



MONASH University

Improving conservation outcomes in threatened species translocation programs

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BSc (honours)



A male mallee emu-wren *Stipiturus mallee*

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Abstract

Conservation translocation refers the human-mediated movement of living organisms from one area, with release in another, where the primary motivation is a conservation benefit. Translocations have had a positive influence on conservation globally, contributing to the recovery efforts of hundreds of threatened taxa. Despite notable successes, translocation programs encounter many challenges and failure is not uncommon. In this thesis, I investigate some of the key knowledge gaps that remain for translocation practitioners across planning, implementation, post-release monitoring and reporting.

Translocated individuals may be sourced from captive or wild populations. Typically, wild-caught individuals have a better chance of persistence following release than their captive-bred counterparts. However, translocation managers must ensure that removing individuals from wild populations for translocation is sustainable. In a structured review, I assess the peer-reviewed literature that addresses wild-sourced translocation programs to assess how frequently impact on source population is addressed in translocation research. Of 292 articles, I identified just 32 instances (11%) where an *a priori* impact on source population was estimated. I propose a standardised framework for reporting on management of translocation source populations: published summaries of wild-sourced translocations should include clear conservation goals, a description of the methods used to assess potential impact, an *a priori* justification based on evidence for the chosen harvesting strategy, an estimated timeline for recovery and a summary of post-removal population trends. Routinely reporting impacts of harvesting on source populations will inform management when source sustainability is uncertain, improve transparency and provide a point of comparison against which improvement in the field may be measured.

As an exemplar for the management of translocation source populations, I implement the framework described above using five threatened passerines, endemic to Norfolk Island, as model taxa. I use demographic data to project population trajectories under alternative harvesting strategies for each taxon to estimate the impact of harvesting for translocation. Despite considerable demographic variation among focal populations, I demonstrate all five taxa have the potential to sustain harvesting at rates required for future conservation translocations. In doing so, I provide a rare example of an *a priori* assessment of the impact of harvesting for translocation.

When key ecological information is lacking, conservation translocations should be conducted within an adaptive, experimental framework to maximise knowledge gained, and to increase the probability of success. I describe the trial translocation of the mallee emu-wren to Ngarkat Conservation Park, with emphasis on experimentally testing factors that may increase probability of successful population establishment for this species. Despite the failure to establish a population, I provide valuable management insights regarding both the mallee emu-wren, and translocation practice more broadly. I show that timing of releases can influence translocation outcomes and that spring releases should be prioritised in future mallee emu-wren translocations.

Finally, I characterise genetic structure and diversity across the global population of the mallee emu-wren and use this information to identify management priorities for this species. The global mallee emu-wren population may be considered a single genetic unit for management purposes. I show that future translocations should incorporate gene pool mixing between individuals from spatially diverse source populations to maximise genetic diversity.



A slender-billed white-eye *Zosterops tenuirostris*, endemic to Norfolk Island.

Publications during enrolment

Mitchell, WF, Clarke, RH (2019) Using infrared thermography to detect night-roosting birds. *Journal of Field Ornithology* **90**, 39-51.

Hunt, T, **Mitchell, W**, Boulton, R, Hedger, C, Ireland, L (2019) Cooperative breeding recorded in the endangered Mallee Emu-wren *Stipiturus mallee*. *Australian Field Ornithology* **36**, 163-167.

Mitchell, WF, Boulton, RL, Ireland, LJ, Hunt, TJ, Olds, LGM, Verdon, SJ, Clarke, RH, Stubbs, W, and Hedger, CJ (2021) Reintroducing the mallee emu-wren to Ngarkat Conservation Park, South Australia. In 'Global Re-introduction Perspective Series 2020: Case studies from around the globe.' (Ed PS Soorae.) pp. 137-142 (IUCN SSC Conservation Translocation Specialist Group: Abu Dhabi and Calgary Zoo).

Nance, AH, **Mitchell, W**, Brown, SM, Clarke, RH, MacGregor, NA, Ward, R, Garnett, ST (2021) Norfolk Island Gerygone *Gerygone modesta*. In 'The Action Plan for Australian Birds 2020.' (Eds ST Garnett, GB Baker.) pp. 651-653. (CSIRO Publishing: Melbourne).

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Verdon, SJ, **Mitchell, WF**, Clarke, MF (2021) Can flexible timing of harvest for translocation reduce the impact on fluctuating source populations? *Wildlife Research* **48**, 458-469.

Thesis including published works

declaration

I hereby declare that this thesis contains no material which has been accepted for the award of any other degree or diploma at any university or equivalent institution and that, to the best of my knowledge and belief, this thesis contains no material previously published or written by another person, except where due reference is made in the text of the thesis.

