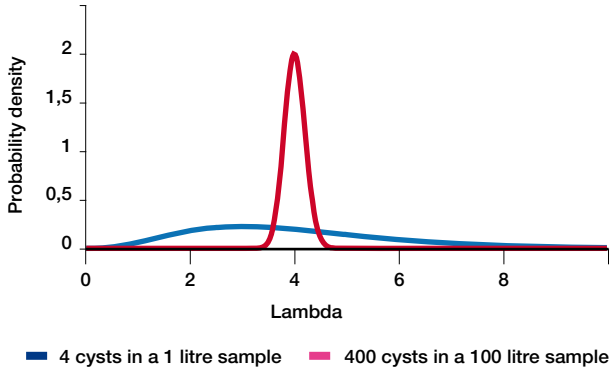


Fig. 43
Estimates of the average number of *Giardia* cysts

Per litre of contaminated drinking water (λ), using the gamma distribution,

$$Gamma\left(x, \frac{1}{t}\right)$$

where x = the number of cysts, t = the space (volume) of observation

Strengths and weaknesses, when to use and interpret with caution

Monte Carlo modelling is reasonably intuitive, relatively easy to implement and avoids the direct use of complex mathematical formulae. It provides a powerful technique whereby many biological processes can be conveniently incorporated into a *model* allowing the impact of various uncertainties that inevitably exist to be properly investigated. Critical steps along a particular biological pathway can be readily identified and various intervention strategies explored to access their relative impact on the outcome of interest. It can provide a useful adjunct to a qualitative assessment to gain further insights into particular aspect of the overall assessment.

Although Monte Carlo modelling involves numbers, it is not necessarily any more *objective*, nor are the results necessarily any more 'precise' than a qualitative assessment. Choosing an appropriate *model* structure, which pathways to include or exclude, the level of aggregation or disaggregation, the actual values used for each of the inputs and the types of distribution applied to them all involve a degree of subjectivity. The results themselves, which are expressed numerically, invariably present significant challenges in interpretation and communication.

Regardless of whether a qualitative or quantitative approach is adopted it is important to appreciate that all *risk assessments* inevitably include a degree of subjectivity. The personal opinions and perceptions of the analyst, experts and decision makers are inescapable. As a result, in order to ensure that a reasonable level of objectivity is attained, it is important to transparently document all the data, assumptions, uncertainties, methods and results. It addition, the conclusions reached must be supported by a well-reasoned and logical discussion. As with any *risk assessment* it should be fully referenced and subjected to peer review.

Case studies

Paisley 2001; Pharo & MacDiarmid 2001.

References

Vose 2000; Murray *et al*. 2004

Software options

Excel (www.microsoft.com) together with Excel-based software that enable simulation modelling to be undertaken: @Risk (www.palisade.com); Crystal Ball (www.oracle.com); Model Risk (www.vosesoftware.com). Refer to the relevant website for details concerning costs, licensing agreements and trial versions.

Appendix 5
A guide to planning a DRA workshop

R.M. Jakob-Hoff, T. Grillo, A. Reiss, H. Hodgkin & R. Barraclough

As noted above, many *wildlife* DRA exercises are likely to be conducted by one or two individuals who may or may not consult others with relevant knowledge or expertise. However, where a DRA workshop is possible, the following is provided to assist in the planning.

Planning a wildlife DRA workshop

Increasingly workshops are used for *wildlife* DRAs, in which the subject matter attracts significant public (and therefore political) interest, is associated with contentious issues such as public health or changes in land use or the results of which have impact on a diverse group of stakeholders. For those who are convening or participating in such a workshop, some understanding of group dynamics will help preparation.

Understanding people in groups

The psychology and behaviour of human beings is well beyond the scope of this *Manual*. However, a basic understanding of some group dynamics that can influence the success of a collaborative enterprise is of value and can be used to anticipate, recognise and appropriately respond to behaviours that reflect the group's stage of development.

Synergy
An increased effectiveness achieved by a number of people working together (Chambers Concise Dictionary).

An ideal DRA team brings together a relatively small group (8–15) of individuals with well-matched skill sets. Over time, a team functioning at its full potential can develop a synergy that produces results far superior to those that could be produced by any one individual (see Box 7). To gain the full benefits of such teamwork, the workshop leader must pay attention to establishing a collaborative culture in which each member feels valued and is able to contribute fully.

The characteristics of the stages are:

Stage 1 – Forming
This occurs when a team is formed *and* when it encounters changes, including changes in group members. There is a high dependence on the group leader for guidance and direction during this stage. Individual roles and responsibilities are unclear, and people need to get to know each other and the task. The leader must guide discussion about the group's purpose, objectives and external relationships.

Box 7:
The four-stage model of team development

All groups go through stages of development and it is useful for workshop convenors and participants to be aware of them. There are numerous ***models*** of this but a common one is Tuckman's four-stage ***model*** of team development (Tuckman 1965). In this ***model***, groups go through four stages termed 'Forming', 'Storming', 'Norming' and 'Performing' (Fig. 44). As shown by the double arrows in this figure, a group may find itself repeating any part of the cycle if significant changes occur.

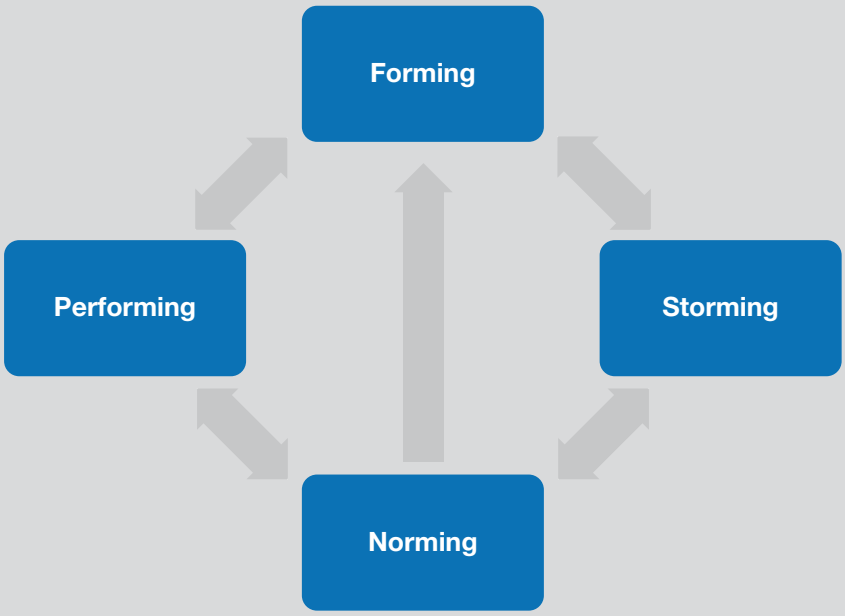


Fig. 44
Stages of team development

Stage 2 – Storming
Boundaries are tested and decisions do not come easily within the group during this stage. Group members vie for position as they attempt to establish themselves in relation to other group members and the group leader, who might receive challenges from group members. Clarity of purpose increases but plenty of uncertainties persist. Cliques and factions may form and there may be power struggles. The team needs to be focused on its goals to avoid becoming distracted by relationships and emotional issues. Compromises may be required to enable progress. Leadership is needed to help move through this stage productively.

Stage 3 – Norming
Roles and responsibilities become clear and accepted and there is agreement on how decisions are made and how the group operates. Norms of behaviour develop, both formal and informal. Smaller decisions can be delegated to individuals or small teams within the group. Commitment and unity is strong. The group may engage in fun and social activities. The group discusses and develops its processes and working style. There is general respect for the group norms and for the leader and some leadership may be shared by the group. People start to feel they are a team.

Stage 4 – Performing
The group knows clearly what it is doing and why. It has a shared vision and requires less hands-on management from the group leader. There is a focus on achieving goals, and the group may develop a high degree of autonomy. Disagreements occur but now they are resolved within the group positively, and changes to processes and structure are made easily. Group members look after each other. Morale and performance are high.

Personal attributes of group members

In an effective group, the attitude of members is as important as skills and knowledge. Ideally, workshop group members are:

- able and willing to work in a team
- willing to listen to other points of view
- open to new information and ideas
- adaptable to a changing political situation
- empathetic to cultural needs and practices
- willing to share professional expertise and information freely within the team.

Working agreement

It is useful to clarify the need for these attributes when inviting individuals to participate in the workshop. One method for encouraging these behaviours is to suggest, at the beginning of the workshop, a working agreement to assist the group to use its time most effectively (see Box 8). It is important that the wording is discussed and understood by all participants and that group consensus on the terms of the agreement is reached. The written agreement can then be placed in a prominent site within the meeting venue where members can refer to it as needed. It is, of course, essential that the workshop leader consistently practices these behaviours as an example to others.

Box 8:
Example of a working agreement for a DRA workshop

- The focus is on the agreed workshop objective(s)
- All other business and agendas are put on hold
- We will be respectful of each other at all times
- Everything will be recorded on paper for the group memory
- Everyone participates; no one dominates
- All ideas, comments and opinions are openly shared
- All ideas are valid
- We will actively listen to each other without interruption
- Differences and problems will be acknowledged
- We will observe agreed time-frames
- Confidentiality is observed whenever requested

Assembling and developing a collaborative DRA team

A workshop will ideally be organised by a small core group that will meet to plan the workshop, organise logistics, assist in ‘running’ the workshop and meet again to debrief after the workshop. The planning group should include representatives of key stakeholders and decision makers. If this is not possible, keeping these people informed and inviting their input to establishing the workshop’s plans and goals will pay dividends.

Meetings

The particular circumstances of the DRA will determine the most appropriate and practical means of meeting with the team. There can be great benefit (in developing synergy, improved communication, relationship building and commitment) in face-to-face meetings. However, time and resources as well as concern for minimising carbon footprint mean that more frequently groups are using Internet and

telecommunications technology to have 'virtual' meetings. Apart from the savings in time, money and carbon emissions, these have the advantage of bringing individuals together who are geographically separated by great distances.

Regardless of the meeting venue, considerable work needs to be done prior to each meeting. More often than not, those who agree to participate in the team will be doing so on a voluntary basis or on behalf of their organisation. Adequate preparation is therefore not only in the interests of getting maximum value from the meeting, but also acknowledges that the time and expertise being donated by participants to the DRA exercise is valued.

All good meetings have a clear, agreed purpose, agenda and time-frame and should conclude with an agreed action plan in which responsibility for each action has a clear deadline and is assigned to a specific individual. If the skills of a facilitator or evaluator are to be used, this is the time to begin working with them.

See Box 9 for a pre-workshop preparation checklist as an aid to the preparation of a DRA workshop. With the exception of venue preparation and catering, the items on the checklist are relevant to both face-to-face and 'virtual' workshops using the Internet.

Value of facilitators

As noted above, one of the values of skilful, independent facilitators, particularly during the early 'forming' and 'storming' phases, is their ability to focus on the process and dynamics of the group and to make timely interventions. A good facilitator will raise the group's awareness of group dynamics, mediate conflicts and bring attention back to the meeting's purpose. This frees the group up to focus on the topic of the meeting. In the absence of a trained facilitator (which is probably the most common situation) raising team awareness of the phenomenon of stages of group development at the outset (e.g. posting a diagram such as Figure 44 with its explanation on the meeting room wall or group website) can be a useful tool to provide context when conflicts arise.

Assembling a wildlife DRA team

For the purposes of this *Manual* the term 'team' refers to any group of two or more individuals collaborating with each other on a *wildlife* DRA. Depending on circumstances, the team may or may not meet face to face, regularly, intermittently or even at all. In many cases discussions may occur only at a distance using e-mail, telephone, the Internet, etc.

Box 9:
Pre-workshop preparation checklist

- Write a project outline for the DRA including all relevant background
- Complete a full literature review on the topic and include as much unpublished information as is available. (The aim is to provide all participants with sufficient background material to bring them on to an equal understanding of the issues, the information available to you and the key information gaps)
- If you are to use the services of a facilitator, an evaluator or a communications professional, meet with them early to seek input into the planning of the meeting and the evaluation and communications plans
- Using the evaluation planning template (Appendix 6, p. 118), draft the goal of the DRA and the specific objectives and methods to be used. These will be reviewed with the participants and the remaining fields completed during the meeting
- Use this *Manual* to select the appropriate DRA tools and ensure that you, or at least one of the other participants, is familiar with them
- Create a list of stakeholders and experts and prioritise according to:
  a) skills and expertise needed; and
  b) influence on communicating and implementing the DRA findings. Avoid inviting more than 10–12 participants but ensure that there is broad representation of experts and stakeholders
- Use the communications plan template (Table XII) to enter full contact details of attendees (title, organisation, mailing address, e-mail, telephone, fax). This plan will be completed during the first meeting. (Note: this register of attendees, with some minor adjustments, could also form the beginning of a skills register.)
- Develop a meeting budget and consider sources of funds including sponsors
- Circulate the project brief with an invitation to the preferred list of attendees
- Draft an agenda that will systematically step the meeting participants through the DRA process as outlined in this *Manual* using any tools chosen to assist. Circulate this prior to the meeting
- If necessary submit sponsorship applications
- Identify and book a suitable venue, if needed
- Organise food and drinks for participants and check if any have special dietary needs
- Check the venue is fully functional and set up for your needs – including comfortable seating, tables, clean, functional and accessible toilets, audiovisual equipment, white boards, etc. and adequate heating, cooling and ventilation
- Organise consumables such as paper, pens, rolls of paper, sticky tape, name tags, etc.
- Print and collate any printed materials for distribution before or during the meeting

As with any team, having the right mix of individuals is critical to the quality of its performance. The specific scenario and DRA questions your team is addressing (refer to the problem formulation step of the DRA process) will influence the range and types of expertise needed.

Members of a DRA team can be broadly categorised as either 'stakeholders' or 'experts'. Some individuals may fall into both categories. When considering the team's composition it is useful to make a list of relevant stakeholder groups and experts (Table XI), prioritise them and then consider specific individuals to contact to check their interest and availability.

Stakeholders

Stakeholders are those people and organisations that have a direct or indirect interest in, or will be affected by, the DRA process and its outcomes. A checklist of some potential stakeholder groups is provided in Table XIV. (A specific example is included as Table II).

Table XIV
Checklist of some potential wildlife DRA stakeholders

Biosecurity advisors or agencies
Captive breeding practitioners or organisations
Community conservation groups
Non-governmental organisations (NGOs), e.g. WWF, Greenpeace
Federal, state and local government agencies
Funding agencies and donors
Media/journalists
Hunting, fishing and other outdoor recreation organisations
Industry representatives, e.g. horse racing, mining, power generation, etc.
Wildlife conservation managers/rangers
Land owners and managers, including farmers, ranchers, property developers, etc.
Regulatory bodies including permit processing officers
Policy advisors/Politicians
Public health organisations
Researchers or universities
Volunteer wildlife groups – e.g. wildlife rehabilitation carers
Pet owners

When selecting stakeholders for the team, priority should be given to those who hold key information or skills and those who will have influence on the communication and implementation of recommendations arising from the DRA.

This list will also form the basis of the all-important communications plan (see risk communication step of the DRA process).

Experts

The level and type of expertise used is one of the most important factors influencing the outcome of the analysis. *Risk analysis* is not the exclusive domain of specialists. While expertise in *risk analysis* can contribute significantly to the process, people who are knowledgeable in appropriate areas of *wildlife* biology and relevant health sciences can carry out a credible assessment of disease risks (Leighton 2002). Each situation will require a specific mix of skills and expertise.

Using the social, political and technical dimensions discussed in the '*Planning and conducting a wildlife DRA*' section of this *Manual*, Table XV summarises a list of skills, attributes and professions that can be of value to those aspects of a *wildlife* DRA process. The wide range of professions listed is a reflection of both the complexity of *wildlife* disease scenarios and the value of taking a transdisciplinary approach.

As not all readers of this *Manual* will be familiar with the skills associated with all of the professions listed, a brief synopsis of the skill sets associated with a selection of them is provided below.

Wildlife managers

These are generally government or NGO (e.g. community conservation group) representatives responsible for coordinating management decisions for endangered or threatened species. They are able to provide context on current species management programmes and advice on requirements for government permits for *risk management* initiatives. Managers of *ex situ* (captive) and *in situ* (free-ranging) *wildlife* can also bring in-depth knowledge of the biology and behaviour of the *wildlife* species under consideration and the practicalities of working with them. They may also be able to access some of the resources available for research targeted at priority knowledge gaps and *risk management* implementation through their affiliated organisations.

