Abstracts of papers presented at the symposium

A brief history of the many faces of detection in ecology and wildlife management

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In the early years of the development of ecological methods, detection was considered a relatively simple parameter to estimate. The early closed population estimation techniques of Lincoln and Petersen and the more sophisticated open population models of Leslie, Chitty, Chitty and Jolly, and Seber assumed a relative ease of estimating the detection probability. Wildlife ecologists who knew their animals were always concerned about unequal catchability, and fisheries biologists like Ricker provided models to compensate for unequal catchability in fishery estimation, but it was not until the Colorado mafia published their monograph in 1978 on a series of models that allowed for certain classes of unequal detection that the problem was formalized for closed populations in Program CAPTURE. From the mid-1970s there was a groundswell of publications and a generation of cooperation between mathematicians and ecologists to attack the problem of detection, not only for population estimation but more importantly for disease analysis and pest management. This new synthesis of mathematical and statistical power with ecological insights of the clever ways that animals and plants avoid detection has produced a series of methods that recognised as a critical part of wildlife management in this century.

Comparing two methods of calculating the probability of absence: the Negative Predictive Value, and a Credible Interval

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If sampling fails to reveal the presence of an invasive species with potential to actually be present, how may we calculate the probability that it is truly absent, e.g. didymo (*Didymosphenia geminate*) in New Zealand's North Island. In statistical terms this is a Bayesian question, concerning the probability of a hypothesis (presence/absence), given the obtained data (all results negative). "Classical" theory doesn't answer this question, because it inverts the required considerations by calculating the probability of all samples being absent *if* the invasive was actually present. Accordingly, the Bayesian view of "probability" must be adopted in order to answer the question. That definition differs from classical probability in that it *always* includes an element of subjective belief, particularly in the choice of an appropriate "prior probability" (this is our belief as to the presence of the invasive organism *before* collecting new data). Bayesian methods can therefore be somewhat controversial – but we seem forced to use them. One Bayesian approach is to use the "Negative Predictive Value", in which a point estimate of the probability of presence (or absence) prior to sample collection (the "prior probability") is updated using data once collected using Bayes' rule. This is in common use in medical studies, where the prior probability is the background disease prevalence, which is generally well understood. It is sometimes used in environmental 'hot-spot' investigations. An alternative approach is to recognise the uncertainty in the prior belief by using a distribution of prior probability and updating that using data once collected to give a Credible Interval in which the probability of presence (or absence) should lie – if all our assumptions have been satisfied. We will compare the merits of these approaches considering didymo, southern salt marsh mosquito (*Aedes camptorhychus*) and the sea squirt *Styela clava*.

Population probability models for insect eradication

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One of the greatest challenges in eradicating pest species is determining when no further individuals remain: terminating the control programme too early means failure to eradicate, whereas continuing for too long can add considerable expense. Since monitoring tools are usually only qualitative and invariably imperfect, there may be considerable uncertainty about when and if eradication has been achieved. However, it is possible to quantify the efficacy of monitoring tools and to use this together with knowledge of the basic ecology of the target pest to robustly quantify the probability of successful eradication over time. Here, I describe one such approach and demonstrate its use in the large-scale eradication of painted apple moth (*Teia anartoides*) from Auckland, New Zealand. A population model for the production of male moths was used in conjunction with spatially-explicit pheromone trap locations and attraction radii to determine the daily probability of detecting a hypothetical wild population at a particular location. Over time, these probabilities compounded to decrease the likelihood of painted apple moth presence given an ongoing lack of detection. In this way, spatio-temporal risk maps were produced to inform managers and to suggest when eradication had been achieved to a predetermined level of certainty. The model suggested that eradication was likely to have been successful in the main infestation areas by mid 2005, with subsequent catches likely to represent further small incursions, as corroborated by evidence from mitochondrial DNA and stable isotope markers. While it was plausible that a wild population was present in the Otahuhu area in 2005, it was very unlikely that it remained by the end of 2006. Population probability models have potential for much wider use in border biosecurity and establishment of area freedom, particularly in combination with future automated trapping systems.

Network theory as a method for developing biosecurity preparedness: Netweork topology of *Paratrechina longicornis* in the Pacific and within New Zealand

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The black crazy ant, *Paratrechina longicornis*, is frequently intercepted at the border and post border in New Zealand.