This thesis includes two original papers published in peer-reviewed journals, one submitted manuscript and a manuscript in preparation for submission. The core theme of the thesis is the science that underpins management of conservation translocation programs. The ideas, development and writing of all the papers in the thesis were the principal responsibility of myself, the student, working within the School of Biological Sciences under the supervision of Rohan Clarke, Paul Sunnucks and Rebecca Boulton.

The inclusion of co-authors reflects the fact that the work came from active collaboration between researchers and acknowledges input into team-based research.

In the case of chapters 2, 3, 4 and 5 my contribution to the work involved the following:

Thesis Chapter	Publication Title	Status	Nature and % of student contribution	Co-author name(s) Nature and % of Co-author's contribution*	Co-author(s), Monash student Y/N*
2	Are we adequately assessing the demographic impacts of harvesting for wild-sourced conservation translocations?	Published in <i>"Conservation Science and Practice"</i>	Concept, analyses and manuscript preparation 85%	1) Rohan Clarke: input to manuscript 5 % 2) Paul Sunnucks: input to manuscript 5 % 3) Rebecca Boulton: input to manuscript 5%	No No No
3	Sustainable harvesting for wild-sourced conservation translocations: A case study using island-endemic passerines	Submitted	Concept, data collection, analyses and preparation of manuscript 70%	1) Rohan Clarke: concept and input to manuscript 10% 2) Alexandra Nance: Data collection and input to manuscript 20%	No Yes

Thesis Chapter	Publication Title	Status	Nature and % of student contribution	Co-author name(s) Nature and % of Co-author's contribution*	Co-author(s), Monash student Y/N*
4	Using experimental trials to improve translocation protocols for a cryptic, endangered passerine	Published in <i>"Pacific Conservation Biology"</i>	Methodology, data collection, analyses and manuscript preparation 65%	1) Rebecca Boulton: concept, data collection and input to manuscript 5% 2) Luke Ireland: data collection and input to manuscript 5% 3) Thomas Hunt: data collection and input to manuscript 5% 4) Simon Verdon: data collection and input to manuscript 5% 5) Liberty Olds: data collection and input to manuscript 5% 6) Chris Hedger: concept, data collection and input to manuscript 5% 7) Rohan Clarke: concept and input to manuscript 5%	No No No No No No No
5	Prioritising genetic diversity of founders in translocation planning for an endangered semi-arid passerine	In preparation for submission	Concept, data collection, analyses and preparation of manuscript 85%	1) Alexandra Pavlova: Analyses and input to manuscript 5 % 2) Rohan Clarke: data collection and input to manuscript 5% 3) Paul Sunnucks: concept, analyses and input to manuscript 5%	No No No

I have renumbered sections of submitted or published papers in order to generate a consistent presentation within the thesis.

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I hereby certify that the above declaration correctly reflects the nature and extent of the student's and co-authors' contributions to this work. In instances where I am not the responsible author I have consulted with the responsible author to agree on the respective contributions of the authors.

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A Norfolk grey fantail *Rhipidura albiscapa pelzelni*, endemic to Norfolk Island.

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1. Introduction

The world is in the grip of a biodiversity crisis (Ceballos *et al.* 2015). Despite decades of concerted effort from a global conservation movement, the natural world is being destroyed at a frightening rate (IPBES 2019; Sandbrook *et al.* 2019). Those engaged in trying to alleviate this destruction face an uphill struggle. The inertia of consumerism does not appear to be dissipating, with global resource use predicted to increase 117% by 2050 (Hatfield-Dodds *et al.* 2017). Climate change poses an ecological and social challenge that may only be addressed through global collaboration, a magnitude of cooperation that humanity has rarely, if ever, been able to achieve (Li *et al.* 2021). Meanwhile, the estimated level of investment required to address global conservation demands is at least an order of magnitude higher than that currently available (McCarthy *et al.* 2012) and governing bodies the world over underperform in addressing these threats (Lindsey *et al.* 2017; Burck *et al.* 2021). In light of these challenges, maximising the conservation gain from the limited resources that are available is critical if we are to safeguard as much of Earth's biodiversity as possible. Conservation is most effective when driven by comprehensive empirical evidence (Sutherland *et al.* 2004). In this thesis, I investigate the science of optimising conservation outcomes with particular focus on threatened species translocation programs.

Translocation as a tool for conservation

Conservation translocation, as defined by the International Union for Conservation of Nature (IUCN/SSC 2013), is the human-mediated movement of living organisms from one area, with release in another, where the primary motivation is a conservation benefit. A number of terms fall within this broad definition (Fig. 1.1, Seddon *et al.* 2014). 'Population restoration' incorporates 'reintroduction', the movement of organisms to an area they once inhabited but from which they have become extinct, and 'reinforcement', the release of organisms within an extant population of conspecifics. 'Augmentation' and 'supplementation' are synonymous with 'reinforcement', which is usually performed to bolster genetic diversity or population size. 'Conservation introduction' incorporates 'assisted colonisation'; the movement of organisms outside their historic range, typically due to absence of suitable conditions within that historic range, and 'ecological replacement', the movement of an organism into a novel habitat to perform an important ecological function of a now locally extirpated, but closely related, taxa (Seddon 2010).