Wildlife veterinarians

All veterinarians receive a broad training in the prevention, investigation, diagnosis and medical and surgical treatment of domestic animal ailments. Their training, which also includes specialist topics such as nutrition, animal reproduction and toxicology, focuses primarily on horses, cattle, sheep, goats, pigs, dogs, cats and poultry. *Wildlife* veterinarians have additional postgraduate training or experience in the application of veterinary skills to captive or free-living *wildlife*. They have a strong focus on disease prevention and, as such, have a good understanding of disease risk assessment and *risk management* (Fowler 1986; Franzman 1986). In addition, *wildlife* veterinarians may bring knowledge and skills in chemical and physical capture, restraint and transport of *wildlife*, disease *surveillance* and *monitoring*, diagnostic sample collection, storage and transport, interpretation of diagnostic results and the development of pre-translocation *quarantine* and health screening protocols.

Epidemiologists

Veterinary and medical epidemiologists study the patterns of disease occurrence in populations and the factors that influence these patterns. (Thrusfield 2007). They focus on investigating animal populations rather than individual animals and aim to:

- determine the origin of a disease the cause of which is unknown
- investigate and control a disease the cause of which is either unknown or poorly understood
- acquire information on the ecology and natural history of a disease
- plan, monitor and assess disease control programmes
- assess the economic effects of a disease.

They can therefore advise on disease event patterns in a population and the factors that influence their occurrence. They can also identify *risk factor*s for disease and determine optimal treatment and management options, advise on the use of methods to compare the impacts of different *risk management* options and provide guidance on outbreak investigation, study design, data collection and analysis and documentation of results.

Table XV
Skills and attributes that can be of value to a wildlife DRA process

	Skill or attribute	Who might have these skills
Social	Working with communities	Social scientists
	Group facilitation	Facilitators
	Cultural understanding	Cultural advisor
	Communication	Communications practitioners (e.g. employed in media, public relations, marketing)
	Project review	Evaluator, auditor
Political	Influence	Individuals whose opinions are likely to influence stakeholders e.g. community leaders (councillors, heads of pertinent local organisations or cultural groups, politicians, prominent scientists and spokespeople?)
	Policy, regulations and guidelines (national/ international)	Policy advisor
	Legal advice	Environmental lawyer
	Up-to-date knowledge of relevant legislation, permits (e.g. CITES), etc.	Government agency representatives
	Understanding of transboundary disease issues	Government agency representatives, e.g. in the areas of customs and biosecurity
Technical	Wildlife management, biology and ecology	Ecologist, biologist, wildlife manager
	Wildlife health and disease including diagnostic tests and their interpretation	Wildlife veterinarian Epidemiologist Laboratory scientist (e.g. pathologist, virologist, microbiologist, toxicologist, etc.)
	Zoonotic diseases	Veterinarian Public health doctor Epidemiologist
	Disease risk analysis	Risk analyst Statistician
	Disease modelling	Disease modeller, Climatologist Population biologist Geneticist Reproductive biologist

Wildlife ecologists

Ecologists study the relationships between organisms and their environments. An ecologist can provide insight into the interactions between organisms within the study site and between them and their habitat. A number of specialist disciplines have arisen from the subject of ecology. For instance, some ecologists specialise in reintroduction biology, the process of translocating populations to re-populate previous habitat from which they have been eliminated, establishing populations in 'safe' locations, or supplementing depressed populations. They bring experience in logistical and animal handling approaches to maximise survival of translocated animals. A disease ecologist can provide insight into factors affecting the *transmission*, rate of spread and maintenance of disease within a population and the dispersal and density of the population (Animal Health Australia 2011).

Public health doctors

The discipline of public health focuses on the prevention of diseases and the promotion of health in people and forms part of the training of both medical and veterinary practitioners. Of value to *wildlife* DRA is their understanding of zoonotic diseases, i.e. diseases naturally transmitted between humans and other vertebrate species, e.g. rabies and psittacosis. Given the widespread and growing interaction between people and *wildlife*, most *wildlife* DRAs should include consideration of zoonotic disease transfer risks. Individuals with this training can provide advice on measures available to manage these risks.

Given their potential value at the planning, problem formulation and implementation steps of the DRA, two further skill sets are described: those of evaluation and facilitation.

Evaluators

Evaluation is 'the process of determining the merit, worth or value of something or the product of that process' (Scriven 1991). Trained evaluators bring a broad range of data-gathering, critical thinking and analytical skills. Where possible, it is valuable to involve an evaluator when developing an evaluation framework at the outset of planning the DRA (Appendix 6, p. 118). A good evaluator will greatly assist the clarification of research questions during the problem formulation step and ensure that data to be gathered to answer the review question 'How will I know if I have succeeded?' is identified and planned for. The inclusion of an evaluation plan (Appendix 6, p. 118) as part of the DRA process and its implementation will provide the basis for the *monitoring* and review stage of *risk management*. This, in turn, will provide the basis of an adaptive management process (Fig. 8) enabling the need for adjustments to the *risk management* programme and improvements to future DRA processes to be identified.

Facilitators

In a DRA workshop setting, a neutral, experienced facilitator can be a valuable resource for the team. Facilitators help groups to clarify their goals and ensure full participation and mutual understanding while fostering inclusive solutions and cultivating shared responsibility (Kaner *et al.* 2007). While it can be an advantage for the facilitator to be familiar with the meeting's subject matter, he or she must remain neutral to the content and focus on the group's processes. This is vital given the passion and strongly held views often aired at *wildlife* DRA workshops, and the occasional need to resolve conflicts! To be effective, facilitators need to be involved during the earliest stages of planning the DRA process.

Appendix 6
Evaluation planning

R.M. Jakob-Hoff

In a DRA project there are two aspects that should be subject to formal evaluation:

– the DRA process itself, and

– the outputs of the process that are the *risk management* actions.

Consequently an evaluation plan should be developed during the problem description step and additional evaluation questions developed as part of the *risk management* step. In both cases goals and strategies are formulated and, for each one, the question asked 'How will success be measured?'.

Table XVI provides an example of an evaluation plan (sometimes referred to as a 'programme logic model') used in planning a DRA for Tasmanian devils within a Conservation Breeding Specialist Group (CBSG)-facilitated conservation planning workshop. This is a tool that can be used to clarify, document and establish a common understanding of the project and to ensure the reasons for pursuing a particular course of action are open and transparent for all involved. The DRA team should collaboratively develop an evaluation plan during the problem formulation step of the DRA project.

Developing and using this framework can involve considerable discussion among team members, and tends to lead to a much clearer and more realistic DRA plan than one drawn up in isolation. *Time must be allowed for this participatory process*. The more participatory the process, the more it can help to ensure common understanding of the project among all participants. In line with the adaptive management approach, evaluation plans are living documents and should be continuously refined as new information comes to hand. They require careful review and, often, several revisions.

An explanation of the steps in developing an evaluation plan follows.

1. Initially the goal for the DRA, as agreed to in the problem description step, is noted above the table. All subsequent objectives are developed as a means of achieving this goal.

2. The first column of Table XVI lists the specific objectives of the *risk analysis*. As far as possible, you should formulate SMART objectives – which are specific, measurable, achievable, realistic and time dependent.

3. The second column of the table explains the reason or rationale behind each objective, i.e. why this objective is important. This is a 'clarification' step and, when discussed, will often lead to a refinement of the objective.

Table XVI
Evaluation plan for a Tasmanian devil DRA workshop (excerpt)

Goal To establish an evidence-based disease risk management plan for Tasmanian devils within the context of an insurance population management plan using the best available information, analytical tools and expertise.

Specific objectives (What?)	Rationale (Why?)	Strategies (How?)	Evaluation questions	Sources of data
By 7 July 2008, to review and analyse the disease risks associated with management of an insurance population of devils	Management of an insurance population will involve *ex situ* management and periodic movement of animals between metapopulations Identification and analysis of associated disease risks will enable appropriate risk mitigation measures to be established	Follow a structured *disease risk analysis* process Involve key stakeholders, experts and decision makers in DRA	Was a structured DRA process followed? Were an appropriate group of stakeholders, experts and decision makers involved in the DRA? If key individuals or groups were not involved, who were they and why were they not involved?	Organiser's evaluation Organiser's and participant's evaluation Participant's evaluation questionnaire and organiser's follow up with missing individuals
Within the same timeframe, to develop a disease risk management plan that is integrated with the insurance population management plan	A disease risk management plan as an integral component of the insurance population management plan is needed to ensure that disease risks are appropriately and consistently understood and applied by all relevant participants.	Conduct the DRA within the broader framework of a CBSG insurance population planning workshop for Tasmanian devils	Was the DRA included as part of a CBSG insurance population planning workshop for Tasmanian devils	Organiser's evaluation Workshop report

4. The third column states the inputs (activities, processes and resources) to be used to attain the objective. This list is the action plan for the DRA. It is important to be as detailed as possible with this step and to take into account any assumptions made in step 2 above.

5. The fourth column lists the questions that will be needed to monitor and evaluate the effectiveness of the strategies used, the extent to which outcomes were achieved and the extent to which each objective has been met. Both qualitative and quantitative measures are valid and important and should be applied as appropriate.

6. The final column lists the sources of the data needed to answer the evaluation questions and this becomes the DRA monitoring plan. Defining these at the outset will ensure that appropriate processes are put in place to collect relevant data in a format that lends itself to *robust* analysis.

Box 10 lists some possible measures of success for a *wildlife* DRA.

Box 10:
Some possible measures of success for a wildlife DRA

In the context of a wildlife DRA, key measures of success could include:

- The best available data have been used
- Data gaps were identified and prioritised for future research
- Data analysis was as robust as possible (i.e. stands up to peer review) given the levels of uncertainty (assumptions are explicitly stated) and the available tools, resources (time, funds, technology, etc.) and expertise.
- Risk management recommendations were supported by key stakeholders and decision makers
- Risk management actions have been, or are being, implemented, monitored, reviewed and refined over time.

These measures could be framed as the objectives for a DRA exercise and used to generate suitable evaluation questions to anticipate and avoid any potential obstacles to success.

Appendix 7
Example wildlife DRA summaries

B. Rideout

As this *Manual* is the first published articulation of the application of *disease risk analysis* from a specific biodiversity conservation perspective, it has not been possible to locate existing publications that follow the format outlined in this *Manual*. The following case studies have been compiled retrospectively from the author's personal experience and are included here to illustrate how a wide variety of DRAs could be summarised following the format outlined in this *Manual*. Given that the examples are based on retrospective material not all components of a full DRA were completed. This in itself provides insight into the potential value of each of the sub-steps of the process as illustrated in Figure 4.

We encourage others who choose to follow the systematic process described in this *Manual* to publish their work and increase the case studies available as examples to colleagues around the world.

Example 1: Interruption of California condor (*Gymnogyps californianus*) release programme

References

Unpublished conservation programme documents.

Risk communication

Stakeholders involved in the *risk analysis* and decision making included our clinical veterinarians, California condor breeding programme managers, and US Fish and Wildlife Service California condor recovery programme staff.

Problem description

Context
The California condor is one of the most endangered birds in North America. By 1987, only 27 birds remained, all in captivity. The recovery programme involves captive propagation in several isolated and relatively *biosecure* facilities, with release at several locations in the south-west United States and Baja California, Mexico. By locating the breeding facilities near the release sites and keeping the breeding flocks relatively isolated from other birds, releases can occur with minimal disease screening (because the wild populations would be exposed to the same pathogens as the captive breeding flocks, neutralising any disease risks). The primary disease surveillance tool is routine health *monitoring* of the population and thorough post-mortem examinations

on all birds that die. Although the mortality rates in the captive breeding flocks are very low, one facility experienced the unexpected loss of a parent-reared nestling at three months of age. A thorough post-mortem examination revealed that the chick died from a poxvirus infection that had spread through all of the internal organs. Poxviruses more typically cause self-limiting skin infections. This type of systemic virus spread had not been seen in any captive or free-ranging California condors in the past and raised questions about the source and significance of the virus. Until these questions could be resolved, no further releases were allowed from this facility. Because the breeding programmes operate at maximum capacity, there is little space to house juvenile birds if releases are interrupted, so this situation created a serious management problem due to lack of holding space for the birds originally destined for release.

Goals, scope and focus
The goal of the recovery programme is to maximise the population of California condors and eventually re-establish self-sustaining populations in the wild. The goal of this risk assessment was to answer the following questions:

1. Was this poxvirus a newly introduced virus in the region that might pose a threat to the wild population or just a low-risk endemic agent that for unknown reasons caused an overwhelming infection in this nestling?

2. What is the normal host for the virus, and would that host probably already be a natural source of exposure for wild California condors?

Assumptions and limitations
The chief limitations with this approach are that it requires a rapid and technically challenging response, and it assumes that in a reasonable time-frame we can characterise the virus and determine its normal host.

Discussion of acceptable levels of risk
The risk tolerance is low for this project because the California condor population size is still low and the geographic range is very restricted. Any introduced disease that could limit the ability to establish self-sustaining populations in the wild would be devastating.

Hazard identification

Hazard list
The only hazard of concern at this point is an unidentified avian poxvirus.

Hazard categorisation (infectious/non-infectious)
Infectious.

Initial hazard prioritisation (identification of hazards of concern for full risk assessment)
Avian poxvirus.

Graphic depiction (e.g. scenario tree) of the biological pathways leading to exposure of the susceptible animals or people to each the hazards of concern)
Not used.

Risk assessment

Release assessment
Although avian poxviruses are not known to cause *latent infections*, there is a possibility of chronic or inapparent infections that could result in release (assuming that this agent is not already present in Condor release areas). In addition, the persistence of the agent in the environment increases the risk of release through mechanical or fomite transmission.

Exposure assessment
Condors frequently congregate at carcases and water sources in the wild, which results in high potential for exposure if release of a novel poxvirus were to occur.

Consequence assessment
Systemic poxvirus infections are normally a rare and isolated occurrence. If this virus has a higher potential to cause systemic infection, the consequences could be significant, such as causing sufficient mortality to prevent the establishment of self-sustaining populations in the wild.

Risk estimation
The risk estimation concluded that the questions above needed to be addressed before releases from this captive breeding population could continue.

Risk management

Option evaluation
Based on the above analyses, the risk mitigation plan required the sequencing of portions of the poxvirus DNA to determine the strain type and then conducting surveillance for this strain in wild birds that would be sympatric with California condors.

Implementation

Action planning
The Wildlife Disease Laboratories at San Diego Zoo Global were responsible for poxvirus sequencing and opportunistic surveillance of wild birds.

Monitoring and review
The highest prevalence of poxvirus infections in wild birds in this geographic region was seen in common ravens (*Corvus corax*) and California towhees (*Pipilio crissalis*). The DNA sequence of the common raven virus did not match the sequence of the California condor virus. However, the sequence of the California towhee virus was a 100% match with the California condor virus. This California towhee poxvirus has also been seen in other native birds throughout North America, indicating that it is an endemic virus in this part of the world. Since California towhees are abundant in California condor release areas, the conclusion was that exposure of the wild population had probably already occurred. Releasing additional California condors from the affected facility would not pose any additional disease risk to the wild population. Releases therefore resumed and no additional problems have been seen.

Example 2: Identification and mitigation of the cause of *Gyps* spp. vulture declines in Asia

Risk communication

Stakeholders involved in the *risk analysis* and decision making included veterinarians, biologists, representatives of NGOs, political officials and government agency representatives in several Asian countries. However, the process was not structured as a formal risk assessment and communication plan, but rather evolved as research results became available and public awareness increased.

Problem description

Context
The oriental white-backed vulture (*Gyps bengalensis*), long-billed vulture (*G. indicus*) and slender-billed vulture (*G. tenuirostris*) were once among the most common birds across south Asia, but a catastrophic decline beginning in the 1990s resulted in a population decline of greater than 95%. This decline has had tremendous conservation, cultural and public health significance, since these vultures are the primary means of carcase clean-up from the agricultural industry and are also important in some human funeral ceremonies.

Goals, scope and focus
The goals were to identify the cause(s) of the decline and implement effective mitigation strategies as rapidly as possible.

Assumptions and limitations
A diverse array of assumptions and limitations made the task very difficult. The pattern and spread of the population declines were assumed by many to be consistent only with transmissible causes (Cunningham *et al.*, 2003), so initial investigations focused primarily on viruses and other infectious agents. The investigations were challenging in part because of the difficulty in obtaining fresh carcases for post-mortem examinations, the lack of local expertise in field investigation of *wildlife* diseases, a lack of rapidly available funding, and the number of countries and government agencies involved. Whatever the cause of the decline, it was assumed that government intervention would be required to address the problem, so conclusive findings and clear risk communication were expected to be critical.

