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Potential cane toad short to medium term control techniques – the biological
feasibility and cost of exclusion as a mitigating control strategy

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1. Executive Summary

- 1.1 Invasive cane toads *Bufo marinus* are spreading rapidly across northern Australia, raising serious public and scientific concerns for the long-term persistence of many potentially vulnerable wildlife populations. A number of mitigating solutions to the cane toad problem have been proposed, including direct killing of toads, biological control, or the establishment of secure areas from which cane toads are excluded.
- 1.2 Here we address the exclusion strategy, seeking in particular to provide estimates of the cost of isolating long-term viable populations of 12 species of susceptible native fauna managed to remain free of cane toads, using advanced methods in population viability analysis modelling combined with our experience in wildlife management in the difficult environments of northern Australia.
- 1.3 Our results reveal a relatively wide disparity across different taxa in the minimum habitat areas required for long-term persistence, ranging from as little as 16 km² for mangrove monitors, to 220 km² for northern quolls, to vast areas of up to 50 000 km² for wide ranging species such as wedge-tailed eagles.
- 1.4 An area the size of the Cobourg Peninsula (2 207 km²), which would be relatively cost-effective to isolate as a landscape-scale exclosure, appears to be large enough to support viable populations of most small mammal and reptile species such as quolls, goannas and predatory snakes (and presumably most amphibians and insects, which also have relatively small home range requirements or high average densities), though it would still fail to capture fully the areas for some of the largest free-ranging species, include most top avian predators such as wedge-tailed eagles. For Garig National Park, the cost of construction of a exclusion fence across the neck of the Cobourg Peninsula of 6 km length would be approximately \$3.6–5.7 million, with annual maintenance costs in the range of \$0.4-0.9 million.
- 1.5 In reality the situation is more complex, because captial and recurring costs for the construction and maintenance of fencing are governed not only by the size of the area to be enclosed, but also by the choice of location (e.g. it is more efficient to fence off the neck of a natural partial exclosure such as the Cobourg Peninsula than it is to create a perimeter around an inland site) and the nature of the materials used in construction (e.g. sourcing local or recycled building materials is more cost-effective). Overall costs could also be reduced by created secure area exclosures that encompass the ranges of multiple

species for which such conservation action is deemed warranted

- 1.6 Although the results presented herein represent preliminary estimates for the logistics of the “secure area” strategy of cane toad impact mitigation, they do nevertheless provide wildlife managers with some of the key information required to rationally and efficiently allocate time, money and habitat areas to maximise conservation benefits in the face of cane toad encroachments.

2. Introduction

Since its introduction in Australia in 1935 the cane toad has spread throughout much of Queensland, northern New South Wales and the Northern Territory (van Dam et al. 2002). The cane toad is predicted to further increase its range, primarily throughout coastal and near-coastal regions of tropical Australia, to encompass an area of approximately 2 million km² (Sutherst et al. 1995).

The spread of the cane toad into the Northern Territory has been documented reasonably comprehensively since about 1980 (e.g. Freeland and Martin 1985), and some preliminary work done on impacts on frog communities (Freeland and Kerin 1988) but recognition of the imminence of the threat to Kakadu National Park did not stimulate significant public investments in research on impacts or control until the 1990s. A substantial investment was then made to explore options for biological control, but few additional impact studies were done, and those completed were too short and unfocused to produce more than ambiguous results (Catling et al. 1999).

A consequence of this neglect has been that Australia is unprepared to respond to local, regional, national and international concern at the threats presented to highly significant sites like the World Heritage listed Kakadu National Park. There are too few data to permit the most basic cost-benefit analysis of proposals for control, or to demonstrate that no attempt at control is a reasonable option

In common with most other pest control programs, it is probable that effective management of cane toad impacts will require a combination of approaches, including (if feasible and socially acceptable) biological control, conventional methods of destruction, and exclusion. This report addresses the role of exclusion, whether employed as a dominant strategy or in combination with other methods.

Here we provide estimates of minimum viable population sizes (MVPs) and the area required to support those MVPs for 12 candidate species chosen for their probable susceptibility to the invasion of the toad and/or public perceptions of their particular significance. Species of particular interest to Indigenous people are included (Altman et al. 2003). It also describes the physical means of applying exclusion structures and analysis's the potential capital and recurring costs.