Translocations have a long and varied history (Fischer and Lindenmayer 2000). Early translocations carried out by Europeans in the southern hemisphere, explicitly for the purpose of conservation, were often framed around the establishment of sanctuaries for species considered rare (Low 2002). During the early twentieth century, 75 Australian animal and plant species were introduced to Wilson's Promontory in Victoria's southeast. When considered a century later, some of the species chosen for introduction during this period leave one scratching their head. Tropical tree kangaroos, arid malleefowl and desert budgerigars were all expected to co-exist on the narrow peninsula, battered by Southern Ocean winter storms. Few survived for long (Low 2002). Translocations to Kangaroo Island in South Australia during the same period have had a greater impact. Originally, introduced in the 1920s, the island's koala population numbered ~27,000 by the early twenty-first century and has caused significant, not to mention expensive, impacts on native vegetation (Low 2002; Masters *et al.* 2004).

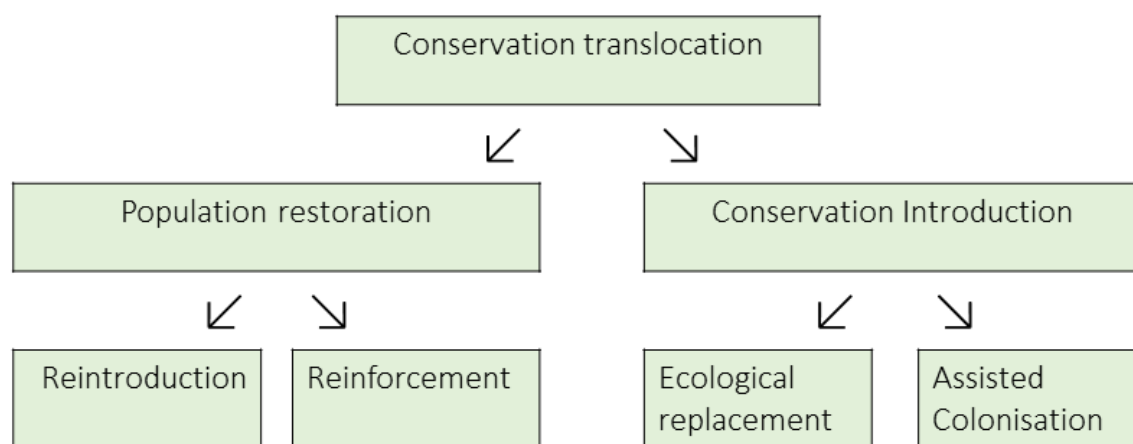


Figure 1.1. A summary of terms that fall within the broad definition of conservation translocation.

Since those early days, the field of translocation science has come a long way. In recent decades, some of the most highly publicised conservation success stories globally have focused on the translocations of threatened species (Lavery and Moseby 2014; Bolam *et al.* 2020). For example, translocation has been a fundamental component in the recovery of the California condor *Gymnogyps californianus*, once extinct in the wild (Walters *et al.* 2010). Population size, genetic diversity and fitness of the Endangered Florida panther *Puma concolor coryi* were all improved by the translocation of individuals of the closely related *P. c. stanleyana* into the Florida panther population (Johnson *et al.* 2010). Translocation to predator-free islands has been instrumental in the ongoing persistence of several southern hemisphere avian species including the hihi *Notiomystis cincta*, little spotted kiwi *Apteryx owenii*, North Island saddleback *Philesturnus rufusater* and North Island robin *Petroica longipes* (Ramstad *et al.* 2013; Parlato and Armstrong 2018; Parlato *et al.* 2021). Globally, the conservation management of hundreds of species incorporates translocation but despite high profile successes, failure is common (Berger-Tal *et*

al. 2019; Langridge *et al.* 2021; Morris *et al.* 2021). A recent review of 293 translocation case studies presented in the IUCN Conservation Translocation Specialist Groups' *Global Re-introduction Perspectives Series* catalogued common difficulties faced by translocation managers. The most common hurdles, in order of frequency, were animal behaviour, monitoring challenges, lack of funding, quality of release habitat, lack of baseline knowledge and lack of public support (Berger-Tal *et al.* 2019).