Discussion of acceptable levels of risk
The risk tolerance for mitigation failure was low because of the rapidity of the decline, the expected slow recovery of such a long-lived and slowly reproducing species, and the public health ramifications of accumulating carcases (such as the expansion of the feral dog population and associated increases in the rabies risk).

Hazard identification
Comprehensive hazards list:

The group that identified the cause of the decline began with a very broad list of potential hazards based on a case definition arising from the field investigations. The hazard list included infectious agents such as novel viruses, mycoplasmas, other bacteria, natural and man-made toxins and environmental conditions.

Hazard categorisation (infectious/non-infectious)
Both infectious (transmissible) and non-infectious hazards were considered.

Initial hazard prioritisation (identification of hazards of concern for full risk assessment)
Because of the broad nature of the hazard list, all categories of causes remained high priorities for investigation. A decision was made to proceed with parallel investigations of:

- toxic aetiologies (causes) through tissue analysis for organic and inorganic toxins,
- a transmission study involving captive birds inoculated with material from affected birds to determine if an unidentified infectious agent was involved.

Ultimately the cause of decline was determined to be the contamination of cattle carcases with the veterinary drug diclofenac (Oaks *et al.* 2004). Birds feeding on carcases of cattle treated with diclofenac experienced acute kidney damage and died rapidly from secondary renal gout.

Graphic depiction (e.g. scenario tree) of the biological pathways leading to exposure of the susceptible animals or people to each the hazards of concern)
Graphic representations were not used, but once diclofenac was identified as the apparent cause of the population declines, a modelling study confirmed that the observed prevalence of diclofenac in cattle carcases was sufficient to explain all of the observed population declines (Green *et al.* 2004). This helped rule out other avenues of exposure, such as water contamination.

Risk assessment

Release assessment
Shortly after the identification of diclofenac as the cause of the vulture's decline, the prevalence of the drug in domestic cattle carcases was assessed and found to be high (Green *et al.* 2004). 'Release' had already occurred on a large geographic scale, requiring high-level government intervention to prevent ongoing release and exposures.

Exposure assessment
Exposure required only a single feeding on a contaminated carcase. Bioaccumulation does not occur in the food chain or the environment, so mitigating exposure required only prevention of exposure to carcases of treated cattle.

Consequence assessment
The consequences of ongoing exposure included the probable extinction of several *Gyps* vulture species, an increasingly unsanitary environment due to accumulation of decomposing carcases, and rapid increases in other scavenger populations, such as feral dogs, with an increased risk of human rabies and other *zoonoses* (Markandya *et al.* 2008).

Risk estimation
The consequences of widespread diclofenac exposure were already being felt by the time the drug was identified as the cause of the vulture's decline, so it was obvious that continued population declines and all of the associated negative outcomes would occur unless there was effective mitigation of the exposure risk.

Risk management

Option evaluation
The only option that could be implemented on a sufficiently large scale and rapid timeline was a government ban on the use of diclofenac in animals.

Implementation

Action planning
Meetings with appropriate stakeholders and government officials led to bans on the veterinary use of diclofenac in India and Pakistan by 2006. In order to improve compliance with the ban, additional research by several groups lead to the identification of non-toxic alternative drugs, as well as the identification of other non-steroidal anti-inflammatory drugs that were as toxic to vultures as diclofenac (Swan *et al.* 2006).

Monitoring and review
Monitoring the effectiveness of the diclofenac ban reveals that the prevalence of contaminated carcases has dropped dramatically, but enough contaminated carcases remain to cause ongoing population declines of approximately18% per year (Cuthbert *et al.* 2011). Obstacles to success include the fact that diclofenac is easy to manufacture and there are hundreds of small factories continuing to produce it, the drug is sold on the human pharmaceutical market without prescription, so it continues to be available to farmers and veterinarians in pharmacies, and the non-toxic replacement drug is perceived as being less effective. A number of NGOs continue to work on improving the effectiveness of the mitigation strategies.

Example 3: Pacific island psittacine translocation

References

Unpublished conservation programme documents.

Risk communication

Stakeholders involved in the *risk analysis* and decision making included agriculture and *wildlife* officials at the national and local government levels for the source and destination islands, as well as independent experts reviewing the plans.

Problem description

Context
A small psittacine species is listed as CITES Appendix II because its distribution is limited to one small South Pacific island and is therefore vulnerable to extinction from a variety of catastrophic events, such as a typhoon.

Goals, scope and focus
The goal of the project is to translocate a small group of these psittacines from the source island to a destination island within its original historical range in order to establish a second population as a hedge against extinction.

Assumptions and limitations
A major assumption in the *risk analysis* was that the sole remaining population of the target species has remained isolated from unnatural disease exposure due to the remoteness of the source island and the historical lack of an airstrip or tourist activities. In addition, the lack of other psittacines on the destination island reduced the list of diseases of concern to those that have a broad host range (beyond psittacines).

In order for the translocation to be acceptable and successful, the destination island had to meet the following limiting criteria:

- be within the original historical range of the species
- be free of other psittacine species
- be free of introduced ship rats (*Rattus rattus*), which are known to have extirpated other native psittacines, and
- have the support of the local people.

Discussion of acceptable levels of risk
Although the risk of significant disease introduction to the destination island is low, the risk tolerance is also very low. This is because there are other endangered avian species on the destination island that would be vulnerable to a catastrophic disease outbreak, and the destination island is under the governance of a different country than the source island.

Hazard identification

Comprehensive hazards list
There was no available disease surveillance data for the population, but historical evidence suggested that the population had been stable and without any documented disease outbreaks or mortality events for at least several decades. The comprehensive hazards list was developed from the global scientific literature on psittacine diseases, but the task was problematic because most of the agents of concern were documented in birds from the global pet trade rather than from wild populations.

Agents of concern with potentially broad host ranges included polyomaviruses, paramyxoviruses, herpesviruses, circoviruses, avian influenza, haemoparasites, gastrointestinal parasites and ectoparasites.

Hazard categorisation (infectious/non-infectious)
The only non-infectious hazard of concern was mortality associated with holding for *quarantine*. Because of this concern, and the long history of isolation on the small source island, there was no strict quarantine period. The translocation plan called for birds to be released in two weeks or less, with daily health *monitoring* during the holding period.

Initial hazard prioritisation (identification of hazards of concern for full risk assessment)
The following hazards were determined to be the highest priority based on expert opinion and the literature regarding their broad host range, transmissibility and potential population-level effects.

- paramyxoviruses
- circoviruses
- avian influenza viruses (H5 and H7 strains owing to regulatory concerns)
- ectoparasites.

Graphic depiction (e.g. scenario tree) of the biological pathways leading to exposure of the susceptible animals or people to each the hazards of concern
Not used.

Risk assessment

Release assessment
The likelihood that the hazard was present or would be released was considered low for paramyxoviruses and avian influenza because recent exposure was considered unlikely, the agents do not survive long in the environment and they do not cause persistent infections.

The likelihood of presence or release was considered low to moderate for polyomaviruses, herpesviruses and circoviruses, and high for haemoparasites, gastrointestinal parasites and ectoparasites (see exposure assessment).

Exposure assessment
The likelihood of exposure for most viral agents was considered low to moderate because close contact would be required. Close physical interaction with other avian species on the destination island was not expected and the target species would be the only nectar and pollen specialist on the island, so exposure at shared feeding sites was considered unlikely. Exposure to haemoparasites was considered likely because comparable arthropod vector populations were present on both the source and the destination islands. Exposure to gastrointestinal parasites and ectoparasites was also considered likely because of the environmental persistence of the infective stages of some agents.

Consequence assessment
For paramyxoviruses, the biological consequences were considered potentially significant if there was a host-adapted virus that was non-pathogenic in the psittacines but had unknown potential to spill over

into other species and cause disease. The likelihood of this was considered low, however. There was also a concern over the regulatory consequences of any positive test results because of potential confusion with exotic Newcastle disease.

The consequences of establishing a novel circovirus or polyomavirus on the destination island were considered significant because of the potential for these agents to cause population-limiting disease, survive for extended periods in the environment and cause persistent infections.

The consequences of avian influenza virus establishment were largely a regulatory concern because a variety of avian influenza strains are probably present already in aquatic birds on both the source and destination islands.

The consequences of establishing new ectoparasites, such as blood-sucking mites, were considered potentially significant. Some ectoparasites can cause lethal infections in individuals, and disrupt nesting behaviour in populations.

The consequences of establishing haemoparasites on the destination island were considered relatively low because any agents present would probably be distributed through all the islands in the region.

Risk estimation

The risk estimation concluded that screening for viruses and parasites with a potentially broad host range was warranted.

Risk management

Option evaluation

Based on the above analyses, a risk mitigation plan was developed that involved testing cloacal swabs by PCR for the viruses of concern (polyomaviruses, circoviruses, paramyxoviruses, and avian influenza H5 and H7 strains). PCR was determined to be the best testing option because it does not rely on species-specific reagents and in this case did not require blood sampling.

The mitigation plan for ectoparasites involved careful inspection of captured birds and treatment with insecticide spray.

However, the birds could not be safely held in quarantine until test results were available. Consequently the mitigation plan called for release of the birds as soon as possible after capture and ectoparasite treatment, but with lethal removal of the released birds if test results later came back positive (and were confirmed by additional testing).

Implementation

Action planning

Consensus on the risk assessment and mitigation plan was achieved with all of the stakeholders. Implementation fell to the *wildlife* disease specialist on the translocation team and the in-country regulatory veterinarians.

Monitoring and review

There were no mortalities or other adverse outcomes during the translocation. PCR testing for the agents of concern was negative in all birds. Feather mites were present on all birds and were treated with insecticide spray. No other ectoparasites were found. Subsequent DNA sequencing data from the feather mites revealed that they were probably a novel host-adapted species. Other birds sharing the same habitat on the source island, such as *Acrocephalus* sp. reed warblers and domestic poultry, had their own unique feather mite species, so it appears that host switching is not common with these ectoparasites.

Post-release *monitoring* was the responsibility of the project leader and assigned staff on the destination island. *Monitoring* has been ongoing since the release, with success determined by the growth of the released population and the absence of negative impacts on other native bird species. Periodic project updates have been submitted to the government agencies overseeing the project.

Appendix 8
DRA example: Mountain gorilla, using Stella™ software

(From Unwin and Travis 2009)

Participants

Laura Hungerford, Patty Klein, Mike Cranfield, Genevieve Dumonceaux, Barbara Corso, Mark Atkinson, Shelley Alexander, Dominic Travis, Tom Meehan, Jim Else, Sue Brown.

Step 1 – Tell the story

Bwindi Park gorillas. Trackers and guides are the source. Scabies originates from the local community and is one of the few diseases that does *not* stem from the trackers and guides. The disease of most concern for the gorillas is measles (affects the population for a few months) and tuberculosis (continually affects the population)

Step 2 – Define the questions

Risk of transmission of disease to the gorillas (from the identified sources).

What is the likelihood of introducing scabies into the habituated gorilla population?

What is the likelihood of introducing cryptosporidia into the habituated gorilla population?

What is the likelihood of introducing measles into the habituated gorilla population?

The species of concern are:

- humans
- gorillas
- other (habituated) primates.

Step 3 – Map the pathways (Fig. 45)

Procedures done at all points:

- In the tracker and guide/community/agricultural activity area: community health programmes (basic) and basic veterinary care
- In the staging/health-screening area: educational programme

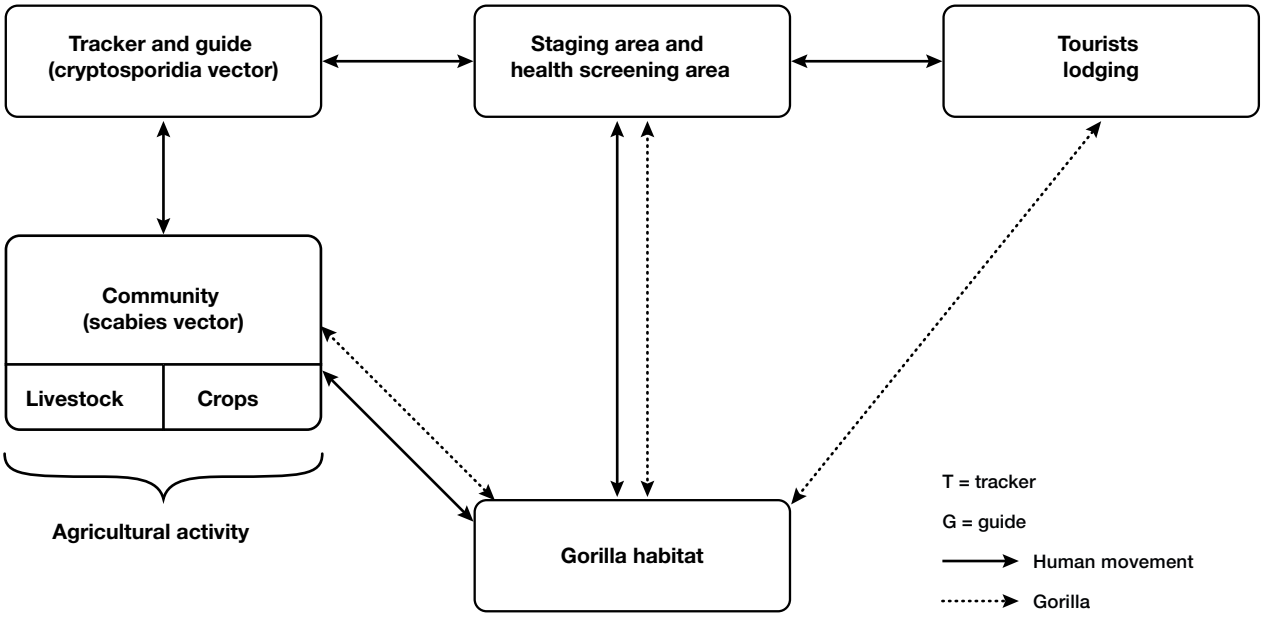


Fig. 45
Step 3 – Map the pathways

Step 4 – Identify all potential sources

a) Scabies transmission pathways (Fig. 46)

Identify all potential sources for scabies transmission

Source point	Hazard risk assessment
Trackers and guides	Low
Local community	High
Livestock/crops	None
Staging/health screening area	Low
Tourist lodging	None
Gorilla habitat	High

Assumptions and conclusions

The probability of transmission from trackers and guides is low.

The critical control point (CCP) is gorilla movement to and from the community.

CCPs are within the community, gorilla to gorilla within the habitat, and community to gorillas.

b) Cryptosporidia transmission pathways (Fig. 47)

Identify all potential sources for *Cryptosporidium* transmission

Source point	Hazard risk assessment
Trackers and guides	High
Local community	Low
Livestock/crops	High
Staging/health screening area	Low
Tourist lodging	Low
Gorilla habitat	High

Assumptions and conclusions

Not critically significant.

The four CCPs are: gorilla to livestock; livestock to trackers and guides; staging area to gorillas; trackers and guides to gorillas.

c) Measles transmission pathways (Fig. 48)

Identify all potential sources for measles transmission

Source point	Hazard risk assessment
Trackers and guides	Low (>0)
Local community	Low (>0)
Livestock/crops	None
Staging/health screening area	Low (>0)
Tourist lodging	Low (>0)
Gorilla habitat	None

Assumptions and conclusions

The probability of transmission from trackers and guides or tourists is extremely low, but the effect if it occurs is really bad.

The risk of transmission is extremely low.

The CCP is within the gorilla population.

There is a need to modify the destination population.

d) Tuberculosis transmission pathways (Fig. 49)

Identify all potential sources for tuberculosis transmission

Source point	Hazard risk assessment
Trackers and guides	Medium to moderate
Local community	Medium to moderate
Livestock/crops	Low
Staging/health screening area	Medium to moderate
Tourist lodging	Low
Gorilla habitat	None

Assumptions and conclusions

There is an extremely low risk of transmission.

There is no effective treatment, and it is a significant health problem in terms of morbidity/mortality.

The CCPs are within the community and gorilla to gorilla.