Interceptions and incursions of *P. longicornis* are invariably connected to shipping containers and sawn timber. Both of these conveyors form large networks in the Pacific region and New Zealand in terms of distance and volume of goods moved. An assessment of the *P. longicornis* conveyor network topology in the Pacific and within New Zealand is made in relation to border and post border interceptions. Management strategies including site election for surveillance and pre-emptive eradication targeting conveyance nodes with high degree distributions are outlined. The utility of the method for targeted biosecurity preparedness projects is discussed.

Using network theory to survey for *Candidatus* Liberibacter solanacearum

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Pathogens are well known to spread through networks of conveyors. The resulting distribution and progress of disease is often quite different to expected distributions made by compartmental models (natural spread). This paper outlines the use of network theory to target risk sites for surveillance of *Candidatus* Liberibacter solanacearum. Results are presented together with a discussion on the likely role that the conveyor network for *Candidatus* Liberibacter solanacearum has played in the spread of the disease and its vector within New Zealand and on-going implications.

Biosecurity surveillance design: detecting non-indigenous vertebrate introductions using risk and power

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Ecosystems can be severely damaged by the introduction, establishment and spread of non-indigenous species (NIS) including vertebrates, invertebrates and plants. Development and use of natural areas poses a biosecurity risk regarding the introduction of increase NIS invasion risks, so biosecurity systems including prevention and detection measures are required. Even with the most rigorous biosecurity efforts, there is potential for NIS to evade quarantine and go on to establish and spread. The cost of such an event can be great, both environmentally and financially (e.g. containment/management or eradication). We have developed a surveillance design methodology, for an application where increased use of a natural area may result in NIS incursions, even with extensive biosecurity systems. The surveillance design methodology acknowledges heterogeneity of risk in the study area and stratifies the area to optimise surveillance deployment, achieving great efficiencies and improvement in statistical power of detection. Many of the risk decisions require lack data and so the system incorporates expert opinion with available data. The design covers the broad range of potential NIS that may be introduced by using exemplar species and a variety of surveillance system components (SSCs) (such as a combination of formal scientific surveys, trapping methods, and casual observation) distributed optimally over time and space. The mix of SSCs can be manipulated to take into account such factors as their relative financial costs and demands on expertise. The methodology has the flexibility to be applied to various groups of potential NIS (e.g. vertebrates, invertebrates and plants), and the design can evolve as data are collected (adaptive management). Overall, the surveillance design methodology allows for an efficient use of resources, providing sufficient power to detect incursions, resulting in reduced environmental and financial costs from NIS incursions.

Eradication of feral goats on Guadalupe Island: absence confirmation

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Insular ecosystems all over the world have been negatively affected by the introduction of ungulates, and it is due to the dramatic impacts that extensive control/eradication programmes have been undertaken. Eradication programmes using sophisticated techniques were recently carried out on Mexican islands. However, the phase of absence confirmation is facing the challenges seen elsewhere: how much effort is needed to confirm success? We present the case of Guadalupe Island in the Mexican Pacific. Eradication of feral goats (*Capra hircus*) was conducted on this volcanic island of 250 km^2 from 2002-2006. Since 2007 we have focussed on confirming absence through use of Judas goats. We discuss our results to date and how future assessments can be improved.

Protected species and predator detection dog use in New Zealand wildlife conservation projects

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In many New Zealand threatened species (birds, lizards, frogs, invertebrates) recovery programmes dogs are a significant conservation management tool. Protected species detection dogs have regularly been used to locate rare birds since the 1970's and more recently lizards. They have been used to detect, but not capture, kakapo, takahe, kiwi, whio, pateke, taiko, skinks and geckos, for monitoring and translocation purposes. Kakapo would possibly be extinct today if dogs had not been used to locate birds on Stewart Island and Fiordland for translocation to predator-free islands before predators and old age eliminated these original remnant populations. Use of these dogs on the kiwi recovery projects has advanced the progress of these projects by about ten years.

Predator detection dogs support threatened species recovery programmes and their role is to enhance other predator control methods. They have been regularly used since 2002 following a successful three-year pilot project to prove their usefulness. These dogs are used to detect the presence of mammalian predators including rodents, mustelids, cat and hedgehog. They are particularly useful when predator numbers are low when other predator detection methods (tracking tunnels, traps, gnaw sticks) have difficulty confirming their presence. Once detected by the dogs the predators are killed using toxins, traps or shooting. Dogs are used for: surveillance of supposedly predator-free sites; as a tool to focus predator

trap placement. A Standard Operating Procedure that includes a process of handler application and interview, and a two-step assessment and certification system for dogs and handlers guide these Department of Conservation dog programmes. There are currently 11 predator dog handlers and 26 protected species dog handlers in the programmes.