Conservation programs are often managed on shoestring budgets, may be risky to focal taxa (e.g. elevated stress associated with capture and handling) and may fail (Dickens *et al.* 2010; Morris *et al.* 2021). Efficiency is, therefore, paramount for achieving success. For this reason, factors that may influence persistence of translocated populations have received considerable research attention. Husbandry, habitat suitability, intra-species social interactions, behaviour, naivety in the face of novel predators, as well as the origin, number and genetic diversity of founders have all been demonstrated as factors affecting the probability of success for a translocation program (Fischer and Lindenmayer 2000; Armstrong *et al.* 2007; Dickens *et al.* 2010; Ewen *et al.* 2012; He *et al.* 2016; Richardson and Ewen 2016; Moseby *et al.* 2018a; Moseby *et al.* 2018b; Franks *et al.* 2020). In short, managers require a comprehensive understanding of the taxa undergoing translocation, its habitat and the complex ecological interactions at play in their focal system. When information is lacking (as is invariably the case), managers are encouraged to make predictions based on the best available information and to design reintroductions within an adaptive experimental framework to inform future management (Armstrong *et al.* 2007). By structuring conservation initiatives in a way that provides opportunities for hypothesis testing, managers are able to gain knowledge about their focal system and incorporate that knowledge into future decisions in an iterative, adaptive process (Armstrong *et al.* 2007; Canessa *et al.* 2019).

This large volume of research has led to the establishment, and maintenance, of comprehensive guidelines for the most effective management of translocation programs (Fischer and Lindenmayer 2000; IUCN/SSC 2013). Strategies such as the IUCN's '*Guidelines for Reintroductions and Other Conservation Translocations*' (2013) may be used as a benchmark to assess performance in the field of translocation science. Key reviews reveal areas in which best practice is typically achieved but also highlight areas in which the field might improve. Translocation research regularly incorporates *a priori* hypotheses with greater emphasis on gaining insight through experimentation, having largely transitioned away from descriptive reporting (Taylor *et al.* 2017). However, a high proportion of translocation literature fails to incorporate long-term monitoring of translocated individuals and considers only short-term metrics of success (Taylor *et al.* 2017). The integration between science and practice could also be improved by uptake of translocation research that explicitly evaluates competing management scenarios, thereby aiding with on-ground decision-making (Taylor *et al.* 2017). The need

for continued translocation research is highlighted by reported rates of failure in translocation literature. Between 25% and 74% of translocations result in failure, depending on review criteria and study period (Griffith *et al.* 1989; Fischer and Lindenmayer 2000; Bricchieri-Colombi and Moehrenschrager 2016; Bubac *et al.* 2019; Resende *et al.* 2020; Morris *et al.* 2021). Despite increased research and investment, success rates have not improved in recent decades (Resende *et al.* 2020; Morris *et al.* 2021). Publication bias, specifically a reduced likelihood for failed conservation initiatives to be published, may further distort perception of success rates in translocation programs. Finally, a subset of authors have demonstrated the potential impact of harvesting individuals from wild populations for the purpose of translocation (Dimond and Armstrong 2007; Margalida *et al.* 2015; Canessa *et al.* 2019; Verdon *et al.* 2021). Indeed, the IUCN's *Guidelines for Reintroductions and Other Conservation Translocations* (2013) recommends that any reduction in viability of translocation source populations should be balanced by expected gain within the release population. However, it is unclear how frequently the sustainability of translocation source populations is considered.

Sustainable management of translocation source populations

Translocated individuals or propagules may be obtained from captive populations (often reared specifically to provide founders for translocation programs) or harvested from wild populations (Ferrer *et al.* 2014). Captive breeding programs are expensive and routinely require permanent staff, enclosures, and access to veterinary facilities (Rahbek 1993; Cruz *et al.* 2016; Harley *et al.* 2018). The scale of captive facilities are also often limited, which may negatively influence genetic diversity within captive populations (Frankham 2008). Careful management is required to mitigate inbreeding depression, the accumulation of deleterious alleles and reductions in genetic diversity (Frankham 2008; Robert 2009). After successive generations in captivity, animals may lose behaviours that provide a fitness advantage in the wild, making them less likely to survive following release (Tetzlaff *et al.* 2019; Crates *et al.* 2021). Wild-harvested organisms are more likely to persist following translocation than their captive-bred counterparts (Rummel *et al.* 2016). Additionally, the probability of successfully establishing a population is increased by translocating a greater number of founders (Deredec and Courchamp 2007; Morris *et al.* 2021). Translocating large numbers of wild-sourced animals is, therefore, an attractive option given the increased probability of success and the challenges associated with captive-bred founders. However, any benefits of using wild animals as a source for translocation must be weighed against the potential harm that might be caused to those populations (Dimond and Armstrong 2007; IUCN/SSC 2013). This is especially the case for threatened species where existing populations are characteristically small and the act of harvesting may exacerbate threatening processes for the source population (Courchamp *et al.* 2008).