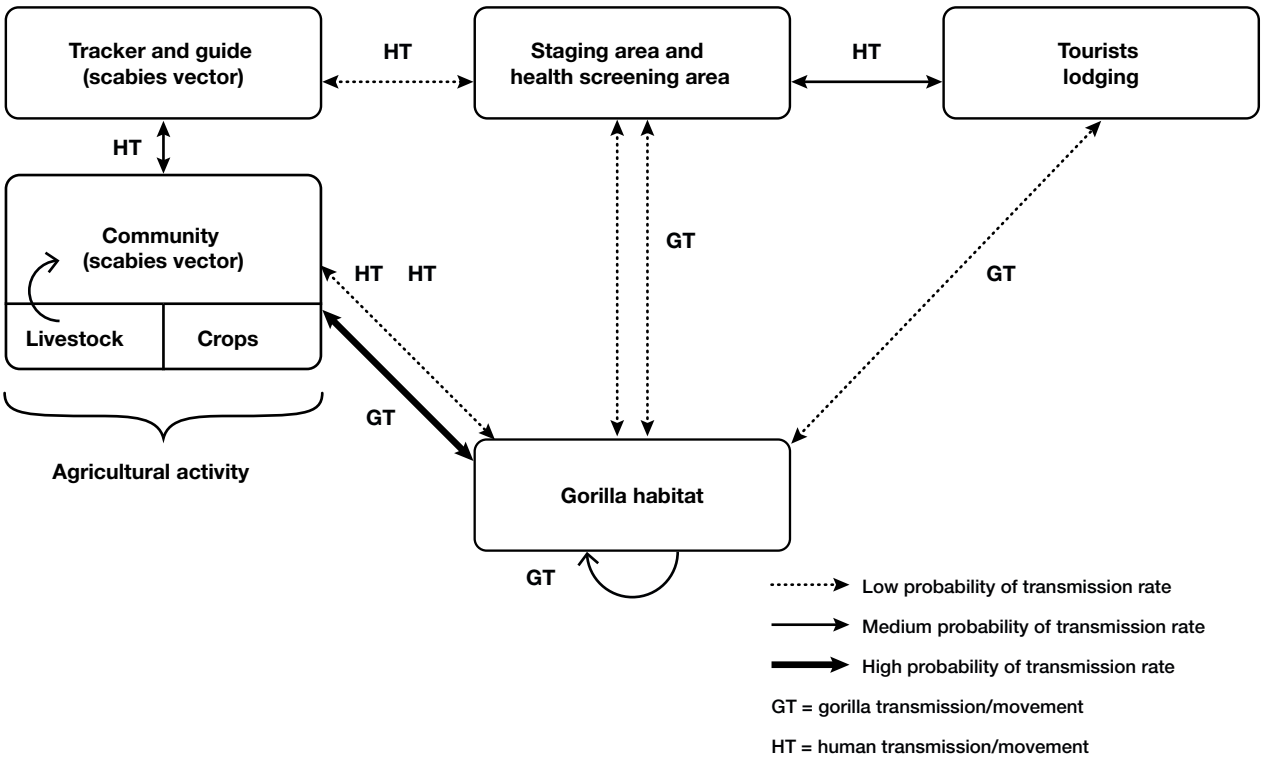


Fig. 46
a) Scabies transmission pathways

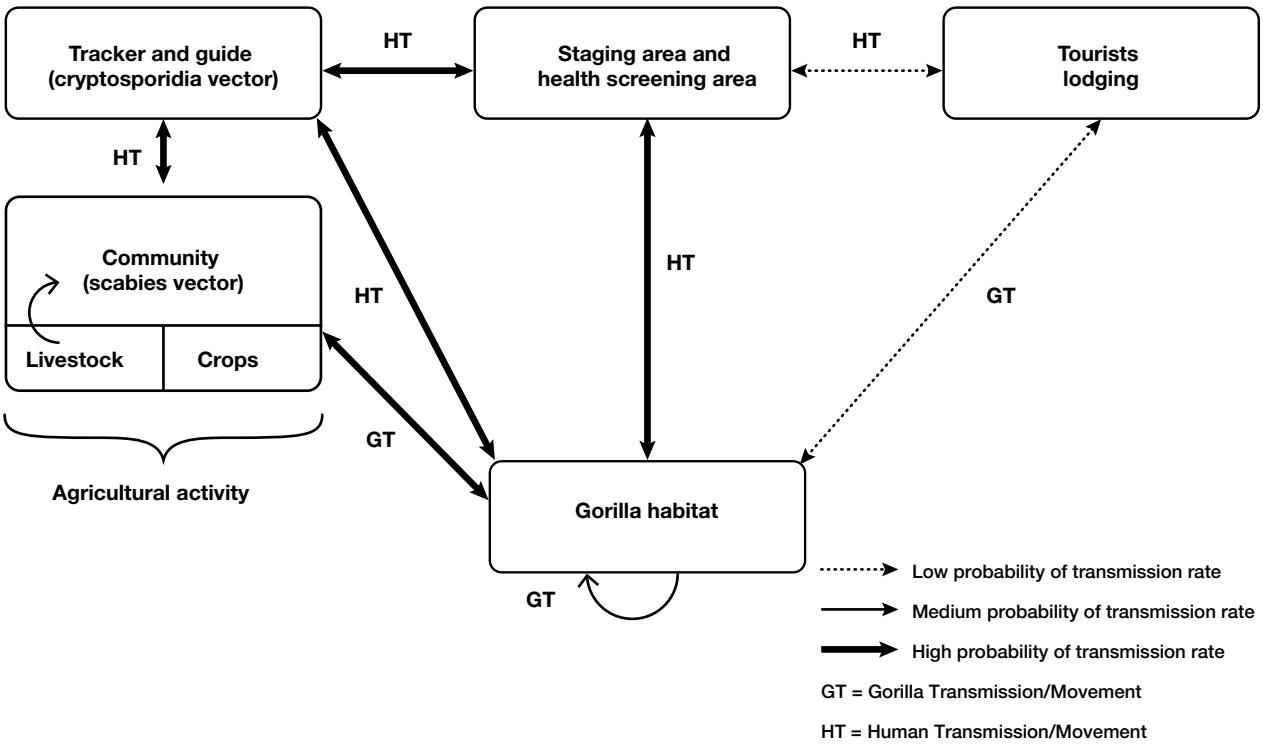


Fig. 47
b) Cryptosporidia transmission pathways

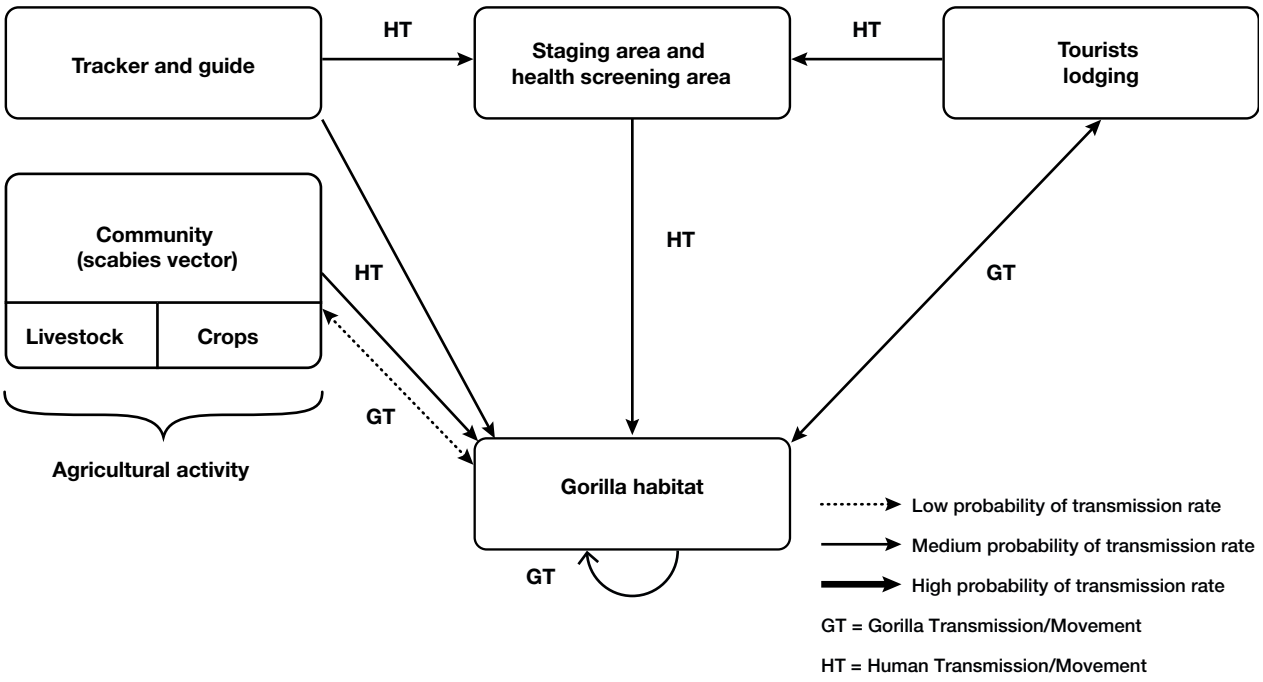


Fig. 48
c) Measles transmission pathways

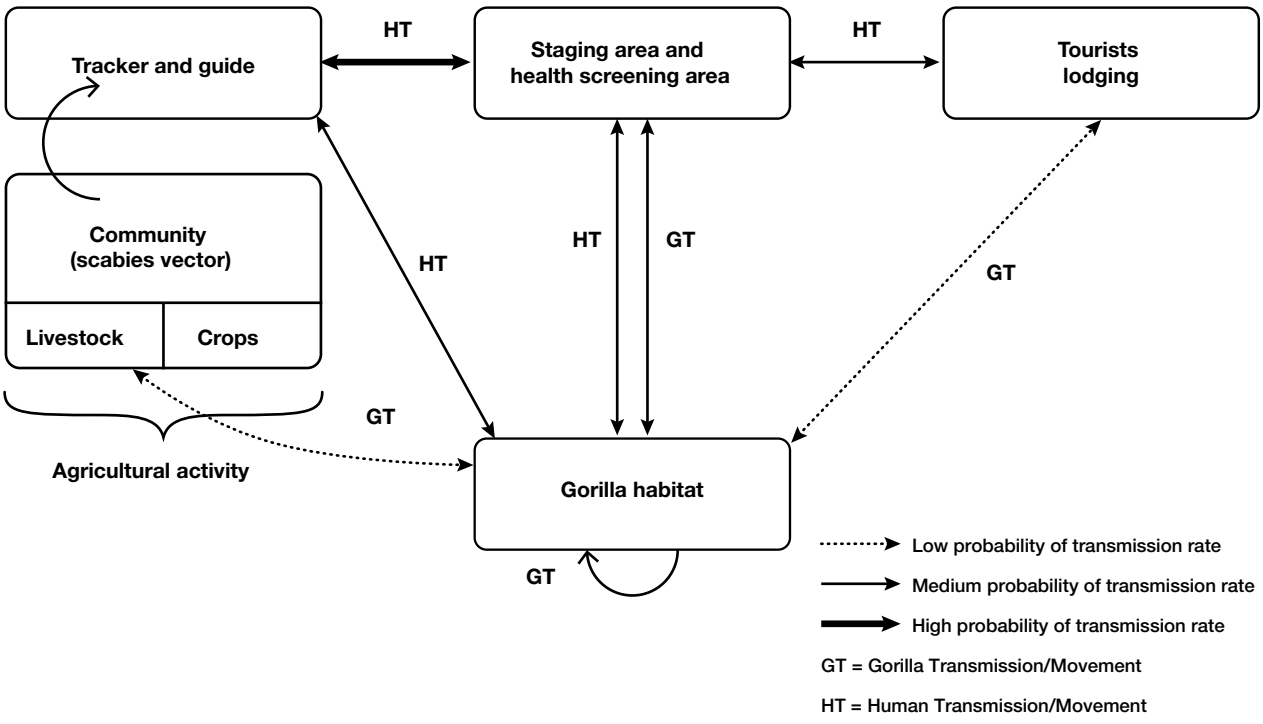


Fig. 49
d) Tuberculosis transmission pathways

Actions

Community control point

- Increase community and public health programmes/education.
- Employee health programmes.
- Increased livestock health programmes/education.
- Create buffer zone.

Staging area control point

- Tracker and guide personal hygiene.
- Tourist personal hygiene.

Habitat control point

- *Vaccination* programme.
- Treatment.

Stella™ Software (www.iseesystems.com)

Working group summary of diagram

The Stella programme is designed to see patterns in dynamic situations. We developed this *model* as a working draft to allow the group to become familiar with the Stella programme.

Set up:
Modelled as transmission of disease among gorillas, transmission among children of trackers, transmission among other children in the village, trackers used as route of exposure of measles to the gorillas.

Assumptions:
gorillas contract measles (from humans and each other)

- humans act as *fomites* for the measles virus
- trackers developed immunity to measles as adults
- naive populations = all but trackers
- negligible impact of transmission tracker to tracker.
- closed populations
- random contacts
- random dispersal
- human adults that are not trackers are irrelevant (only trackers have contact with gorillas)
- all people infected recover and gain immunity.

Identifying data:
other children= 5,000

- trackers' children= 700
- trackers = 110
- gorilla population = 320
- non-contact gorillas = 60
- contact gorillas = 260
- vaccine programmes have 98% efficacy for gorillas and people
- contact rate sick child to child is 1:10
- contact rate for trackers to gorillas in contact groups is 1:20
- contact rate for non-contact gorillas to contact gorillas is 1:2

Run and evaluate scenarios

1. Measles goes through the population.
2. Vaccinate just the trackers children.
3. Vaccinate all children.
4. Vaccinate gorillas only.

Results of simulations

Vaccinating the gorillas only was the most effective way to minimise the incidence of measles in the gorilla population.

Re-evaluate *model* again, and again and again …

Summary

Process of developing the model
Identification of the problems to address. Assemble a group of individuals with diverse experience and training. Employ someone who has knowledge of Stella. Begin to draw a conceptual picture of the problems you are addressing. Develop assumptions.

Determine the CCPs of the *model*.

Input data into the *model* (if possible use real data, otherwise best estimates). Run the *model*.

Evaluate the data, *model* and graphs resulting.

Re-evaluate the appropriateness of the data entered and the relationships created. Continue to refine and improve the *model* (to infinity).

Question: Does this approach provide benefit in exploring a complex problem?

Answer: Yes, it allows you to visualise the process, to identify CCPs, identify relationships that may not have been obvious and get a clearer idea of the information you need to acquire.

Question: Can this approach give you a quantitative answer?

Answer: With more refinement and enough good data it may give you quantitative answers.

Decision tree cost analysis for human–gorilla measles

Description and interpretation

Three scenarios were assessed. The first involved an assumed prevalence in the in-contact human population of 10% and screening for the disease in these individuals conducted by cursory inspection and observation of clinical signs only. The sensitivity of this method was assumed to be 50%. The cost was assumed to be zero.

Scenario 1: Physical inspection of trackers

In the second scenario the screening test method used was a hypothetical PCR of clinical samples from every in-contact human. The sensitivity of this method was assumed to be 99%. Specificity was assumed to be 75%. Additional assumptions were that positive in-contact humans were excluded from the workforce. Based on this specificity the probability of a false-positive individual is 0.225. This created the requirement for an additional 25 (rounded) individuals on the workforce with resulting labour cost increases. This was also based on a daily application of the method (which may not be realistic at all). The effect of the frequency of PCR testing (daily, weekly, quarterly, annually) on the sensitivity value of the method (not of the test) must be considered. The costs incurred were the test costs and the labour costs. The probability of disease (agent) introduction into the gorilla population was reduced to 0.00005 in this *model*.

Scenario 2: PCR testing of trackers

Assumptions
100 trackers/guards at USD 3/day

PCR test cost = USD 20. Increased sensitivity of PCR increases false-positive rate so that $p = 0.225$, therefore workforce required increases.

The third scenario implemented *vaccination* of the in-contact humans. Vaccine efficacy was assumed to be 99% and therefore prevalence dropped to 1%. Testing was limited to inspection for signs and therefore 50% efficacy was assumed. This approach dropped cost to a one-time investment of USD 2.00 per vaccination or an initial outlay of USD 200 outlay. The risk probability was 0.000025.

Scenario 3: Vaccination of trackers

Assumptions
Vaccine cost = USD 2/dose.

100 trackers/guards vaccinated.

Vaccination reduces prevalence to 1%.