Canine detection of radio-telemetered brown treesnakes

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We are investigating canine teams (dogs and their handlers) on Guam as a potential tool for finding brown treesnakes (BTS) (*Boiga iregularis*), especially incipient populations on other islands. Canine teams have demonstrated proficiency at finding captive snakes in hidden tubes. Teams also find free-ranging BTS in various habitats, but detection rates for the latter are unknown. Dog handlers usually rely on visual searchers to locate BTS once a dog has signalled snake presence. At times, dogs signal but the visual search team cannot locate the snake; this complicates attempts to quantify detection rates. Our research aimed to estimate detection rate of free-ranging BTS by canine teams as a function of snake attributes, characteristics of snake refugia, and environmental conditions. Canine teams searched a defined 40m × 40m forested area with a snake that had consumed a dead mouse containing a radio-transmitter. Trials were conducted during the morning, when snakes were usually hidden in refugia. A tracker knew the snake's location, but dog handlers and data recorders did not. We recorded data on dog alerts and on-scent behaviour during trials. Out of 86 trials, the two canine teams had an average success rate of 36%. This study provides initial estimates of canine team efficacy when searching in complex habitats in information on optimizing visual search strategy after dog signals snake presence (defining size of area to search, identifying preferred refugia, etc.). We discuss experimental design, challenges and initial results.

Reliable mop-up of surviving pests: a more cost-effective and fail-safe approach to local extirpation

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Achieving very low densities of small mammal pests is routinely attained by expensive, large-scale, broadcast poisoning. There are two strategic responses to maintaining these low pest densities (or attempting to eradicate the survivors) – repeat the poisoning at regular intervals, or attempt to detect and mop-up the survivors. Here we report preliminary trials working toward the latter approach for possums (*Trichosurus vulpecula*) in a large mainland forest in New Zealand, and show that detection-and-mop-up is not only feasible but also possibly the most economically sensible and reliable way of achieving 100% kills. We use a simple bioeconomic model to predict the optimal surveillance (detection) strategy for possum mop-up, based on the characteristics of the detection device, and the few data available on the aggregation patterns of possums at extreme low density.

Using genetics and Bayesian modelling to evaluate the eradication of stoats (*Mustela erminea*) from Resolution Island, Fiordland, New Zealand

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The New Zealand Department of Conservation recently (May 2008) began a programme to eradicate stoats (*Mustela erminea*) from Resolution Island (Fiordland, New Zealand) using kill traps. In conjunction with this eradication effort we have the following 3 objectives: (1) to measure the population abundance of stoats prior to trapping using hair tubes and forensic DNA methods; (2) optimise techniques for detecting individual stoats, in order to quantify the probability of stoat persistence given no detections after several months of trapping; and (3) use genetic analyses to identify the possible origins (mainland incursions or *in situ* breeding) of new stoats captured in a control zone. We present Bayesian modelling techniques used to determine the probability of stoat persistence on the island after the initial population reduction, when individual stoats are no longer captured in traps. We also provide details on an effective level of monitoring and trapping effort required to maintain a comfortable level of confidence that stoats no longer persist on the island. Improving these techniques adds to variety of valuable tools for management of invasive mammal species in a range of natural environments worldwide.

Random exploratory behaviour by individual island colonists

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The post-arrival behaviour of individuals in novel environments influences survival and population establishment. For pest species early detection and elimination of new arrivals is vital to prevent invasion, and this requires a thorough understanding of movement patterns post-arrival. Studies have previously investigated exploratory movements in novel laboratory environments, but not during colonization of natural systems. We individually released five adult male brown rats (*Rattus norvegicus*) onto a rat-free island and monitored their movements hourly for three weeks. We demonstrate that (i) in the period immediately following arrival individual movements are apparently random; (ii) individuals effectively remain around their release site for three days before dispersing further; (iii) range size is much larger compared to individuals at high-density; (iv) exploration rate is mediated by central place foraging behaviour. These low-density movement behaviours have implications for understanding animal colonization dynamics, and intercepting wide-ranging individuals of invasive species as they arrive at new locations.

Searching for weeds – how to search where the weeds are?