3. Objectives

- a. Estimate minimum viable population sizes and habitat areas (MVPs) for a range of fauna thought to be at greatest risk from cane toad invasion.
- b. Assess MVPs at a range of thresholds for probability of population failure over selected time-frames.
- c. Using available empirical data on the home range size and population densities of the target species, determine the area required to support MVPs.
- d. Estimate costs of capital and recurring costs of enclosing MVPs in a number of plausible landscape settings and at different levels of risk of population failure.
- e. Describe relationships between capital and recurring expenditures and the probability of securing viable populations within toad exclosures.

4. Minimum viable populations – an overview

Predicting the persistence of small populations has become a key issue in ecology and conservation biology. A large and growing number of species are threatened with extinction from human associated factors (habitat loss, over-exploitation, pollution and invasive species such as the cane toad) and stochastic factors (demographic & environmental fluctuations, inbreeding, loss of genetic variation, and natural catastrophes) (World Conservation Monitoring Centre 1992). Empirical studies have shown population size and habitat area to be strong predictors of extinction vulnerability (Terborgh and Winter 1980; Berger 1990). Given that the resources available to conservation programs are finite, and data on many endangered species are inadequate or unavailable, there is a critical need for general rules for predicting minimum reserve size and the minimum viable size of wildlife populations. With

this key information, time, money and habitat areas can be rationally and efficiently allocated (Lacy 1992). Further, since political and administrative decisions are frequently made without the time or data for detailed, case-specific evaluations (Pressey et al. 1993), general, yet scientifically reliable, estimates of minimum viable population sizes and habitat areas (MVPs) are essential. An MVP can be broadly defined as the smallest size required for a population or species to have a predetermined probability of persistence for a given length of time, given real-world constraints (see reviews by Simberloff 1988; Nunney & Campbell 1993).

The MVP approach is already widely applied as a heuristic decision-making tool. For example, the concept is employed (consciously or sub-consciously) each time a land-use planning decision sets aside habitat to conserve a species. The area set aside translates to an estimated population size considered to be sufficient to persist for some unspecified period. Similarly, the World Conservation Union (IUCN) specifies population size cut-offs for all taxa in its rules for categorising endangerment under the Red List criteria (e.g. a "lower risk" population has a greater than 90% probability of survival over 100 years; IUCN 2000). The conservation of wild nature often requires that decisions be made immediately, and without the benefit of complete information. The options in decision-making are to use the best, albeit imperfect, scientific information and tools available given the data to hand (e.g. MVP estimates), or for humans to make subjective decisions that are notoriously inaccurate, or wait for the collection of copious and more precise data while species go extinct.

Various attempts have been made to estimate MVP. Being primarily theoretical, these approximations of MVP have been based on genetics (Franklin 1980; Lande and Barrowclough 1987), demography (Lande 1988; Menges 1992), environmental stochasticity (Shaffer 1981; Lande 1988), and all factors combined (Soule 1987). These estimates imply MVPs ranging from a few hundred to many thousands of individuals, with considerable variance likely to be found among taxa and species (Shaffer 1987). The few empirical estimates made have been based on observed extinction rates of mammals in National Parks in North America and of boreal mammals on mountain tops in the United States (Belovsky 1987). Thomas (1990) compiled data from island biogeography and other sources, suggesting a median number of 5,500, but concluded that MVPs would likely be an order of magnitude greater in species with high variation in population sizes, such as small mammals and insects.

5. Procedures used to estimate MVPs

It is not possible to do deliberate field experiments to estimate MVP on a range of taxa as is required for a study such as the present one. A feasible and flexible approach is to use population viability analysis (PVA) procedures to estimate MVP for a wide range of species (Shaffer 1981; Burgman et al. 1993). Conceptually, MVP and PVA are closely linked (Ewens et al. 1987). PVA is a means for predicting the probability of extinction by using life history information to build a model of a species and its environment, and projecting the population's fate using stochastic computer simulation (Gilpin and Soule 1986; Boyce 1992). PVA implicitly or explicitly models the synergism between stochastic factors (necessary to avoid underestimating MVP), and permits large numbers of MVPs to be estimated in a reasonable time-span. Further, the tools of PVA have been validated using retrospective tests of well studied systems and shown to be unbiased (Brook et al. 2000).