Scenario 1: Physical inspection of trackers

COST?	Parameter	p	Value (USD)	Comment
–	Prevalence	0.1	0	
+	Test	0.5	0	Cursory observation for signs of infection
–	Viability	0.01	0	
–	Transmission	0.5	0	
TOTAL		0.0002	0	

Scenario 2: PCR testing of trackers

COST?	Parameter	(p)	Value (USD)	Comment
–	Prevalence	0.1	0	
+	Test	0.01	25 x 100	PCR oronasal swab
–	Viability	0.01	0	
–	Transmission	0.5	0	
TOTAL		0.00005	2,500	Per test application; need to factor in change in sensitivity due to change in testing frequency

Scenario 3: Vaccination of trackers

COST?	Parameter	p	Value (USD)	Comment
–	Prevalence	0.01	200	Vaccine efficacy reduces prevalence to 1%
+	Test	0.5	0	Inspection for signs
–	Viability	0.01	0	
–	Transmission	0.5	0	
TOTAL		0.00025	200	One time cost

Recommendations

Based on these data and *models* it is clearly more cost beneficial to vaccinate the in-contact humans; however, the use of PCR as a screening test reduces the risk of measles introduction five-fold. These conclusions appear to differ from those obtained using the Stella model. However, this disparity may be due to the complexity of the Stella model, that is, the addition of temporal considerations and additional variables which may affect the outcome.

Risk management/mitigation

Blood sample – minimum 10 mL (6 mL serum, 4 mL whole blood in EDTA [ethylenediaminetetra-acetic acid]), plus enough for at least three blood smears and several drops on filter paper. All samples to be duplicated.

This is a living document and will need to be updated on a regular basis. The samples here are a minimum. All sanctuaries must have access to blood collection and storage equipment and formalin as a bare minimum. Training in the correct use of this equipment will also be required for several sanctuaries.

Notes for on-site veterinarian, in-house laboratory: this refers to the apes only. A second sheet for monkeys will need to be completed.

Table XVII of this section shows part of a disease management chart, this one an example from Limbe Wildlife Centre. For each disease of concern, diagnostic methods and potential management strategies are given, both what is done, and what is ideal. Collation of this data is helpful so risk can be managed, (in this case, across the Pan African Sanctuary Alliance), by highlighting, for example, what everyone considers important to test for, and potential laboratories to assist in investigating those pathogens.

Risk management strategies can be prioritised by creating a risk matrix (Table XVIII). For example, for the new Gorilla Rehabilitation Centre near the Tayna Nature Reserve in the Democratic Republic of Congo, the likelihood of Ebola virus at the centre might be considered medium or high, and the severity would also be high, based on what we know about the pathology of this disease. Therefore it is a disease of high concern. However, if this matrix was at Chester Zoo in the United Kingdom, although the severity for Ebola would still be very high, the likelihood would be very low (we do not currently import animals from areas where Ebola virus is known to exist!). There is software available to assist in the development of risk matrices. For now, it is enough to know that risk matrices exist, and they may be a useful tool in risk management.

Table XVII
Part of a disease management chart – Limbe Wildlife Centre

Disease category	Aetiology (those in bold for inclusion in quarantine disease special interest)	Species	Relative risk	Clinical signs	Diagnostics	If blood samples, what tube, what volume?	For each sample, way and period of conservation	Who can test? (red current)	Treatment if possible/ required	Husbandry	References/ comments	Test as part of normal protocol (T), test in face of outbreak (S)
Viral	Hepatitis A, B, C	All	L	Various – liver associated	Serology	Serum (plain) and plasma (EDTA) 0.5 mL	Freezing, months	JHI, Pasteur/ GAHMU			Not a disease issue, but may need to test for legal reasons?	T (Hep A and B only)
	Encephalomyocarditis virus	All	**M**	Sudden Death	Histopathology	N/A	Formalin, months	JHI/ GAHMU	N/A	Rodent control, cockroach control	More information required?	S
	SIV/ HIV	Chimps	L	Usually asymptomatic	Serology	Serum (plain) and plasma (EDTA) 0.5 mL	Freezing, months	JHI, Pasteur/ GAHMU	N/A		Humans raise antibodies	T
	STLV	Chimps	L	Usually asymptomatic	Serology	Serum (plain) and plasma (EDTA) 0.5 mL	Freezing, months	JHI, Pasteur/ GAHMU	N/A			T
	Ebola/ Marburg	All	**M**	Sudden Death	Serology	Serum (plain) and plasma (EDTA) 0.5 mL	Freezing, months	CIRMF/ GAHMU	N/A			S
	Measles (morbillivirus)	All	L	Maculopapular exanthema	Clinical signs, virus isolation, seroconversion	Serum (plain) and plasma (EDTA) 0.5 mL	Freezing, months	JHI, Pasteur/ GAHMU	N/A		Vaccination?	S
	Polio (enterovirus)	All	L	Asymptomatic or, CNS	Clinical signs	Serum (plain) and plasma (EDTA) 0.5 mL	Freezing, months	JHI, Pasteur/ GAHMU	N/A		Vaccination?	S

GAHMU, Great Ape Health Monitoring Unit
JHI, John Hopkins Institute, Cameroon

Table XVIII
Risk matrix for various primate diseases

Likelihood	Severity: Very low	Low	Medium	High
High	Non-pathogenic Escherichia coli		Gastrointestinal parasite infections	Ebola virus
Medium			Introduction of anthelmintic-resistant strains of helminths	
Low	Exotic strains of non-pathogenic organisms		Stress-induced secondary infections following move	Introduction of human metapneumo-virus
Very low				

Contingency planning – being prepared

The focus of our contingency planning is to keep the sanctuary operational and avoid entry of the disease, disease in staff, culling animals or closure of the sanctuary.

Example: Tuberculosis

First assess the risk to determine if a contingency plan is required.

Risk assessment: hazard
Infection with tuberculosis complex (human/ bovine):

- primates
- hooved stock.

Legislation/statutory control of tuberculosis:

- OIE
- Public health (country dependant)
- Public perception of human health risk.

Risk assessment: likelihood
Infection of sanctuary animals with tuberculosis:

- currently increasing
- constantly changing.

Legislation to control tuberculosis imposed by government/OIE:

- Often non-existent.

Public perception of human health risk:

- high
- influenced by media coverage.

Likelihood x hazard = risk
Likelihood currently moderate but increasing.

Hazard/stakes – very high:

- limited control of source of infection and potential human health risk.

= Contingency planning necessary …

Aim
To decrease the likelihood of introduction of tuberculosis to, or dissemination from, a sanctuary.

Principles
Control measures are designed to reduce the risk of transmission. The routes of possible transmission and contingencies undertaken are listed below.

Main routes of transmission	Contingencies to reduce risk of transmission to/from sanctuary animals
Wildlife and domestic animals	**Aim – to reduce contact between wild animals and sanctuary animals:** – Domestic cattle around the sanctuary can be vectors – Wildlife mammal vectors are likely and will vary between sanctuaries **Preventative measures:** – Prevent contact between primate's enclosures and domestic cattle, not allowing them to graze in the same area – Minimise contact between wildlife mammals and primates as much as is practical
New arrivals	**Aim – to prevent the introduction of infected animals** **Control measures:** If possible, ask for certified diagnostic test before arrival. Obtain as much history on tuberculosis in all populations, from the area of origin, as is possible **Quarantine:** – Different animal care staff from the sanctuary should administer quarantine – Length: 90 days to identify classic symptoms – Intradermal skin test: two tests to be undertaken during quarantine, 42 days apart, using mammalian old tuberculin, avium and bovine tuberculin – Utilise serology rapid test (Stat-pak) if available – Thoracic radiology, if possible – Sputum and tracheal lavage, if possible. Definitely take tracheal lavage for culture if other testing reveals a possible positive
Food	**Aim – to prevent entry of the disease in infected food products. Food items are not a common source of tuberculosis** **Control measures:** – Controlled origin of the food, specially the green feed that we often offer to our animals
Fomites (vehicles, equipment, crates, clothing and shoes etc.)	**Aim – to prevent disease being transferred to animals, their food or anything they may come in direct contact with** **Control measures should disease be widespread (outbreak):** – Footwear disinfected and all trucks and cars (wheels and wheels arches) that enter the quarantine and sanctuary area
Faeces, waste food, soiled bedding, etc.	**Control measures in the event of outbreak:** – Waste products from suspected animals or enclosures must be packed and sealed carefully and separately from all other items – Daily disinfection of soil with approved products recommended for mammalian tuberculosis
Infected humans	**Aim – to prevent the transfer of a disease strain that can infect both humans and animals:** – We would like to make a difference between working staff and visitors – Efforts should concentrate on keeping staff healthy **Recommendations for visitors:** – In the event of an outbreak restrict access to the centre – Always wear facial masks when entering the centre – A short questionnaire on health status is to be undertaken – Prevent visitor access if exhibiting respiratory symptoms – Not less than 10–15 metres between animals and visitors **Recommendations for staff:** – Prophylactic health programme: *in vitro* quick test and Mantoux test – Work wearing facial masks and gloves

Additional points

These contingency measures (Table XIX) are liable to revision as the threat changes and our knowledge of the disease and its control develops. They will be reviewed on a regular basis (minimum monthly).

The contingency of how we would operate and provide care for our animals in the event of a human pandemic is also not covered within this document.

Risk communication

The most important step in the risk analysis process is communication of the risk to all interested parties (your manager, your staff, other veterinarians, your government, peer-reviewed journals, news media, etc.) *and* encouraging dialogue between them. Risk communication is particularly important because the perception of risk by people who do risk analyses can often vary from that of the general public (such

Table XIX
Summary contingency plan

Measures in place (date)	– Test of intradermal reaction against *M. tuberculosis* and *M. bovis* – Quarantine
Measures to be put into effect as quickly as possible **Timing to be supplied as soon as they are known**	Control measures – biosecurity: – Housing/exclusion of wild primates – Restrict human access – Aerosol minimisation – Graded biosecurity – citadel approach Sanctuary dependant
Measures to be put in place in event of outbreak	– Isolation of the sanctuary and positive animals – creation of epidemiological units (Fig. 50) – Stop animal movements – Check all of the collection with quick test and intradermal reaction (*M. tuberculosis*, *M. avium* and *M. bovis*) – Inform the authorities – Possible sacrifice of positive animals

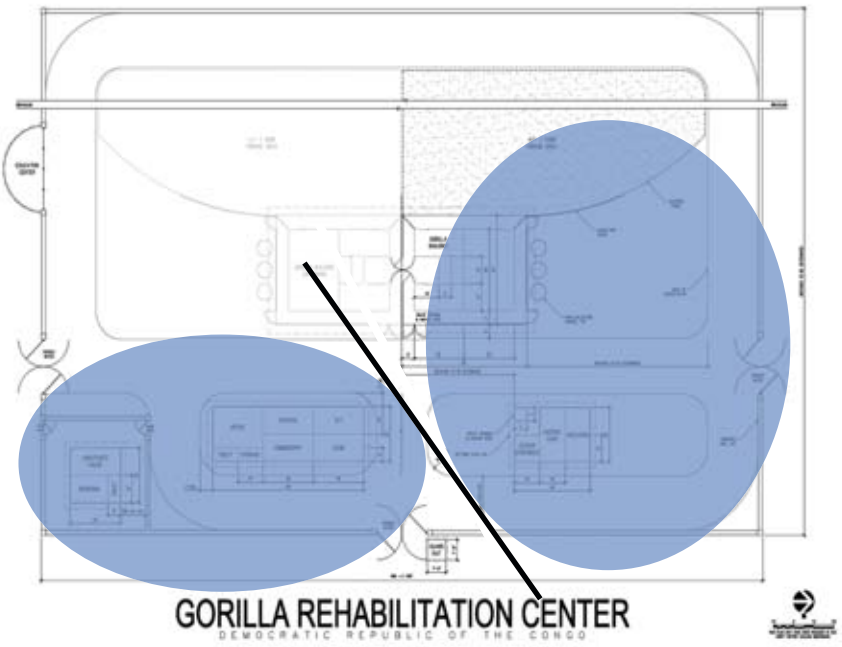


Fig. 50
Creation of epidemiological units
This highlights how your facility can be separated into areas, to prevent the spread of an outbreak to other areas of your facility.

as the local village elders) or your manager. The former (us) may argue that risk should be determined objectively by the 'data alone', whereas the latter may 'irrationally' colour their perception of risk by subjective factors, often called 'outrage factors'. Reality is usually somewhere in the middle.

Since society generally reacts more to outrage than 'mere hazard', an important part of risk communication is to make serious hazards 'more outrageous', and modest hazards less so. Gruesome graphic government campaigns highlighting the dangers associated with driving under the influence of drink or drugs, or some of the educational material used to inform on the transmission of Ebola virus (Fig. 51) are examples of increasing outrage. The extent to which the 'public' accepts risks is clearly related to the degree of outrage.

So, risk communication should not be an afterthought. Consideration of communication of the results of a risk assessment is essential in both defining the hazard and the risk question, as well as formulating the approach to the whole risk analysis. Otherwise the whole exercise will be rendered useless.

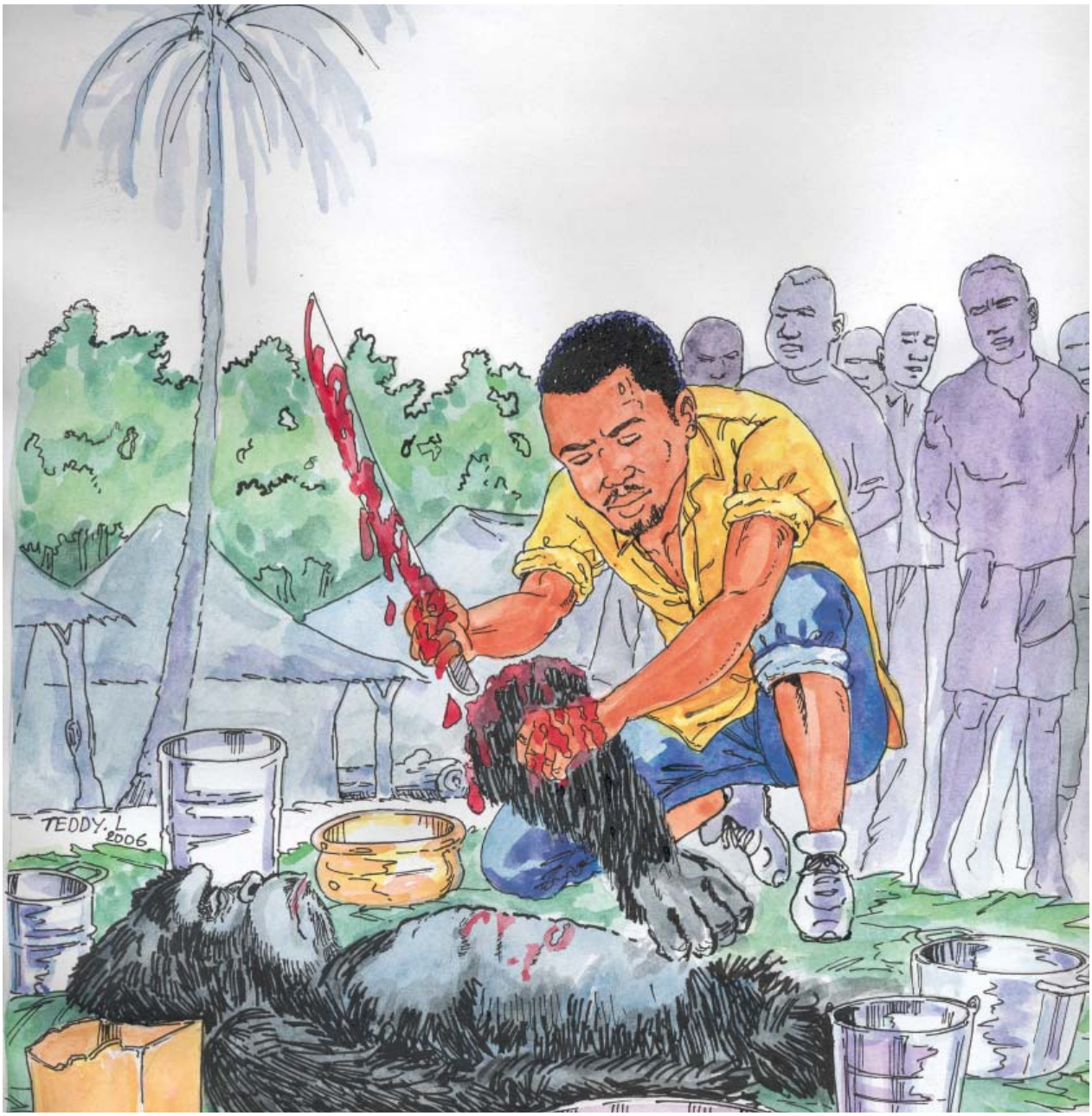


Fig. 51
Image from a series of educational cartoons on the spread of Ebola virus in the Democratic Republic of Congo
(Thanks to Ken Cameron, Wildlife Conservation Society Field Veterinarian)

References

Aguirre A.A., Ostfeld R.S., Tabor G.M., House C. & Pearl M.C. (eds) (2002). – Conservation Medicine: Ecological Health In Practice. Oxford University Press, Oxford, United Kingdom.