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Sampling for rare events, such as a new weed incursion, is not easy. At most of the sample points the species of interest is absent and only occasionally the species is recorded. Very often surveillance and monitoring for rare events (e.g. new weed incursions) is done using local knowledge and a statistical sampling design is not used. The stated reason for this approach is usually because the biodiversity managers knew where to look and didn't need statistics. Adaptive, unequal probability survey designs can be used in these situations, ensuring both sample effort is focused on locations where there is a high likelihood of a weed being present. Time in the field is spent within locations where weeds are present and minimal time spent where weeds are absent. Any relevant information on where weeds are likely to be found (e.g. local knowledge and expertise) can be used to target survey effort in unequal probability survey designs. The advantage of an adaptive, unequal probability survey design is that not only can field effort be focused on areas where the weeds are thought to be. In addition, important weed parameters can be estimated and reported along with estimates of uncertainty. Weed parameters include the proportion of the total area that weeds are present, the diversity of weed species, the total abundance of weeds, and the total area covered by weeds. With reliable and consistent estimates of these weed parameters (e.g. weed cover or abundance) the efficacy of weed management can be tracked. Over time, with regular reporting of weed cover or abundance, the success (or otherwise) of weed management strategies can be measured.

Searching for weeds – a GIS tool

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Sampling for rare events, such as a new weed incursion, can be surprisingly efficient when adaptive, unequal probability survey designs are used. Spatially explicit habitat models and expert knowledge of weedy species can be used to identify areas of varied survey intensity. We introduce a GIS-based tool that can be used for designing such a survey. The user-friendly tool interfaces (behind the scenes) with the US Environmental Protection Agency's spatially balanced sampling design functions in R. The functions ensure that the location of the sample points are spatially balanced while at the same time, allowing the user to specify survey intensity in area of special interest (preferred habitats, areas of high conservation value, areas of high public use, etc). We discuss the use of the GIS tool in a case study where we designed a 5-year weed monitoring plan for a local authority in New Zealand. The plan includes 'over sample' sites to replace any original sample sites that were impractical or costly to visit. Initial results include estimates of what proportion of the total region has weeds present and an estimate of weed density. More detailed results are produced for specified known weed hot spots, such as areas adjacent to roads and rivers. These estimates are available for all weed species, and for individual species. Because the

system is GIS-based, spatial information is stored. Over time, as the weed surveillance and monitoring progresses, regional changes in weed distribution can be tracked, and species and locations that require more targeted weed management can be identified. Further results of such a probability-based design can be used to develop habitat models for predicting future distributions.

Quantitative evaluation of complex surveillance systems for pest and disease detection

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Surveillance for disease detection is used primarily for early detection of incursions and to support assertions of freedom from disease. Analytical techniques used to evaluate the efficacy of such surveillance are equally applicable across the domains of invasive species (both plant and animal), diseases and pests of agriculture crops, livestock, and of wildlife. Scenario tree models of surveillance activities may be used to estimate their diagnostic sensitivities, or the probability that the target organism will be detected given that it is present at a defined level. This paper will outline techniques for estimating the sensitivity of both targeted and general surveillance activities, and for the surveillance system as a whole. Probability of freedom from the target organism may be estimated from the surveillance sensitivity, and this Bayesian approach may be extended to estimate current probability of freedom from appropriate use of historical and ongoing surveillance evidence.

Application of techniques for the quantitative analysis of complex surveillance systems to disease and wildlife management

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Scenario tree modelling and associated methods provide tools to quantify the combined value of multiple complex surveillance activities over time. The outputs of this analysis are an estimate of the sensitivity of a surveillance system, and the cumulative probability of disease freedom that surveillance provides over time. The ability to quantify the performance of complex surveillance systems provides a number of new opportunities in the design and application of search and detection activities. One of these is the ability to objectively compare alternative detection strategies. The sensitivity of a strategy (the probability that the target biota would be detected, given that they are present at a defined level) may be balanced against cost and practicality considerations to determine the most effective strategy for a given situation. The paper provides an example of the comparison of two surveillance strategies (structured surveys and abattoir surveillance) for disease detection in animal health (Classical Swine Fever). These techniques may also play an important role in the certification of success in pest eradication operations. The ability to use multiple sources of evidence to evaluate success means that a higher level of confidence can often be achieved at lower cost. Examples of the application of scenario tree modelling in plant health and invasive pests are provided to illustrate its use within eradication programs.