Population monitoring for translocation purposes

To make informed decisions that maximise the likelihood of translocation success while ensuring that harvesting is undertaken sustainably, conservation managers require a detailed understanding of their target populations (MacKenzie and Kendall 2002). In most cases, this information is derived from surveys of a subset of those populations. Drawing conclusions from such surveys without accounting for false negative observations, i.e. when a species is present but not detected, can lead to significant bias (Bibby and Buckland 1987; MacKenzie and Kendall 2002; Tyre *et al.* 2003). Common modelling approaches developed to address varying detectability in surveys include dynamic occupancy modelling (MacKenzie *et al.* 2017), distance sampling (Buckland *et al.* 2012) or mark-recapture (Royle and Young 2008). Such methods allow probability of detection and population size to be estimated with greater precision and accuracy but also increase labour and expense in the field (Kery and Royle 2015). Automating aspects of the data collection process is one way that efficiency may be improved, without sacrificing accuracy, in population surveys.

Autonomous acoustic recording units, paired with automated signal detection software, show promise as a method for increasing efficiency of field surveys of vocal taxa (Knight *et al.* 2017; Shonfield and Bayne 2017). Data captured using ARUs may be used to populate dynamics occupancy models, allowing population trajectories to be estimated (Metcalf *et al.* 2019). Translocation literature infrequently incorporates post-release monitoring to verify long-term persistence, despite best-practice recommendations (Taylor *et al.* 2017). Incorporating automated data collection into translocation management may reduce expenses associated with extended field seasons over multiple years, thereby increasing the feasibility of maintaining long-term monitoring following translocation.

Genetic diversity in the context of translocation

Maintenance of genetic diversity is fundamental for species' ability to respond to environmental change, including that brought about by humans (Frankham *et al.* 2017). Populations of threatened species are often characterised by inbreeding and associated low genetic diversity (Frankham *et al.* 2017). The resultant reduction in fitness can exacerbate threatening processes. Despite recommendations, the genetic diversity of focal taxa is often poorly considered in conservation management (Pierson *et al.* 2016; Cook and Sgro 2017; Liddell *et al.* 2021). It is essential that translocations be managed in a way that maximises genetic diversity (IUCN 2013). This is usually achieved through careful selection of founders (He *et al.* 2016). In cases where sufficient genetic material is no longer available in extant populations, genetic rescue, or the introduction of genetic material from closely related taxa, is increasingly considered as a means to conserve threatened species (Ralls *et al.* 2018).

Model systems

A translocation program recently implemented in Australia, and another in the early stages of planning, provide valuable opportunities to investigate the science underpinning translocation. Norfolk Island is located in the Pacific Ocean some ~1700 km east of the Australian mainland and ~1100 km north of New Zealand. Seven avian taxa on Norfolk Island have become extinct since European settlement and all five extant passerines are considered threatened (Garnett and Baker 2021). Island endemic taxa suffer an elevated rate of extinction compared with that of mainland taxa (Wood *et al.* 2017). Disproportionately high endemism, spatially limited distributions and naivety to novel predators contribute to this phenomenon (Kier *et al.* 2009; Wood *et al.* 2017). Invasive rodents were a major driver of avian extinctions on Norfolk Island and the persistence of extant passerines is likely dependent on ongoing rat suppression efforts (Nance *et al.* 2021). Translocation may provide a means to establish a haven for Norfolk's threatened passerines on a predator-free island. Such an approach has been instrumental in the conservation and subsequent reintroductions of several threatened avian taxa in New Zealand and other Pacific islands (Miskelly and Powlesland 2013). However, the passerines of Norfolk Island have very small distributions with three taxa restricted to the ~460 ha Norfolk Island National Park. It is essential that any conservation interventions made in this system are informed by comprehensive ecological data to minimise risk to these populations (Sutherland *et al.* 2004). I estimate population parameters for Norfolk Island's five threatened taxa and then use these data to investigate the number of individuals that could be sustainably removed from these populations for the purpose of translocation.

The second case study I investigate in this thesis is the translocation of the Endangered mallee emu-wren *Stipiturus mallee*. The mallee emu-wren is specialised to live amongst the dense interwoven spines of spinifex grass *Triodia scariosa*, and is rarely found in areas where *Triodia* is absent (Howe 1910; Verdon *et al.* 2020). Historic land-clearing, senescence of *Triodia* habitat, drought and wildfire have led to a precipitous decline in mallee emu-wren abundance and distribution (Brown *et al.* 2009). Landscape scale wildfires have led to the extirpation of mallee emu-wrens from many of the reserves they once occupied, including all South Australian populations (Verdon *et al.* 2019). By 2014, the global population of the species was restricted to a fragmented network of reserves comprising Nowingi State Forest and Murray-Sunset, Hattah-Kulkyne and Wyperfeld National Parks in the north-west of Victoria. In this fragmented landscape, mallee emu-wrens do not have the dispersal capability to re-colonise many areas of suitable habitat that have recovered following reserve-scale wildfire. The establishment of new populations through translocation has been recommended as a priority conservation strategy for mallee emu-wrens to provide insurance against destruction of extant populations by wildfire and restore the species to parts of its historic range (Brown *et al.* 2009; Boulton and Lau 2015).