Akçakaya, H.R. & Atwood J.L. (1997). – A habitat-based metapopulation model of the California gnatcatcher. *Cons. Biol*., **11**, 422–434.

Alderman D.J. (1996). – Geographical spread of bacterial and fungal diseases of crustaceans. *In* Preventing the spread of aquatic animal diseases (B.J. Hill & T. Håstein, eds). *Rev. sci. tech. Off. int. Epiz*., **15** (2), 603–632.

Alley M. & Gartrell B. (2006). – A *Salmonella* outbreak in hihi (*Notiomystis cincta*), Kokako. *Bull. wildl. Soc. N.Z. vet. Assoc.*, **13** (1).

Alley M.R., Connolly J.H., Fenwick S.G., Mackereth G.F., Leyland M.J., Rogers L.E., Haycock M., Nicol C. & Reed C.E.M. (2002). – An epidemic of salmonellosis caused by *Salmonella typhimurium* DT160 in wild birds and humans in New Zealand. *N.Z. vet. J.*, **50** (5), 170–176.

Animal Health Australia (2011). – Wild Animal Response Strategy, Australian Veterinary Emergency Plan (AUSVETPLAN), Edition 3, Primary Industries Ministerial Council, Canberra.

Armstrong D., Jakob-Hoff R. & Seal U.S. (eds) (2003). – Animal Movements and Disease Risk – A Workbook, 5th Ed. IUCN/SSC Conservation Breeding Specialist Group, Apple Valley, Minnesota.

Arrioja A. (2008). – Book Review: Handbook on Import Risk Analysis for Animals and Animal Products, Vols. 1 and 2. *Can. vet. J.*, **49**, 1036.

AUSVETPLAN WARS Manual. Available at: www.animalhealthaustralia.com.au/wp-content/uploads/2011/04/WARS3.3-18-FINAL21Jun11.pdf.

Bartholomew J.L., Hedrick R.P., Kerans B., MacDiarmid S.C. & Winton J.R. (2005). – Development of a risk assessment based approach for the prevention, management and control of whirling disease. *Rev. Fisheries Sci.*, **13**, 205–230.

Bengis R.G., Kriek N.P.J, Keet D.F., Raatch J.P., De Vos V. & Huchzermeyer H.F.A.K. (1996). – An outbreak of bovine tuberculosis in a free-living African buffalo (*Syncerus caffer,* Sparrman) population in the Kruger National Park: a preliminary report. *Onderstepoort J. vet. Res.*, **63**, 15–18.

Bengis R.G., Kock R.A. & Fisher J (2002). – Infectious animal diseases: the wildlife/livestock interface. *In* Infectious diseases of wildlife: detection, diagnosis and management (Part One) (R.G. Bengis, ed.). *Rev. sci. tech. Off. int. Epiz.,* **21** (1), 53–65.

Berstein P.L. (1996). – Against the Gods: The Remarkable Story of Risk. John Wiley and Sons, New York.

Biosecurity New Zealand (2005). – Import Risk Analysis – Ornamental Fish, Ministry of Agriculture and Forestry, Wellington, New Zealand.

Bolortsetseg S., Shiilegdamba E., Nyamsuren D., Weisman W., Fine A., Yang A. & Joly D.O. (2012). – Serosurveillance for foot and mouth disease in Mongolian gazelles (*Procapra gutturosa*) and livestock on the Eastern Steppe of Mongolia. *J. Wildl. Dis.*, **48** (1), 33–38.

Bradshaw C.J.A., McMahon C.R., Miller P.S., Lacy R.C., Watts M.J., Verant M.L., Pollack J.P., Fordham D.A., Prowse T.A.A. & Brook B.W. (2012). – Novel coupling of individual-based epidemiological and demographic models predicts realistic dynamics of tuberculosis in alien buffalo. *J. appl. Ecol.*, **49** (1), 268–277.

Briones V., Fernandez A., Blanco M., Ramiro F., De Vincente M.L., Garcia J., Mendez J.L. & Goyache J. (1998). –Haemorrhagic septicaemia by *Aeromonas salmonicida* subsp. *salmonicida* in a black-tip reef shark (*Carcharhinus melanopterus*). *J. vet. Med. B*, **45** (7), 443–445.

Brückner G., MacDiarmid S.C., Murray N., Berthe F., Müller-Graf C., Sugiura K., Zepeda C., Kahn S. & Mylrea G. (2010). – Handbook on Import Risk Analysis for Animals and Animal Products, Volume I. Introduction and Qualitative Risk Analysis, 2nd Ed. World Organisation for Animal Health (OIE), Paris.

Budke C. M., Campos-Ponce M., Qian W. & Torgerson P.R. (2005). – A canine purgation study and risk factor analysis for echinococcosis in a high endemic region of the Tibetan plateau. *Vet. Parasitol.*, **127** (1), 43–49.

Calle P.P. (1999). – Tuberculin responses in orang-utans. *In* Zoo and Wild Animal Medicine. Current Therapy 4 (M.E. Fowler & R.E. Miller, eds). WB Saunders Company, Philadelphia, Pennsylvania, 650–657.

Carey C., Cohen N. & Rollins-Smith L. (1999). – Amphibian declines: an immunological perspective. *Dev. Comp. Immunol.*, **23**, 459–472.

Clancy D., Billinghurst A. & Cater H. (2009). – Hazard identification and risk assessment – understanding the transition from the document plan to assessing dynamic risk in biosecurity emergencies. World Conference on Disaster Management, 13–14 October, Sydney, Australia.

Clark E.L., Munkhbat J., Dulamtseren S., Baillie J.E.M., Batsaikhan N., Samiya R. & Stubbe M. (eds) (2006). – Mongolian Red List of Mammals. Regional Red List Series. Volume 1. Zoological Society of London, London, United Kingdom.

Clemen R.T. (1997). – Making Hard Decisions: An Introduction to Decision Analysis. Duxbury Press, Pacific Grove, California.

Clemen R.T. & Reilly T. (2001). – Making Hard Decisions with Decision Tools®. Duxbury Thomson Learning, Pacific Grove, California.

Clements C.A. & Pfeiffer D.U. (2009). – Emerging viral zoonoses: Frameworks for spatial and spatiotemporal risk assessment and resource planning. *Vet. J.*, **182**, 21–30.

Conservation Breeding Specialist Group (CBSG) (2008). – Tasmanian Devil PHVA Final Report. IUCN/SSC Conservation Breeding Specialist Group, Apple Valley, Minnesota.

Covello V.T. & Merkhofer M.W. (1993). – Risk Assessment Methods: Approaches for Assessing Health and Environmental Risks. Plenum Publishing, New York.

Cowell R.R. (1997). – Microbial biodiversity and biotechnology. *In* Biodiversity II: Understanding and Protecting our Biological Resources (E.O. Wilson, ed.). National Academy of Sciences, Washington, District of Columbia, 279–299.

Cunningham A.A., Prakash V., Pain D., Ghalsasi G.R., Wells G.A.H., Kolte G.N., Nighot P., Goudar M.S., Kshirsagar S. & Rahmani A. (2003). – Indian vultures: victims of an infectious disease epidemic? *Anim. Cons.*, **6** (3), 189–197.

Cuthbert R., Taggart M.A., Prakash V., Saini M., Swarup D., Upreti S., Mateo R., Chakraborty S.S., Deori P. & Green R.E. (2011). – Effectiveness of actions in Indian to reduce exposure of Gyps vultures to the toxic veterinary drug diclofenac. *PloS One*, **6** (5), e19069. doi: 10.1371/jounal.pone.0019069.

Dambacher J.M., Shenton W., Hayes K.R., Hart B.T. & Barry S. (2007). – Qualitative modelling and Bayesian network analysis for risk-based biosecurity decision making in complex systems. Report for the Australian Centre of Excellence in Risk Analysis, Melbourne.

Daszak P., Cunningham A.A. & Hyatt A.D. (2000). – Emerging infectious diseases of wildlife – threats to biodiversity and human health. *Science*, **287** (5452), 443–449.

Daszak P., Cunningham A.A. & Hyatt A.D. (2003). – Infectious disease and amphibian population declines. *Diversity Distributions*, **9** (2), 141–150.

Davis M.A. (2008). – Population dynamics of the New Mexico ridge-nosed rattlesnake (*Crotalus willardi obscurus*) in the Madrean Archipelago: a threatened species in a changing ecosystem. MS thesis, Colorado State University, Fort Collins, Colorado.

Decker D.J., Wild M.A. & Riley S.J. (2006). – Wildlife disease management: a manager's model. *Human Dimensions Wildl.*, **11** (3), 151–158.

Dohoo I.R., Martin W.S. & Stryhn H. (2003). Veterinary Epidemiologic Research. AVC Inc., Calgary, Canada.

Di Stefano J., Anson J.A., York A., Greenfield A., Coulson G., Berman A. & Bladen M. (2007). – Interactions between timber harvesting and swamp wallabies (*Wallabia bicolor*): space use, density and browsing impact. *Forest Ecol. Manage.*, **253** (1–3), 128–137.

Donaldson A.I., Alexandersen S., Sorensen J.H. & Mikkelsen T. (2001). – Relative risks of uncontrollable (airborne) spread of FMD by different species. *Vet. Rec.*, **148**, 602–604.

Donnelly C.A., Woodroffe R., Cox D.R., Bourne J., Gettinby G., Le Fevre A.M., McInerney J.P. & Morrison W.I. (2003). – Impact of localised badger culling on tuberculosis incidence in British cattle. *Nature*, **426** (6968), 834–837.

Fowler M.E. (1986). – Introduction and overview. *In* Zoo and Wild Animal Medicine, 2nd Ed. (M.E. Fowler, ed.). W.B. Saunders, Philadelphia, Pennsylvania, 4–6.

Franzman A.W. (1986). – Wildlife medicine. *In* Zoo and Wild Animal Medicine, 2nd Ed. (M.E. Fowler, ed.). W.B. Saunders, Philadelphia, Pennsylvania, 8–11.

Friend M. (2006). – Disease Emergence and Re-emergence: The Wildlife–Human Connection. US Geological Survey, Reston, Virginia.

Gale P., Brouwer A., Ramnial V., Kelly L., Kosmider R., Fooks A.R. & Snary E.L. (2010). – Assessing the impact of climate change on vector-borne viruses in the EU through the elicitation of expert opinion. *Epidemiol. Infect.*, **138**, 214–225.

Gál J., Vincze Z., Jakab C., Ari C. & Lefler K.K. (2005). – Multiplex shafted fibroma on the upper jaw of a sand-tiger shark [*Carcharias (Odontaspis) taurus*]. *Magyar Allatorvosok Lapja* [*Hungarian vet. J.*], **127** (5), 242–245.

Gallagher E., Ryan J., Kelly L., Leforban Y. & Wooldridge M. (2002). – Estimating the risk of importation of foot and mouth disease into Europe. *Vet. Rec.,* **150**, 769–772.

Garratt K.J. & Chimed-Ochir B. (2001). – Biodiversity conservation and sustainable livelihood options in the Grasslands of Eastern Mongolia. MON/97/G32. Report of the independent mid-term evaluation mission, August 2001.

Gartrell B.D., Alley M.R., Mack H., Donald J., McInnes K. & Jansen P. (2005). – Erysipelas in the critically endangered Kakapo. *Avian Pathol.*, **34** (5), 383–387.

Green R.E., Newton I., Shultz S., Cunningham A.A., Gilbert M., Pain D.J. & Prakash V. (2004). – Diclofenac poisoning as a cause of vulture population declines across the Indian subcontinent. *J. appl. Ecol.*, **41** (5), 793–800. doi: 10.1111/j.0021–8901.2004.00954.x.

Gregory R., Failing L., Harstone M., Long G., McDaniels T. & Ohlson D. (2012). – Structured Decision-Making: A Practical Guide to Environmental Management Choices. Wiley-Blackwell, Chichester, United Kingdom.

Grimes D.J., Stemmler J., Hada H., May E.B., Maneval D., Hetrick F.M., Jones R.T., Stoskopf M. & Colwell R.R. (1984). – *Vibrio* species associated with mortality of sharks held in captivity. *Microb. Ecol.*, **10**, 271–282.

Gubler D.J. (2007). – The continuing spread of West Nile virus in the Western hemisphere. *Clin. infect. Dis.*, **45**, 1039–1046.

Hannon B. & Ruth M. (2009). – Dynamic Modelling of Diseases and Pests. Springer-Verlag, Berlin.

Harvey T., Mahaffey K.R., Velazquez S. & Dourson M. (1995). – Holistic risk assessment: an emerging process for environmental decisions. *Regul. Toxicol. Pharmacol.*, **22**, 110–117.

Heffernan D.E. (2005). – A report on an assessment of the protected areas of the Eastern Steppe of Mongolia. Report prepared by US Peace Corps volunteer assigned to the Ministry of Nature and Environment Mongolia, Ulaanbaatar.

Heiner M., Galbadrakh D., Kiesecker J., McKenney B., Evans J., Enkhtsetseg T., Zmburelmaa D., Ulziisaikhan V., Oyungerel B., Sanjmyatav D., Gankhuyag R., Enkhbat D., Ochirhuyag L., Sergelen G., Girvetz E. & McDonald R. (2011). – Identifying Conservation Priorities in the Face of Future Development: Applying Development by Design in the Grasslands of Mongolia. The Nature Conservancy, April 2011.

Hickling G.J. (1991). – The ecology of brush-tailed possum populations infected with tuberculosis. *In* Proceedings of a Symposium on Tuberculosis (R. Jackson, ed.). Publication 132, Massey University, Palmerston North, New Zealand.

Hirsch D.C. (2004). – *Enterobacteriaceae*: Salmonella spp. *In* Veterinary Microbiology, 2nd Ed. (D.C. Hirsch, N.J. MacLachlan & R.L. Walker, eds). Blackwell Publishing, Oxford, United Kingdom, 69–74.

Holdich D.M. & Reeve I.D. (1991). – Distribution of freshwater crayfish in the British Isles, with particular reference to crayfish plague, alien introductions and water quality. *Aquat. Conserv. marine freshwater Ecosyst.*, **1** (2), 139–158.

Hood G.M., Barry S.C. & Martin P.A.J. (2009). – Alternative methods for computing the sensitivity of complex surveillance systems. *Risk Anal.*, **29** (12), 1686–1698. doi:10.1111/j.1539–6924.2009.01323.x0.

Hugh-Jones M.E., Hubbert W.T. & Hagstad H.V. (2000). – Zoonoses: Recognition, Control and Prevention. Iowa State University Press, Ames, Iowa.

Hunter D., Bayley A. & Tailor B. (1995). – The Zen of Groups: The Handbook for People Meeting with a Purpose. Fisher Books, Tucson, Arizona.

International Life Sciences Institute (ILSI) (2000). – Revised Framework for Microbial Risk Assessment. ILSI Press, Washington DC.

Jacobson S.K. (2009). – Communication Skills for Conservation Professionals, 2nd Ed. Island Press, Washington, District of Columbia.

Jakob-Hoff R. (2001). – Disease risk assessment for translocation of kaki (black stilt), *Himantopus novaezeelandiae*, from captivity to the wild. DOC Science Internal Series 16. Department of Conservation, Wellington, New Zealand.

Jakob-Hoff R.M. (2008). – Kakapo disease risk assessment and management plan. Proceedings of Kakapo Science and Technical Advisor Committee Workshop, NZCCM, 17–18 November, Auckland Zoo. Copies available by contacting richard@cbsgaustralasia.org

Johnston M.R.L. (1975). – Distribution of *Pirhemocyton* Chatton & Blanc, and other, possible related, infections of poikilotherms. *J. Protozool.,* **22** (4) 529–535.

Kaner S., Lind L., Toldi C., Fisk S. & Berger D. (2007). – Facilitator's Guide to Participatory Decision-making, 2nd Ed. John Wiley and Sons, Chichester, United Kingdom.

Keet D.F., Davies-Mostert H., Bengis R.G., Funston P., Buss P., Hofmeyr M., Ferreira S., Lane E., Miller P. & Daly B.G. (eds) (2009). – Disease Risk Assessment Workshop Report: African lion (*Panthera leo*) bovine tuberculosis. Conservation Breeding Specialist Group (CBSG SSC/IUCN)/CBSG Southern Africa. Endangered Wildlife Trust.