There is no generally agreed upon definition of over what time frame population persistence should be measured, nor what extinction probabilities should be used. We therefore evaluated a range of risk levels and time-frames, ranging from 1 to 50% probability of extinction over 20 to 1000 years. However, a standard definition of a <10% probability of extinction over 100 years was used unless otherwise specified. Since the practical imperative was to define a minimum habitat area for each species, we specifically estimated the carrying capacity (equilibrium population size, given density dependent effects) required to deliver a MVP that satisfies the relevant risk-time definition (see Beissinger and Westphal 1998). The MVPs here reported are expressed as in terms of total population size (males and females).

The underlying statistical models upon which the inferences presented in this report are based on PVA modelling and associated statistical analysis of a large compilation of well-studied, long-monitored species from across the globe with good information on population dynamics (Brook et al., manuscript in preparation). These 1198 species spanned a wide range of taxa, biomes and life histories. Population dynamics time-series data were obtained from various online, text and primary sources. A major reference source was the Global Population Dynamics Database (cpbnts1.bio.ic.ac.uk/gpdd/), which provides time-series data for nearly 5,000 populations spanning over 1400 species. Other sources were used where the data was either superior to that of the GPDD, or where time-series data were unavailable from the GPDD. However, due to ambiguities and inconsistencies within the GPDD, as well as

inherent differences among the many data sources, a strict set of filtering criteria were subsequently derived, permitting the objective removal of time-series data deemed unworthy or inconsistent. This allowed for the establishment of a reduced and coherent database which was suitable for cross-species analysis.

Information-theoretic model selection procedures were used to assign relative weights (strength of evidence) to an *a priori* candidate set of five population dynamics time-series models fitted to the long-term monitoring data of each species and based upon variants of the generalized population dynamics model:

$$\log\left(\frac{N_{t+1}}{N_t}\right) = a\left(1 - \frac{N_t}{K}\right)^\theta + \varepsilon$$

Depending on the values of a , K , and θ (as estimated from the population time-series data), the stochastic population model can represent a random walk, exponential growth or density dependent growth/limitation at varying levels of intensity (Dennis and Taper 1994). Model parameterisation and time-series data analysis was conducted using @RISK (Palisade Corporation 2000), a stochastic simulation "add-in" for Microsoft Excel[®]. The model variants used for this study were as follows:

- Random walk (RW) 1p (σ)
- Exponential (EX), 2p (a , σ)
- Logistic (LG), 3p (a , K , σ)
- Gompertz (GZ), 3p (a , $\ln[K]$, σ)
- θ -Logistic (TL), 4p (a , K , σ , θ)

MVPs were generated using each of the above models by conducting a series of runs with different initial population sizes and carrying capacities (e.g. 50, 100, 500, 1,000, and 5,000). When these did not encompass the threshold MVP probabilities of population survival for the required definition of MVP, higher or lower starting values were added until the desired

thresholds were attained. Extinction risk was regressed against $\log K$ (to linearise the results), and the predicted MVP then interpolated. Subsequently, runs around this predicted value were performed to refine the MVP estimate, until the results were within 1% of the required probability. 100 simulation replicates of each run were used initially, to keep computer time to reasonable levels, and for the final assessments, 1,000 replicate simulations are used to provide greater precision. The final, model-averaged MVP estimates were calculated by scaling each individual model prediction by the model's AIC_c weight estimated during the maximum likelihood fitting procedure for each species (refer to Burnham and Anderson 2002, for methodological details).

The results of the model-averaged simulations were then used to derive a statistical approximation relating the estimated MVP for all of the 1198 species to the ecological correlates described in sections 7 and 8. To do this, multivariate generalized linear mixed models (GLMM) were fit using the *R* statistical package v1.8.1 (Ihaka and Gentleman 1996), specifying a normal error distribution with an identity link function, where $\log(\text{model-averaged MVP})$ was the response variable. The error structure of GLMM corrects for non-independent of statistical units (species), in this case due to phylogenetic relatedness, and permits the 'random effects' variance explained at different levels of hierarchical clustering (Class/Order/Family) to be decomposed. The seven derived predictor variables were modelled as 'fixed effects'. This procedure was repeated for a range of risk levels and simulation duration to provide estimates across a range of different MVP definitions.