I was a core member of the team that implemented a 2018 trial reintroduction of 78 mallee emu-wrens from extant populations in Victoria to Ngarkat Conservation Park in South Australia. This experimental reintroduction was implemented within an adaptive management framework to optimise release protocols and assess the feasibility of additional translocations. Considerable uncertainty existed around factors that might influence the likelihood of successful establishment of the mallee emu-wren following translocation. Furthermore, the size, cryptic behaviour, and the potential danger radio trackers, and even multiple colour bands, pose to this species make monitoring of the mallee emu-wren a challenge (e.g. Hill and Elphick 2011). In this thesis, I use the mallee emu-wren as a model species to investigate establishment and persistence following translocation, as well as to assess survey methods for cryptic species. The 2018 translocation also provided an opportunity to collect genetic material from mallee emu-wrens across their range. I investigate genetic diversity and structure across the global mallee emu-wren population and use these data to provide insight and recommendations regarding the source of founders for future translocations that will maximise genetic diversity in newly established populations.

General aims and thesis outline

Together, these translocation programs present a timely opportunity to address some of the key knowledge gaps that remain for translocation practitioners across planning, implementation and post-release monitoring. Specifically, my research has enabled me to:

- assess recent literature to assess current practice with regards to management of translocation source populations and use this insight to make recommendations aimed at improving current practice;
- use population vital rates to provide managers with a case study for estimating sustainable harvesting rates for source populations;
- identify factors that maximise the probability of translocation establishment success while minimising costs and effort;
- develop methods to accurately and precisely monitor persistence of reintroduced populations when the translocated species is cryptic or difficult to survey;
- assess the genetic characteristics of the global mallee emu-wren population and investigate avenues for broadening genetic diversity; and
- determine whether reintroduction is an effective long-term conservation strategy for the mallee emu-wren and for the endemic passerine species of Norfolk Island.

This thesis is presented as four primary chapters, each structured as a standalone research output developed for publication in the refereed literature. In chapter two, I evaluate 292 peer-reviewed

primary research articles with a focus on wild-sourced conservation translocation programs to assess how frequently impact on source population is addressed in translocation research and whether this frequency has increased during the last decade. I summarise current methods used for assessing impact and rate their effectiveness. Finally, I present a framework for increasing transparency in the field and ensuring that benefits of conservation programs are not outweighed by harm to extant source populations.

In the third chapter, I use Norfolk Island's endemic passerines as a model system to implement the framework presented in chapter two. I use demographic data collected on Norfolk Island between 2018 and 2020 to estimate population size and reproductive rates for Norfolk Island's five endemic passerines. I project population trends for these five taxa under several alternative harvesting strategies. I estimate the rate of harvest that is sustainable over a ten-year period from each population and discuss the factors that influence the capacity of each population to recover following harvesting. The five taxa assessed have contrasting population demographics and life histories, providing a useful comparison of how these factors influence rate of recovery following harvest. This chapter provides an exemplar for sustainable management of translocation source populations, while providing key management insight for the threatened passerines of Norfolk Island.

In chapter four, I provide a summary of the trial reintroduction of the mallee emu-wren to Ngarkat Conservation Park. A key aim of this program was to optimise release protocols and investigate factors that may promote successful establishment of mallee emu-wren following translocation. Specifically, I evaluate the effect of timing of release and familiarity of release groups on post-release dispersal, survival and reproductive output. I also present population trends following translocation at harvest sites to assess the capacity of extant mallee emu-wren populations to sustain harvesting for additional translocations. This chapter provides an important example of how familiarity may influence translocation of social taxa and the potential effects of climatic conditions and season of release on translocation outcomes.

An important consideration in any conservation program is the genetic diversity of the population undergoing management. My fifth chapter addresses genetic diversity and structure across the global mallee emu-wren population. I use these data to identify founder sites and subpopulations for future translocations that will maximise genetic diversity of newly established populations. I also assess whether existing isolated subpopulations would benefit from reciprocal translocations to introduce novel genetic material, i.e. gene flow augmentation.

A key focus of my research program also sought to investigate acoustic recording units, paired with automated call recognition, as a method for inexpensive long-term monitoring of mallee emu-wren

population trends following translocation. I aimed to assess the effectiveness of this approach by comparing it with typical observer surveys in a paired study design. Unfortunately, my candidature coincided with fieldwork restrictions associated with the Covid19 pandemic and this aspect of my research program was abandoned. However, I present a mallee emu-wren call recognition template, capable of batch detection of mallee emu-wren calls from field recordings, as an appendix to this thesis. I assess the efficacy of this tool using standardised performance metrics and its discuss future applications.

Finally, I summarise the central findings of each chapter and highlight the contributions I have made to the field of translocation science generally, as well as to the conservation of both the mallee emu-wren and endemic passerines of Norfolk Island. I close by outlining future research opportunities made possible by my work.