Khan R.A. & Newman M.W. (1981). – Blood parasites from fish of the Gulf of Maine to Cape Hatteras, Northwest Atlantic Ocean, with notes on the distribution of fish hematozoa. *Can. J. Zool.*, **60**, 396–402.

Kuhn T.S. (1962). – The Structure of Scientific Revolutions. University of Chicago Press, Chicago, Illinois.

Leighton F.A. (2002). – Health risk assessment of the translocation of wild animals. *In* Infectious diseases of wildlife: detection, diagnosis and management (Part One) (R.G. Bengis, ed.). *Rev. sci. tech. Off. int. Epiz.,* **21** (1), 187–195.

Lhagvasuren B. & Milner-Gulland E.J. (1997). – The status and management of Mongolian gazelle *Procapra gutturosa* population. *Oryx*, **31** (2), 127–134.

Lowrance W.W. (1980). – The nature of risk. *In* Societal Risk Assessment: How Safe is Safe Enough? (R.C. Schwing & W.A. Albers Jr, eds). Proceedings of an International Symposium, 8–9 October 1979, General Motors Research Laboratories, Warren, Michigan, 5–17.

Markandya A., Taylor T., Longo A., Murty M.N., Murty S. & Dhavala K. (2008). – Counting the cost of vulture decline – an appraisal of the human health and other benefits of vultures in India. *Ecol. Econ.*, **67**, 194–208.

MacDiarmid S.C. (2001). – Risk analysis in aquatic animal health. *In* Risk Analysis in Aquatic Animal Health (C.J. Rodgers, ed.). World Organisation for Animal Health (OIE), Paris, 1–6.

MacDiarmid S.C. (2003). – Risk analysis, international trade, and animal health. *In* Fundamentals of Risk Analysis and Risk Management (V. Molak, ed.). CRC Lewis, Boca Raton, Florida, 377–387.

MacDiarmid S.C. (ed.) (2011). – The spread of pathogens through international trade in animals and animal products. *Rev. sci. tech. Off. int. Epiz.,* **30** (1).

MacDiarmid S.C. & Pharo H.J. (2003). – Risk analysis: assessment, management and communication. *In* Veterinary Services: organisation, quality assurance and evaluation (E. Correa Melo & F. Gerster, eds). *Rev. sci. tech. Off. int. Epiz.,* **22** (2), 397–408.

McLean R.G. & Ubico S.R. (2007). – Arboviruses in birds. *In* Infectious Diseases of Wild Birds (N.J. Thomas, D.B. Hunter & C.T. Atkinson, eds). Blackwell Publishing, Ames, Iowa, 77–62.

McMahon C., Gordon A.W., Edgar H.W.J., Hanna R.E.B., Brennan G.P. & Fairweather I. (2012). – The effects of climate change on ovine parasitic gastroenteritis determined using veterinary surveillance and meteorological data for Northern Ireland over the period 1999–2009. *Vet. Parasitol.*, **190** (1–2), 167–177.

McMichael A.J. (2004). – Environmental and social influences on emerging infectious diseases: past, present and future. *Phil. Trans. R. Soc. Lond. B biol. Sci.*, **359** (1447), 1049–1058.

Markandya A., Taylor T., Longo A., Murty M.N., Murty S. & Dhaval K. (2008). – Counting the cost of vulture declines – an appraisal of the human health and other benefits of vultures in India. *Ecol. Econ.*, **67** (2), 194–204.

Marsh W. (1999). – The economic of animal health in farmed livestock at the herd level. *In* The economics of animal disease control (B.D. Perry, ed.). *Rev. sci. tech. Off. int. Epiz.,* **18** (2), 357–366.

Ministry of Agriculture and Forestry (MAF) Regulatory Authority (1999). – Import risk analysis: chicken meat and chicken meat products; Bernard Matthews Foods Ltd turkey meat preparations from the United Kingdom. MAF, Wellington. Available at: www.biosecurity.govt.nz/files/regs/imports/risk/chicken-meat-ra.pdf

Michel A.L., Coetzee M.L., Keet D.F., Mare L., Warren R., Cooper D., Bengis R.G., Kremer K. & van Helden P. (2009). – Molecular epidemiology of *Mycobacterium bovis* isolates from free ranging wildlife in South African game reserves. *Vet. Microbiol.*, **133**, 335–343.

Mörner T., Obendorf D.L., Artois M. & Woodford M.H. (2002). – Surveillance and monitoring of wildlife diseases. *In* Infectious diseases of wildlife: detection, diagnosis and management (Part One) (R.G. Bengis, ed.). *Rev. sci. tech. Off. int. Epiz.,* **21** (1), 67–76.

Morgan M.S. & Morrison M. (eds) (1999). – Models as mediators: perspectives on natural and social sciences. Cambridge University Press, Cambridge, United Kingdom.

Morrell V. (1999). – Are pathogens felling frogs? *Science*, **284**, 728–731.

Mueller T., Olson K.A., Fuller T.K., Schaller G.B., Murray M.G. Bolorsetseq S. & Leimgruber P. (2008). – In search of forage: predicting dynamic habitats of Mongolian gazelles using satellite-based estimates of vegetation productivity. *J. Appl. Ecol.,* **45**, 649–658.

Murata M., Masunaga S. & Nakanishi J. (2003). – Population-level ecological risk assessment of planar polychlorinated aromatic hydrocarbons in great cormorant (*Phalacrocorax carbo*) around Tokyo Bay, Japan. *Environ. Toxicol. Chem.*, **22** (10), 2508–2518.

Murayama A., Gracia A.P., Reed D., Traylor-Holzer K., Jakob-Hoff R. & Miller P.S. (eds) (2006). – Tsushima Leopard Cat Conservation Planning Workshop. Conservation Breeding Specialist Group (SSC/IUCN), Apple Valley, Minnesota.

Murray G., Hind-Lanoiselet T., Moore K., Simpfendorfer S. & Edwards J. (2006). – Primefact 408: Crop diseases after drought. New South Wales Department of Primary Industry. Available at: www.dpi.nsw.gov.au/__data/assets/pdf_file/0004/123718/crop-diseases-after-drought.pdf

Murray N., MacDiarmid S.C., Wooldridge M., Gummow B., Morley R.S., Weber S.E., Giovannini A. & Wilson D. (2004). – Handbook on Import Risk Analysis for Animals and Animal Products, Volume 2. Quantitative Risk Assessment. World Organisation for Animal Health (OIE), Paris.

Murray N., MacDiarmid S.C., Wooldridge M., Gummow B., Morley R.S., Weber S.E., Giovannini A. & Wilson W. (2010). – Handbook on Import Risk Analysis for Animals and Animal Products, Volume 2. Quantitative Risk Analysis, 2nd Ed. World Organisation for Animal Health (OIE), Paris.

National Center for Biotechnology Information (NCBI) (2009). – Available at: www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi.

Nease R.F. Jr & Owens D.K (1997). – Use of influence diagrams to structure medical decisions. *Med. Decis. Making*, **17**, 263–275.

Noordhuizen J.P.T.M. (2001). – Analysis techniques commonly used in economics. *In* Applications of quantitative methods in veterinary epidemiology (J.P.T.M. Noordhuizen, F. Frankena, M.V. Thrusfield & E.A.T. Graat, eds). Wageningen Press, Wageningen, Netherlands, 351–357.

North D.W. (1995). – Limitations, definitions, principles and methods of risk analysis. *In* Risk assessment for veterinary biologicals (E.G.S. Osborne & J.W. Glosser, eds). *Rev. sci. tech. Off. int. Epiz.,* **14** (4), 913–923.

Nyamsuren D., Joly D.O., Enkhtuvshin S., Odonkhuu D., Olson K.A., Draisma M. & Karesh W.B. (2006). – Exposure of Mongolian gazelles (*Procapra gutturosa*) to foot and mouth disease virus. *J. Wildl. Dis.*, **42** (1), 154–158.

Oaks J.L., Gilbert M., Virani M.Z., Watson R.T., Meteyer C.U., Rideout B.A., Shivaprasad H.L., Ahmed S., Chaudhry M.J.I., Arshad M., Mahmood S., Ali A. & Khan A.A. (2004). – Diclofenac residues as the cause of vulture population decline in Pakistan. *Nature*, **427**, 630–633.

Oberauer K. & Kliegl R. (2006). – A formal model of capacity limits in working memory. *J. Mem. Lang*., **55**, 601–626.

Olson K.A. (2007). – Mongolian Gazelle Conservation Plan. Unpublished internal report. Wildlife Conservation Society, Bronx, New York.

Olson K.A, Mueller T., Bolortsetseg S., Leimgruber P., Fagan W.F. & Fuller T.K. (2009). – A mega-herd of more than 200,000 Mongolian gazelles *Procapra gutturosa*: a consequence of habitat quality. *Oryx*, **43** (1), 149–153.

Olson K.A., Fuller T.K., Mueller T., Murray M.G., Nicolson C., Odonkhuu D., Bolortsetseg S. & Schaller G.B. (2010). – Annual movements of Mongolian gazelles: nomads in the Eastern Steppe. *J. Arid Environ.*, **74**, 1435–1442.

Ostfeld R.S., Glass G. E. & Keesing F. (2005). – Spatial epidemiology: an emerging (or re-emerging) discipline. *Trends Ecol. Evol*., **20**, 328–336.

Paisley L.G. (2001). – A Monte Carlo simulation model for assessing the risk of the introduction of *Gyrodactylus salaris* to the Tana River, Norway: a second scenario. *In* Risk Analysis in Aquatic Animal Health (C.J. Rodgers, ed.). World Organisation for Animal Health (OIE), Paris, 185–192.

Patel K., Lopez M., Roberts H. & M. Sabirovic M. (2009). – West Nile Virus: Potential Risk Factors and the Likelihood for the Introduction of the Disease into the United Kingdom, Version 2, revised 24 February 2009. Department for Environment, Food and Rural Affairs (Defra), London, United Kingdom.

Pedersen K., Verdonck L., Austin B., Austin D.A., Blanch A.R., Grimont P.A.D., Jofre J., Koblavi S., Larsen J.L., Tiainen T., Vigneulle M. & Swings J. (1998). – Taxonomic evidence that *Vibrio carchariae* (Grimes *et al.* 1985) is a junior synonym of *Vibrio harveyi* (Johnson and Shunk 1936; Baumann *et al.* 1981). *Int. J. syst. Bacteriol.*, **48**, 749–758.

Pharo H.J. & MacDiarmid S.C. (2001). – Quantitative analysis of the risk of disease introduction through the importation of salmon for human consumption. *In* Risk Analysis in Aquatic Animal Health (C.J. Rodgers, ed.). World Organisation for Animal Health (OIE), Paris, 51–60.

Pollino C. A., Woodberry O., Nicholson A. & Hart B.T. (2007). – Parameterisation and evaluation of a Bayesian network for use in an ecological risk assessment. *Environ. Modelling Software*, **22** (8), 1140–1152.

Porphyre T., Stevensen M.A. & McKenzie J. (2008). – Risk factors for bovine tuberculosis in New Zealand cattle farms and their relationship with possum control strategies. *Prev. vet. Med.*, **86** (1–2), 93–106.

Power M. & McCarty L.S. (2002). – Trends in the development of ecological risk assessment and management frameworks. *Hum. Ecol. Risk Assess.*, **8** (1), 7–18.

Rabinowitz P.M. & Conti L.A. (2010). – Human–Animal Medicine: Clinical Approaches to Zoonoses, Toxicants and Other Shared Health Risks. Saunders Elsevier, Philadelphia, Pennsylvania.

Ricci P.F. (2006). – Causal models: influence diagrams, Bayesian networks, classification and regression trees. *In* Environmental and Health Risk Assessment and Management: Principles and Practices (P.F. Ricci, ed.). Springer, Houten, Netherlands, 257–274.

Risebro H., De Franca Doria M., Yip H. & Hunter P.R. (2005). – Intestinal illness through drinking water in Europe. *In* Microrisk: Microbiological Risk Assessment: a scientific basis for managing drinking water safety from source to tap. Available at: www.microrisk.com/uploads/microrisk_intestinal_illness_through_drinking_water.pdf

Robinson T.P. (2000). – Spatial statistics and geographical information systems in epidemiology and public health. *In* Advances in Parasitology (T.P. Rollinson & S.I. Hay, eds). Academic Press, Philadelphia, Pennsylvania, 81–128.

Sainsbury A.W., Ewen J.G. & Armstrong D.P. (2012). – Methods of disease risk analysis for reintroduction. *In* Reintroduction Biology: Integrating Science and Management (J.G. Ewen, D.P. Armstrong, K.A. Parker & P.J. Seddon, eds). Wiley-Blackwell, Oxford, United Kingdom.

Saito K.E., Sileo L., Green D.E., Meteyer C.U., McLaughlin G.S., Converse K.A. & Docherty D.E. *(*2007). – Raptor mortality due to West Nile virus in the United States, 2002. *J. Wildl. Dis.*, **43**, 206–213.

Salman M.D., Stärk K.D.C. & Zepeda C. (2003). – Quality assurance applied to animal disease surveillance systems. *In* Veterinary Services: organisation, quality assurance and evaluation (E. Correa Melo & F. Gerster, eds). *Rev. sci. tech. Off. int. Epiz*., **22** (2), 689–696.

Sarnet J.M., Schnatter R. & Gibb H. (1998). – Invited commentary: epidemiology and risk assessment. *Am. J. Epidemiol.*, **148** (10), 929–936.

Scriven M. (1991). – Evaluation Thesaurus, 4th Ed. Sage Publications, London, United Kingdom.

Sgrillo R.B., Moura J.I.L. & Sgrillo K.R.P.A. (2005). – Simulation model for phytomona epidemics in coconut trees. *Neotrop. Entomol.*, **34** (4), 527–538.

Sharp D. (2006). – Meloxicam to prevent rabies? *The Lancet*, **367**, 887-888.

Shiilegdamba E., Carpenter T.E., Perez A.M. & Thurmond M.C. (2008). – Temporal–spatial epidemiology of foot and mouth disease outbreaks in Mongolia 2000–2002. *Vet. Res. Commun.*, **32** (3), 201–207.

Skerratt L.F., Berger L., Speare R. *et al.* (2007). – Spread of chytridiomycosis has caused the rapid global decline and extinction of frogs. *Ecohealth*, **4** (2), 125–134.

Smith K.F., Acevedo-Whitehouse K. & Pedersen A.B. (2009). – The role of infectious diseases in biological conservation. *Anim. Conserv.*, **12**, 1–12.

Smith M.D., Warmolts D., Thoney D. & Hueter R. (eds) (2004). – The Elasmobranch Husbandry Manual: Captive Care of Sharks, Rays and their Relatives. Special Publication of the Ohio Biological Survey, Columbus, Ohio.

Starr C. (1969). – Social benefits vs. technological benefits. *Science*, **165** (3899), 1232–1238.

Stoskopf M.K. (1993). – Bacterial diseases of sharks. *In* Fish Medicine (M.K. Stoskopf, ed.). W.B. Saunders Company, Philadelphia, Pennsylvania, 774–776.

Swan G., Naidoo V., Cuthbert R., Green R.E., Pain D.J., Swarup D., Prakash V., Taggart M., Bekker L., Das D., Diekmann J., Diekmann M., Killian E., Meharg A., Patra R.C., Saini M. & Wolter K. (2006). – Removing the threat of diclofenac to critically endangered Asian vultures. *PLoS Biology,* **4** (3), e66. doi: 10.1371/journal.pbio.0040066.

Terrell S.P. (2004). – An introduction to viral, bacterial and fungal diseases of elasmobranchs. *In* The Elasmobranch Husbandry Manual: Captive Care of Sharks, Rays and their Relatives (M.D. Smith, D. Warmolts, D. Thoney & R. Hueter, eds). Special Publication of the Ohio Biological Survey, Columbus, Ohio, 427–431.

Thomson G. (2011). – Current disease control policies and 'knowledge gaps' in the epidemiology of foot and mouth disease on Mongolia's eastern Steppe. Report on a consultancy conducted on behalf of the Wildlife Conservation Society. Pretoria, South Africa.

Thrusfield M. (2005). Veterinary Epidemiology. Blackwell Science, Oxford, United Kingdom.

Thrusfield M. (2007). – Veterinary Epidemiology, 3rd Ed. Blackwell Science, Oxford, United Kingdom.

Thrush M.A., Murray A.G., Brun E., Wallace S. & Peeler E.J. (2011). – The application of risk and disease modelling to emerging freshwater diseases in wild aquatic animals. *Freshwater Biol.*, **56**, 658–675.