The final GLMM models so derived were used to determine the MVPs for the candidate taxa evaluated in this report, after arriving at adequate estimates of the six composite predictor variables described on p. 6-7. Minimum habitat areas (MHAs) were determined as the product of the estimated MVP for a given species and the habitat area required per individual (based on known or inferred home range size or average density, listed later in Table 2). For a worked example, consider the northern quoll, which has an average home range size for females of 2.3 ha (Schmitt et al. 1989). The estimated MVP for this species for a <10% risk of extinction over 100 years was 19 100 individuals. The minimum habitat area, assuming overlap of male and female home ranges, would be determined as follows:

$$\text{MHA} = 19100 \times 2.3 \times 0.5 \text{ [sex ratio]} = 21\,965 \text{ hectares} = 220 \text{ km}^2, \text{ or a fenced area of roughly } 14.8 \text{ km} \times 14.8 \text{ km}.$$

There are three fundamental assumptions associated with the approach used. 1) No habitat loss (since the concern is with the minimum habitat area to be maintained over a given time

frame). 2) Current threats and life history parameters do not change in the future (e.g. human impacts do not get worse). 3) Individual populations are discrete and isolated (not distributed in a source-sink or metapopulation configuration). However, these assumptions are stringent only as concerns the MVP estimate for that particular population.

6. Ecological correlates

Twenty-four morphological, life history, ecological and behavioral attributes that have been shown or postulated to correlate with extinction risk were collected for a suite of 1198 species (Brook et al. in preparation).

C1 Body weight: average adult weight (male and female) measured in grams.

C2 Body length: average adult length (male and female) measured in millimetres. Body length or size was defined as tip-of-beak to tip-of-tail for birds, tip-of-snout to vent for reptiles, tip-of-nose to tip-of-tail for mammals.

C3 Reproductive type: 1) sexual, 2) asexual, 3) hermaphroditic.

C4 Age at sexual maturity: average age at which individual's first mate (female), given in months. Note that all of the species considered in this report reproduce sexually.

C5 Lifespan: maximum age attained by individuals in the wild, measured in months.

C6 Generation length: average age of breeding adults at the time their young are born, in months.

C7 Social grouping: taken to be grouping of breeding adults. Categorized as 1) solitary (single parent), 2) monogamous pair (where young expelled once mature), 3) small family group (includes minor polygamy, polyandry), 4) gregarious (territorial mammals with harems, promiscuous species.), 5) colonial (large breeding colonies in birds, breeding ponds - frogs, non-guarding fish).

C8 Dispersal ability: Categorized as 1) immediate (<1 km), 2) local (up to 10 km), 3) landscape (up to 100 km), 4) regional (up to 1000 km), 5) continental/trans-oceanic (1000 - 10 000 km), 6) greater (10 000km +).

C9 Disturbance type: Direct loss (culling etc) or indirect loss (pollution, competition with weeds etc.) were scored by either 1 where experienced otherwise 0.

C10 Fragmentation (range decline): Scores for range decline were given according to the

extent of loss, thus: 1) species occupies < 1% of former range or almost all habitat unsuitable, 2) species occupies 1-10% of former range or suitable habitat, 3) species occupies 10-50% of former range area, 4) species occupies 50-100% of former range or decline unknown/thought to be small.

C11 Geographic distribution: Score criteria were: 1) very narrow endemic - < 50 square km's or 20km (linear), 2) narrow endemic - < 500 square km's or 100 km (linear), 3) confined to single biome (see notes for definition), 4) regional, 5) continental and greater (transoceanic & migratory).

C12 Population size: categorical estimation of effective adult population at time of study.

Categories were: 1) <50, 2) 50-500 (or unknown and thought to be small), 3) 500-5000, 4) 5000-50 000, 5) 50 000-500 000, 6) >500 000

C13 Fertility: number of eggs laid or young born per female, per annum.

C14 Population trend: trend at time of study, given as 1) increasing, 2) stable, 3) declining.

C15 Trophic level: 1) primary producer, 2) detritivore, 3) herbivore, 4) omnivore, 5) carnivore.

C16 Niche breadth: 1) specialist or 2) generalist.

C17 Relationship with Homo sapiens: scored as 1) positive - benefit from human disturbance or have been successfully introduced out of native range, 2) negative - no benefit gained by species.

C18 IUCN listing: Following IUCN, categories were extinct (EX), extinct in the wild (EW), critically endangered (CR), endangered (EN), vulnerable (VU), near threatened (NT), least concern (LC), data deficient (DD) or not evaluated (NE).

C19 Legal protection: categorised according to whether a species was either 1) protected in native region, or listed under CITES Appendices II or I or 2) unprotected.