Combining surveillance data from, and comparing the relative utility of wildlife sentinels for detecting bovine tuberculosis in New Zealand

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Brushtail possums (*Trichosurus vulpecula*) are the main wildlife host of bovine tuberculosis in New Zealand. The disease cycle can be broken by intensive large-scale reduction of possum populations to low levels. That strategy has been successfully applied over much of New Zealand, to the point that a key question now is whether the disease has indeed been locally eliminated, so that the expensive disease control programme can be stopped. However, it is usually too expensive to survey the few possums left. We have therefore developed a new approach to characterising the Tb detection capabilities of any wild animal species that can host the disease. The approach assigns each individual animal and spatially-explicit "detection kernel" that combines data on average range utilisation with probabilities of becoming infected when Tb is present in possums at the lowest sustainable level. We describe the principles involved, and compare the detection capabilities and cost-effectiveness across the species that are commonly being used for this purpose – wild pigs (*Sus scrofa*), ferrets (*Mustela furo*), and deer (*Cervus* spp.).

Spatially-explicit wildlife surveillance to prove freedom from diseases or pests

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Surveillance undertaken to prove freedom from a disease has traditionally focussed on sampling a specified proportion of the population to determine the presence of the infective agent. Based on a sample of individuals testing negative for disease, standard probability theory using the binomial or hypergeometric distribution can be used to make inference about the probability of disease being absent. However, if the disease agent involves a wildlife host, then determining what proportion of the population was sampled becomes problematic as it requires an estimate of population abundance, which may be difficult and expensive to obtain. Surveillance during the eradication of pests such as feral ungulates often make use of the Judas technique, whereby radio-collared individuals are released and followed in the hope that the sociality of the individuals will betray the locations of conspecifics, which can then be dispatched. Data collected during such surveillance is explicitly spatial, containing information about the 'search area' of the Judas animal. However, there has been no attempt to use such data to make inference about the probability of the area being free of the pest, given Judas animals fail to detect any conspecifics.

We present a framework for making specific use of the spatial nature of such wildlife surveillance data to make inference about the probability of freedom from the disease or pest. Underlying the sampling framework is a model of the detection process by sampled individuals. Estimates of individual detection probability are spatially smoothed using the extent of individual movements to produce a spatially-explicit detection surface. Bayes theorem is then used to combine this 2-dimensional surface with prior information on the probability of pest or disease presence, prior to sampling, to estimate the probability that the area is free from the disease or pest, given surveillance fails to detect evidence of their presence. We illustrate the method with examples of the detection of bovine Tb in wildlife in New Zealand and the detection of pigs (*Sus scrofa*) using the Judas technique during the feral pig eradication programme on Santa Cruz Island, California.

Combining livestock and wildlife surveillance data to assess the likelihood of freedom from bovine tuberculosis in New Zealand

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Bovine tuberculosis (Tb) has historically occurred in livestock throughout most of New Zealand, and also in wildlife over about 40% of the country. Using a test-and-cull strategy to eliminate Tb from livestock, intensive control of the major wildlife host (brushtail possums), and surveillance of key spillover hosts (wild ferrets, pigs and deer), the Animal Health Board has reduced the number of infected cattle herds by over 90% since 1994. Many formerly infected areas appear to now be free of the disease, so a key question is whether the disease control programme can be stopped in those places. We have developed a Bayesian framework for combining spatially explicit data derived from livestock testing and surveys of Tb prevalence in key wildlife hosts, and using those data to updating or refine an estimate of the probability of Tb freedom from wildlife provided by a priori prediction derived from a model of how Tb levels in possum are likely to have been affected by the duration and intensity of control. This paper outlines the conceptual framework, and some preliminary "case-study" steps toward implementation.

Caught between validation of results and the case definition

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A highly sensitive and timely detection system is the cornerstone of an effective response to either incursions of exotic diseases and pests or the emergence of new organisms. The trade-off is a reduction in system specificity. This presentation describes a number of investigations and responses involving MAFBNZ Investigation and Diagnostic Centre which were the result of specificity issues (false positive results). How and why did false positives occur, why are they important, the IDC approach to investigation of false positives and how this differs to traditional outbreak investigation together with some *a priori* decisions to reduce the impact of false positive results are explored.

Aspects of eradicating disease from wildlife vectors

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Bovine tuberculosis (Tb) occurs in cattle and in wildlife, with various species infected in a range of countries. The control or eradication of Tb can be empirically based or based on understanding of disease processes such as described in mathematical models. The eradication of Tb from Australia was largely empirically based, with water buffalo (*Bubalus bubalis*) apparently being the only significant wildlife disease host. Buffalo populations were apparently greatly reduced to achieve Tb eradication. This paper examines the alternative approach of basing control or eradication on mathematical models, and compares some predictions of one-host (wildlife) and two-host (cattle and wildlife) disease models with empirical data on Tb in both cattle and in wildlife. The one-host and two-host models were based on those published and also derived. For example, reported positive regressions between prevalence's of Tb in cattle and in brushtail possums in New Zealand and also between prevalence's of Tb in red deer and in brushtail possums in New Zealand, are consistent with two-host disease models assuming frequency dependent transmission. However most models of Tb in wildlife, e.g. the Barlow models, assume density dependent transmission. The implications for disease eradication are that models assuming density dependent transmission have a threshold host (wildlife) density about zero. Hence, if frequency dependent, not density dependent, transmission actually occurs, then host (wildlife) density would have to be reduced much lower, in order for eradication of Tb from cattle.