References

- Armstrong, DP, Castro, I, Griffiths, R (2007) Using Adaptive Management to Determine Requirements of Re-Introduced Populations: The Case of the New Zealand Hihi. *Journal of Applied Ecology* **44**, 953-962.
- Berger-Tal, O, Blumstein, DT, Swaisgood, RR (2019) Conservation translocations: a review of common difficulties and promising directions. *Animal Conservation* **23**, 121-131.
- Bolam, FC, Mair, L, Angelico, M, Brooks, TM, Burgman, M, Hermes, C, Hoffmann, M, Martin, RW, McGowan, PJK, Rodrigues, ASL, Rondinini, C, Westrip, JRS, Wheatley, H, Bedolla-Guzmán, Y, Calzada, J, Child, MF, Cranswick, PA, Dickman, CR, Fessl, B, Fisher, DO, Garnett, ST, Groombridge, JJ, Johnson, CN, Kennerley, RJ, King, SRB, Lamoreux, JF, Lees, AC, Lens, L, Mahood, SP, Mallon, DP, Meijaard, E, Méndez-Sánchez, F, Percequillo, AR, Regan, TJ, Renjifo, LM, Rivers, MC, Roach, NS, Roxburgh, L, Safford, RJ, Salaman, P, Squires, T, Vázquez-Domínguez, E, Visconti, P, Woinarski, JCZ, Young, RP, Butchart, SHM (2020) How many bird and mammal extinctions has recent conservation action prevented? *Conservation Letters* **14**, e12762.
- Boulton, RL, Lau, J, 2015. Threatened Mallee Birds Conservation Action Plan, Report June 2015. Report to the Threatened Mallee Birds Implementation Team, Birdlife Australia.
- Brichieri-Colombi, TA, Moehrensclager, A (2016) Alignment of threat, effort, and perceived success in North American conservation translocations. *Conservation Biology* **30**, 1159-1172.

- Brown, S, Clarke, M, Clarke, R (2009) Fire is a key element in the landscape-scale habitat requirements and global population status of a threatened bird: The Mallee Emu-wren (*Stipiturus mallee*). *Biological Conservation* **142**, 432-445.
- Bubac, CM, Johnson, AC, Fox, JA, Cullingham, CI (2019) Conservation translocations and post-release monitoring: Identifying trends in failures, biases, and challenges from around the world. *Biological Conservation* **238**, 108239.
- Buckland, ST, Anderson, DR, Burnham, KP, Laake, JL (2012) 'Distance sampling: estimating abundance of biological populations.' (Springer Science & Business Media: Berlin, Germany).
- Burck, J, Uhlich, T, Bals, C, Höhne, N, Nascimento, L (2021) 'Climate Change Performance Index 2022. Results. Monitoring Climate Mitigation Efforts of 60 Countries plus the EU—covering 92% of the Global Greenhouse Gas Emissions.' (Germanwatch and NewClimate Institute: Berlin, Germany).
- Canessa, S, Ottonello, D, Rosa, G, Salvidio, S, Grasselli, E, Oneto, F (2019) Adaptive management of species recovery programs: A real-world application for an endangered amphibian. *Biological Conservation* **236**, 202-210.
- Ceballos, G, Ehrlich, PR, Barnosky, AD, García, A, Pringle, RM, Palmer, TM (2015) Accelerated modern human-induced species losses: Entering the sixth mass extinction. *Science advances* **1**, e1400253.
- Cook, CN, Sgro, CM (2017) Aligning science and policy to achieve evolutionarily enlightened conservation. *Conservation Biology* **31**, 501-512.
- Courchamp, F, Berec, L, Gascoigne, J (2008) 'Allee effects in ecology and conservation.' (Oxford University Press: New York).
- Crates, R, Langmore, N, Ranjard, L, Stojanovic, D, Rayner, L, Ingwersen, D, Heinsohn, R (2021) Loss of vocal culture and fitness costs in a critically endangered songbird. *Proceedings of the Royal Society B: Biological Sciences* **288**, 20210225.
- Cruz, CEF, Cerva, C, Andretta, I (2016) Financial Costs of Conserving Captive-bred Wild Birds. *Der Zoologische Garten* **85**, 354-362.
- Deredec, A, Courchamp, F (2007) Importance of the Allee effect for reintroductions. *Ecoscience* **14**, 440-451.
- Dickens, MJ, Delehanty, DJ, Michael Romero, L (2010) Stress: An inevitable component of animal translocation. *Biological Conservation* **143**, 1329-1341.