Tompkins D.M., Dunn A.M., Smith M.J. & Telfer D. (2011) – Wildlife diseases: from individual to ecosystems. *J. anim. Ecol*., **80**, 19–38.

Towse J., Hitch G.J. & Hutton U. (2000). – On the interpretation of working memory span in adults. *Mem. Cogn.*, **28** (3), 341–348.

Travis D.A., Watson R.P. & Tauer A. (2011). – The spread of pathogens through trade in wildlife. *In* The spread of pathogens through international trade in animals and animal products (S.C. MacDiarmid, ed.). *Rev. sci. tech. Off. int. Epiz.,* **30** (1) 219–239.

Tuckman B.W. (1965). – Developmental sequence in small groups. *Psychol. Bull.*, **63**, 384–399.

Tuttle A.D., Burrus O., Burkart M.A., Scott P.W., Stoskopf M.K. & Harms C.A. (2008). – Three cases of gastric prolapse through the gill slit in sand tiger sharks, *Carcharhinus taurus* (Rafinesque). *J Fish Dis.*, **31**, 311–315.

Unwin S.J. & Travis D. (2009). – Notes on disease risk analysis for primate reintroduction programmes, Chester Zoo, and IUCN SSC Conservation Breeding Specialist Group unpublished report for the Pan African Sanctuaries Alliance (PASA). Contact Steve Unwin (s.unwin@chesterzoo.org).

US Environmental Protection Agency (US EPA) (1998). – Guidelines for Ecological Risk Assessment. EPA/630/R-95/002F. Risk Assessment Forum, Washington, District of Columbia.

US Food and Drug Administration (US FDA) (2002). – Initiation and conduct of all 'major' risk assessments within a risk analysis framework, A report by the CFSAN Risk Analysis Working Group. Available at: www.fda.gov/food/foodscienceresearch/risksafetyassessment/ucm242929.htm

Vose D. (2000). – Risk Analysis: A Quantitative Guide, 2nd Ed. John Wiley, Chichester, United Kingdom.

Walker S.F., Bosch J., James T.Y., Litvintseva A.P., Valls J.A.O., Pina S., Garcia G. & Rosa G.A. (2008). – Invasive pathogens threaten species recovery programs. *Curr. Biol.*, **18** (18), R853–R854.

Walshe T. & Burgman M. (2010). – A framework for assessing and managing risks posed by emerging diseases. *Risk. Anal.*, **30** (2), 236-249. doi: 10.1111/j.1539-6924.2009.01305. Available at: www.ncbi.nlm.nih.gov/pubmed/19878485 (accessed on 6 January 2014).

Weldon C., du Preez L.H., Hyatt A.D. Muller R. & Speare R. (2004). – Origin of the amphibian chytrid fungus. *Emerg. infect. Dis.*, **10** (12), 2100–2105.

Westley F. & Vredenburg H. (1997). – Interorganizational collaboration and preservation of global biodiversity. *Organ. Sci.*, **8** (4), 381–403.

Wildlife Conservation Society (WCS) (2009). – Best of the Wild: Wildlife Conservation Society and the Eastern Steppe of Mongolia. WCS Asia Program, Bronx, New York, June 2009.

Wildlife Conservation Society (WCS) (2010). – The Global Conservation Program: achievements and lessons learned from 10 years of support for threat-based conservation at a landscape and seascape scale. The Eastern Steppe Living Landscape (Mongolia). The Living Landscape Program, Wildlife Conservation Society, Bronx, New York.

Wobeser G.A. (1997). – Diseases of Wild Waterfowl, 2nd Ed. Plenum Press, New York.

Wobeser G.A. (2006). – Essentials of Disease in Wild Animals. Blackwell Publishing, Ames, Iowa.

Woodford M.H. & Rossiter P.B. (1994). – Disease risks associated with wildlife translocation projects. *In* Creative conservation: interactive management of wild and captive animals (P.J.S. Olney, G.M. Mace & A.T.C. Feistner, eds). Chapman & Hall, London, United Kingdom, 178–200.

World Health Organization (2000). – Fact Sheet No. 192: El Niño and its healt impacts. Weekly Epidemiological Record, 1998, **73** (20): 148-152. Available at: http://www.who.int/inf-fs/en/fact192.html

World Organisation for Animal Health (OIE) (2010). – Animal health surveillance. *In* Terrestrial Animal Health Code, 19th Ed. OIE, Paris. Available at: www.oie.int/en/international-standard-setting/terrestrial-code/access-online/.

World Organisation for Animal Health (OIE) (2011). – Terrestrial Animal Health Code, 20th Ed. OIE, Paris. Available at: www.oie.int/en/international-standard-setting/terrestrial-code/access-online/.

Worthington R. & MacDiarmid S.C. (2011). – Import Risk Analysis: Zoo Primates from Australia, Canada, the European Union, USA and Singapore. MAF Biosecurity New Zealand, Wellington, New Zealand. Available at: www.biosecurity.govt.nz/files/biosec/consult/import-risk-analysis-zoo-primates-draft-public-consultation.pdf

Yoshiharaa Yu., Chimeddorj B., Buuveibaatar B., Lhagvasuren B. & Takatsuki S. (2008). – Effects of livestock grazing on pollination on a steppe in eastern Mongolia. *Biol. Cons*., **141** (9), 2376–2386.

Zeller H.G. & Schuffenecker I. (2004). – West Nile virus: an overview of its spread in Europe and the Mediterranean basin in contrast to its spread in the Americas. *Eur. J. Clin. Microbiol. Infect. Dis.*, **23**, 147–156.

Glossary of terms

D. Travis, S.C. MacDiarmid, D. Tompkins, B. Rideout & C. Lees

This glossary has been assembled for this *Manual* only. It is not an attempt to standardise or prescribe terminology across the field of wildlife management. Rather the aim is to ensure that terms are used consistently throughout the *Manual* and to help users have a common understanding of what has been written. For instance the terms 'risk analysis' and 'risk assessment' are often used interchangeably. In this *Manual* we have followed the terminology used by the World Organisation for Animal Health (OIE) in using the term 'risk assessment' as a sub-component of 'risk analysis'. Italicised words within definitions refer to other words included in this glossary.

Acceptable risk	A level of *risk* that is so small in terms of likelihood of occurrence or consequences that, in comparison with the expected benefits, stakeholders are willing to accept it
Clinical sign	A behavioural or physical change from normal expressed by an individual when suffering from a *disease*
Consequence assessment	The process of describing the relationship between specified exposures to a hazard and the consequences of those exposures. A causal process must exist by which exposures produce adverse health or environmental consequences, which may in turn lead to socioeconomic consequences and consequences for conservation. The *consequence assessment* describes the consequences of a given exposure and estimates the probability of them occurring
Contagious disease	A *disease* caused by a *parasite* that is acquired directly or indirectly from other hosts without involvement of a *vector* (a subset of *transmissible diseases*; all *contagious diseases* are transmissible, but not all *transmissible diseases* are contagious)
Diagnostic test	Any procedure used to aid in the characterisation of the cause or nature of a *disease* (see *screening test*)
Disease	Any impairment of the normal structural or physiological state of a living organism resulting from its physiological response to a *hazard*
Disease risk analysis	The application of *risk analysis* to identify diseases that may enter a specified animal population to identify the likelihood of such introductions, assess their consequences and identify measures that may be applied to mitigate either the likelihood of introduction or the magnitude of consequences
Ecosystem	A community of organisms together with its physical environment, viewed as a system of interacting and interdependent relationships
Endemic	A disease or *parasite* the *prevalence* of which does not exhibit wide fluctuations through time in a defined location. The term 'enzootic' is sometimes applied when referring to non-human populations

Epidemic	A sudden, rapid spread or increase in the *prevalence* or *intensity* of a *parasite* or *disease*. An *epidemic* is often the result of a change in circumstances that favour parasite *transmission* such as a rapid increase in *host* population density or the introduction of a new parasite. Having an established baseline is essential for detecting *epidemics*. The term 'epizootic' is sometimes applied when referring to non-human populations
Exotic	In relation to disease, a *pathogen* not known to be present in a specified geographic area
Exposure assessment	The process of describing the biological pathway(s) necessary for exposure of animals and humans in a particular environment to the *hazards* (in this case the pathogenic agents) released from a given risk source, and estimating the probability of the exposure(s) occurring, either qualitatively or quantitatively
Fomite	Any inanimate object that is capable of harbouring *parasites* and thereby playing a role in the *transmission* of those *parasites*
Hazard	A biological, chemical or physical agent in, or a condition of, an animal or animal product with the potential to cause an adverse health effect. See also *disease*
Hazard identification	The process of identifying the pathogenic or hazardous agents that could potentially be introduced into a specified animal population or environment by the activity being considered
Holding	Confinement in a non-*biosecure setting* for purposes other than prevention of the acquisition or spread of *parasites* (see *quarantine*)
Host	Any animal that is capable of harbouring a *parasite*, regardless of whether it plays a role in the further *transmission* of the *parasite*
Incidence	The number of new health events (*infection*, *disease*, etc.) experienced by a given population over a specific period of time. (cf. *prevalence*, the total number, new and old, in a given population in a specified time period)
Incubation period	The time that elapses between *infection* with a *parasite* and the onset of *disease*
Infection	The entry and development or multiplication of a *parasite* in the body of a *host*, where it may or may not cause *disease* (see *infestation*)
Infectious disease	The debilitating effects of *infection* or *infestation* by a *parasite*. It is possible for a *host* to be infected by a *parasite* but to show no *clinical signs* of *disease*
Infectious period	Period during which the infected individual is able to transmit the *infection*
Infestation	Subsistence of a *macroparasite* on the external surface of a *host* regardless of whether the *infestation* results in *disease*
Intensity	The mean number of *parasites* within infected individuals of the *host* population. (A different usage is sometimes used: the mean *parasite* burden of the entire population. It is important to distinguish between these two usages)
Latent infection	A persistent *subclinical infection* in which the *parasite* is dormant but has the potential to become active and cause disease or be transmitted in the future
Latent period	The period when an individual is infected but not yet capable of transmitting the *infection*

Macroparasites	*Parasites* that in general do not multiply within their hosts but instead produce *transmission* stages (eggs and larvae) that pass into the external environment (e.g. the parasitic helminths (worms) and arthropods). Typically macroparasites are visible to the naked eye
Model	In the context of DRA, a graphical or computational representation of an actual system used to predict *disease* dynamics and impacts, and the effect of management interventions on those dynamics and impacts
Monitoring	The intermittent performance and analysis of routine measurements and observations, aimed at detecting changes in the environment or health status of a population
Objective	Considering or representing facts, information, etc., without being influenced by personal feelings or opinions
Parasite	An agent that lives on or within a host and that survives at the expense of the *host* regardless of whether a *disease* state follows. This definition includes both *microparasites* (e.g. bacteria, viruses) and *macroparasites* (e.g. helminths, arthropods)
Pathogen (pathogenic agent)	Any *disease*-causing *parasite*
Pathogen pollution	The human-driven (anthropogenic) movement of parasites outside their natural geographic or host species range
Pathogenicity	The degree to which a *parasite* tends to cause *disease* in its *host* and the severity of the *disease* caused
Predictive value	Used in describing the ability of a *diagnostic test* to correctly identify infected and uninfected individuals in a population. A positive *predictive value* is the proportion of individuals with a positive test who have a condition, and a negative *predictive value* is the proportion of individuals with a negative test who do not have the condition
Prevalence	The proportion of the host population with *infection, disease* or antibody presence, often expressed as a percentage. A measure of how widespread an *infection*, *disease* or exposure to an infectious agent is at a point in time
Qualitative risk assessment	An assessment in which the outputs on the likelihood of the outcome or the magnitude of the consequences are expressed in qualitative terms such as high, medium, low or negligible
Quantitative risk assessment	An assessment in which the outputs of the *risk assessment* are expressed numerically
Quarantine	Isolation and observation in a *biosecure setting* for a specified period of time to allow *diseases* of concern to be detected and treated, and to prevent all new exposures to *parasites* of concern
Release assessment	The process of describing the biological pathway(s) necessary for a particular activity to 'release' (that is, introduce) *hazards* into a particular environment or *ecosystem*, and estimating the probability, either qualitatively or quantitatively, of that complete process occurring
Reservoir	Any animate (humans, animals, insects, etc.) or inanimate object (plant, soil, faeces, etc.) or any combination of these serving as a habitat of a *parasite* that reproduces itself in such a way as to be transmitted to a susceptible *host*

Risk	The likelihood of the occurrence and the likely magnitude of the consequences (biological, economic, etc. as defined by a specific *risk analysis* question) of an adverse event or effect to animal or human health
Risk analysis	The process composed of problem description, *hazard identification*, *risk assessment*, *risk management* and *risk communication*
Risk assessment	The evaluation of the likelihood and the consequences of entry, establishment or spread of a pathogenic agent within a specified animal population or environment
Risk communication	The interactive exchange of information and opinions throughout the *risk analysis* process concerning risk, risk-related factors and risk perceptions among risk assessors, risk managers, risk communicators, the general public and other interested parties
Risk estimation	The process of integrating the results from the *release assessment*, *exposure assessment*, and *consequence assessment* to produce overall measures of risks associated with the *hazards* identified at the outset
Risk evaluation	The process of comparing the risk estimated in the *risk assessment* with the level of risk, determined through consultation with stakeholders that is acceptable
Risk factor	Factor associated with an increase in the probability of occurrence of an outcome of interest (e.g. *disease*, reduced fecundity, mortality, etc.)
Risk management	The process of identifying, selecting and implementing measures that can be applied to reduce the level of *risk*
Robust	In the context of *disease risk analysis*, will withstand strong intellectual challenge
Screening test	Any procedure used to aid in the identification of individuals in a population that have *subclinical infections*, so that appropriate action can be taken (see *diagnostic test*)
Sensitivity analysis	A technique commonly used in computer modelling that quantifies the proportional change observed in *model* outcome as a function of proportional changes in the value of any one *model* input parameter. Thus, the relative 'importance' of *model* input parameters for their contribution to *model* performance can be directly evaluated
Subclinical infection	An *infection* that does not result in *clinical signs* of *disease*
Surveillance	The systematic ongoing collection, collation and analysis of information related to animal health and the timely dissemination of information to those who need to know so that action can be taken
Transdisciplinary	The collaborative exploration of an issue or problem that integrates the perspectives of multiple disciplines in order to connect new knowledge and deeper understanding to real life experiences
Transmission	The process by which a *parasite* passes from a source of *infection* to a new *host*
Transparency	In the context of *disease risk analysis*, comprehensive documentation of all data, information, assumptions, methods, results, discussion and conclusions used in the *risk analysis*. Conclusions should be supported by an *objective* and logical discussion and the document should be fully referenced

Uncertainty	The lack of precise knowledge of the input values that is due to measurement error or to lack of knowledge of the steps required, and the pathways from hazard to risk, when building the scenario being assessed
Vaccination	The use of vaccines to stimulate antibody production for the prevention of specific diseases
Variability	A real-world complexity in which the value of an input is not the same for each case owing to fluctuations in parameter values among individuals, populations and species over time and space
Vector	An insect or any living carrier that transports an infectious agent from an infected individual to a susceptible individual or its food or immediate surroundings. The organism may or may not pass through a development cycle within the *vector*
Wildlife	Animals that have a phenotype unaffected by human selection and live independent of direct human supervision or control
Zoonosis	A *disease* naturally transmitted between humans and other vertebrate species

Manual
of Procedures for Wildlife Disease Risk Analysis

Co-published by: the World Organisation for Animal Health (OIE) and the International Union for Conservation of Nature (IUCN)

The IUCN–OIE *Manual of Procedures for Wildlife Disease Risk Analysis* provides a 'how-to' guide that will be useful to the growing and diverse range of professionals involved in assessment and management of wildlife-associated disease risk scenarios. This document has been co-written by 22 specialists in the fields of wildlife disease ecology, epidemiology, risk analysis, modelling, disease surveillance, diagnostics, wildlife management, research, teaching and conservation planning. These authors have pooled their knowledge and experience to make tools and processes at the cutting edge of wildlife disease risk analysis accessible to a broad global audience in an effort to ensure healthy ecosystems through better decision-making. This is a companion volume to the *Guidelines for Wildlife Disease Risk Analysis*.

INTERNATIONAL UNION
FOR CONSERVATION OF NATURE

WORLD HEADQUARTERS
Rue Mauverney 28
1196 Gland, Switzerland
mail@iucn.org
Tel +41 22 999 0000
Fax +41 22 999 0002
www.iucn.org

WORLD ORGANISATION FOR ANIMAL HEALTH
Protecting animals, preserving our future