Evaluation of feral pig removal in Hawaiian preserves

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The Nature Conservancy of Hawaii (TNC) recently embarked on an ambitious ungulate control programme throughout their preserves on the islands of Maui and Molokai. The aim of the programme was local eradication of feral pigs (*Sus scrofa*) and they wanted some way of evaluating their progress. Catch-effort models have previously been applied to cumulative pig dispatches during an island eradication programme (Ramsey et al. 2009; Conservation Biology 23: 449-459). These models simultaneously estimate the parameters describing the initial population size and the probability of detecting an individual per unit of hunting effort, which can then be used to evaluate the likelihood of eradication. However these models rely on a number of assumptions including that the system is closed except for removals and that the relationship between hunting effort and the probability of detection is constant throughout the experiment. As the TNC control programme progressed it became clear the both these assumptions were violated and more pigs were often caught per unit of effort on the later compared with the earlier hunts. There was ongoing immigration into the preserves through breaks in the fence and via unfenced boundaries. Also, later hunts seemed to be more successful per unit of effort than earlier ones, presumably because hunters learnt the best way to cover the area and where the sites most likely to contain pigs were. We described how we incorporated this learning process into a catch-effort model using Bayesian updating in order to evaluate the efficacy of the control programme.

Evaluating black rat eradications on islands in the Gulf of California, Mexico

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Techniques for eradicating rodents from islands have experienced a significant development during the last decades, achieving success on around 300 islands worldwide. Aerial broadcast techniques facilitate eradication on big and complex islands. However, it remains difficult to confirm success. Failure is assessed by waiting until such time as survivors could have produced enough offspring for the population to become easily detectable, which usually means two years of intensive post-eradication monitoring. Moreover, the effort and cost involved may be even higher than the eradication itself. We examine the case of the aerial rat eradication on Farallón de San Ignacio and San Pedro Mártir islands in the Gulf of California, México, in fall 2007. Confirmation of the eradication is an ongoing task on these islands. We discuss the cost-benefit tradeoffs of implementing additional detection studies and conducting spatial simulations to improve the assessment of eradication success.

Absence of evidence is not evidence of absence

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Imperfect detection of a species is often a problem when attempting to establish its presence or absence at a set of locations. Failing to find the required evidence that a species is present at a location does not imply that the species is absent, merely that it has not been found. Some of the consequences of imperfect detection is that assessments of factors influencing species presence/absence can be misleading, and how certain can one be that the species is really absent given it has not detected at a location. In this talk I shall briefly review some of the consequences of imperfect detection, methodological advances that enable the detection process to be explicitly accounted for, and practical ways in which the required additional information can be collected.

Modelling the policy and economic context for detection-based monitoring tools: the costs and benefits of detecting last survivors and first re-colonisers

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Establishing and maintaining the success of pest or weed eradication programmes requires interpretation of failures to detect survivors and first re-colonisers. Recent developments provide statistical frameworks that allow sequences of such failures to be interpreted in a probabilistic context. For example, application of these methods allow managers of eradication programmes to decide *a priori* an acceptable risk of programme failure, and to use this decision to design monitoring regimes that deliver this level of certainty, given the detection characteristics of the search techniques at their disposal. Similar methods could be use to design monitoring regimes to detect an incursion by a previously eradicated species

(i.e. an eradication breakdown), which have an acceptable risk of failure. However, the availability of these methods begs questions about how "acceptable" risks of eradication failure or breakdown should be specified, and the consequent effort that should be expended to locate last survivors and first re-colonisers. We use a risk-based bioeconomic framework to model and analyse these decisions. The analysis demonstrates critical trade-offs between the cost and efficacy of the detection techniques available, the "value" of the eradication programme, and the perceived risk that a breakdown can occur. While our focus is on island pest eradication, we suggest how the bioeconomic framework used could be usefully applied to the detection of rare, at risk species, and the management of sporadically frequent diseases.