C20-24 Biome: Temperate (includes coniferous forest, mixed hardwood-conifers, temperate deciduous forest, montane forest, Mediterranean shrubland or chaparral and eucalyptus woodland), Tropical (tropical savanna or thorn forest and tropical forest), Arid (Tundra, semi-desert, desert and grassland), Freshwater (lakes, rivers, wetlands and swamp regions) and Marine (shoreline, pelagic and benthic).

Home range: Average home range size.

Seven composite predictors were derived from the 24 attributes listed above:

P1, Biome (5 level factor): An additive score index was used to assign a species to one of the five biomes (temperate, tropical, arid, freshwater and marine). For example, a species whose geographic range extended across coniferous forest, mixed hardwood-conifers and temperate deciduous forest (temperate) as well as tropical savanna (tropical), would be assigned to the biome temperate since the score of occurrence here would have been greater than that within tropical.

P2, Conservation status (2 level factor): species were considered to be *threatened* (score = 1) if they scored 1) under legal protection, were listed under the IUCN red list as anything other than *least concern* (excluding *data deficient* and *not evaluated*), or where the global population numbered less than 500 individuals. Otherwise deemed *lower risk* (score = 0).

P3, Geographic range (continuous predictor 0-1): Geographic distribution scores were assigned categorically (see above) and then converted to a continuous predictor 0-1 (by subtracting the total by minimum score possible and then dividing by the range). A high score indicated assumed narrow distribution.

P4, Human impact (continuous predictor 0-1): This considered the extent of range of habitat loss, as well as direct loss or indirect loss. $\text{Human impact} = ((\text{range decline (1-3)} + \text{direct loss (0-1)} + \text{indirect loss (0-1)}) - 1) / 4$. Final score converted to a range from 0-1 by subtracting minimum possible value from end value and dividing by the range. Range decline was given greater weighting here.

P5, Body size: Measurements were converted using the natural logarithm.

P6, Ecological flexibility (continuous predictor 0-1): Dispersal ability, trophic level and the extent of ecological specialization are taken to be surrogates of 'ecological flexibility', assuming that those species thought to be more 'flexible' than others are better adapted to change. A high score indicated assumed less flexibility. Species at the top of the food web were assumed to be less flexible ecologically than those at the bottom. Ecological specialisation or niche breadth considered synthetically both feeding specialisation and habitat specialisation. The final algorithm here was thus $(\text{dispersal ability (1-6)} / 6) + (\text{trophic level (1-4)} / 4) + (\text{specialisation (1-2)} / 2) - (1/6 + 1/4 + 1/2) / (3 - (1/6 + 1/4 + 1/2))$.

P7, Demographics (continuous predictor 0-1): Considered as the reproductive life history of a

species i.e. age at sexual maturity, fertility, reproductive strategy and longevity. Highly fecund, short-lived species are assumed to be more resilient than long-lived species with extended gestation periods, at least in response to short term and major change related to human impacts. Generation length was not used owing to inadequate data. These parameters were categorised and additive values allowed for a final score (high score indicated assumed high demographic risk). Algorithm used was $(\text{fertility} + \text{longevity} + \text{sexual maturity} + \text{reproductive strategy}) - 4 / (11 - 4)$.

7. Rationale for selection of candidate species

The set of candidate species evaluated in this report were selected on the basis of the following considerations:

- (a) Identified or suspected vulnerability to cane toad impacts (van Dam et al. 2002);
- (b) To represent a broad taxonomic spectrum of vertebrates;
- (c) To capture a variety of life history types;
- (d) To encompass iconic north Australian species;
- (e) Likelihood of sufficient demographic and environmental preference data to estimate minimum viable population size and minimum habitat areas using the indirect inference methods developed by one of this report's authors (Brook).

Twelve candidate species were chosen, being the dingo *Canis lupus dingo*, northern quoll *Dasyurus hallucatus* (mammals), black-necked stork or Jabiru *Epippiorhynchus asiaticus*, blue-winged kookaburra *Dacelo leachii*, wedge-tailed eagle *Aquila audax*, black bittern *Ixobrychus flavicollis*, Australian bustard *Ardeotis australis* (birds), black-headed python *Aspidites melanocephalus*, northern death adder *Acanthophis praelongus*, northern sand goanna *Varanus panoptes*, mangrove monitor *Varanus indicus*, and frill-necked lizard *Chlamydosaurus kingii* (reptiles). A detailed description of each species ecology and life history are given later in the report in the appendix.