- Dimond, WJ, Armstrong, DP (2007) Adaptive Harvesting of Source Populations for Translocation: A Case Study with New Zealand Robins. *Conservation Biology* **21**, 114-124.
- Ewen, JG, Armstrong, DP, Parker, KA, Seddon, PJ (2012) 'Reintroduction biology: integrating science and management.' (Wiley-Blackwell: Oxford, UK).
- Ferrer, M, Newton, I, Muriel, R, Báguena, G, Bustamante, J, Martini, M, Morandini, V, Pärt, T (2014) Using manipulation of density-dependent fecundity to recover an endangered species: the bearded vulture *Gypaetus barbatus* as an example. *Journal of Applied Ecology* **51**, 1255-1263.
- Fischer, J, Lindenmayer, DB (2000) An assessment of the published results of animal relocations. *Biological Conservation* **96**, 1-11.
- Frankham, R (2008) Genetic adaptation to captivity in species conservation programs. *Molecular Ecology* **17**, 325-33.
- Frankham, R, Ballou, JD, Ralls, K, Eldridge, MDB, Dudash, MR, Fenster, CB, Lacy, RC, Sunnucks, P (2017) 'Genetic management of fragmented animal and plant populations.' (Oxford University Press: Oxford).
- Franks, VR, Andrews, CE, Ewen, JG, McCready, M, Parker, KA, Thorogood, R (2020) Changes in social groups across reintroductions and effects on post-release survival. *Animal Conservation* **23**, 443-454.
- Griffith, B, Scott, JM, Carpenter, JW, Reed, C (1989) Translocation as a Species Conservation Tool: Status and Strategy. *Science* **245**, 477-480.
- Harley, D, Mawson, PR, Olds, L, McFadden, M, Hogg, C (2018) The contribution of captive breeding in zoos to the conservation of Australia's threatened fauna. In 'Recovering Australian Threatened Species: A Book of Hope.' (Eds S Garnett, J Woinarski, D Lindenmayer, P Latch.) pp. 281-294. (CSIRO Publishing: Melbourne, Australia).
- Hatfield-Dodds, S, Schandl, H, Newth, D, Obersteiner, M, Cai, Y, Baynes, T, West, J, Havlik, P (2017) Assessing global resource use and greenhouse emissions to 2050, with ambitious resource efficiency and climate mitigation policies. *Journal of Cleaner Production* **144**, 403-414.
- He, X, Johansson, ML, Heath, DD (2016) Role of genomics and transcriptomics in selection of reintroduction source populations. *Conservation Biology* **30**, 1010-1018.
- Hill, JM, Elphick, CS (2011) Are grassland passerines especially susceptible to negative transmitter impacts? *Wildlife Society Bulletin* **35**, 362-367.
- Howe, F (1910) Notes on the mallee emu-wren. *Emu* **10**, 336-337.

IPBES (2019) 'Global assessment report on biodiversity and ecosystem services of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services.' (IPBES secretariat: Bonn, Germany).

IUCN/SSC (2013) 'Guidelines for Reintroductions and Other Translocations. Version 1.0.' (IUCN Species Survival Commission: Gland, Switzerland).

Johnson, WE, Onorato, DP, Roelke, ME, Land, ED, Cunningham, M, Belden, RC, McBride, R, Jansen, D, Lotz, M, Shindle, D (2010) Genetic restoration of the Florida panther. *Science* **329**, 1641-1645.

Kery, M, Royle, JA (2015) 'Applied Hierarchical Modeling in Ecology: Volume 1: Prelude and Static Models.' (Academic Press: London, United Kingdom).

Kier, G, Kreft, H, Lee, TM, Jetz, W, Ibisch, PL, Nowicki, C, Mutke, J, Barthlott, W (2009) A global assessment of endemism and species richness across island and mainland regions. *Proceedings of the National Academy of Sciences* **106**, 9322-9327.

Knight, EC, Hannah, KC, Foley, GJ, Scott, CD, Brigham, RM, Bayne, E (2017) Recommendations for acoustic recognizer performance assessment with application to five common automated signal recognition programs. *Avian Conservation and Ecology* **12**, 14.

Langridge, J, Sordello, R, Reyjol, Y (2021) Existing evidence on the outcomes of wildlife translocations in protected areas: a systematic map. *Environmental Evidence* **10**, 1-29

Lavery, T, Moseby, K, (2014) 'From the frontline: saving Australia's threatened mammals.' *The Conversation*.

Li, Y, Sewell, DK, Saber, S, Shank, DB, Kashima, Y (2021) The climate commons dilemma: how can humanity solve the commons dilemma for the global climate commons? *Climatic Change* **164**, 4.

Liddell, E, Sunnucks, P, Cook, CN (2021) To mix or not to mix gene pools for threatened species management? Few studies use genetic data to examine the risks of both actions, but failing to do so leads disproportionately to recommendations for separate management. *Biological Conservation* **256**, 109072.

Lindsey, PA, Chapron, G, Petracca, LS, Burnham, D, Hayward, MW, Henschel, P, Hinks, AE, Garnett, ST, Macdonald, DW, Macdonald, EA, Ripple, WJ, Zander, K, Dickman, A (2017) Relative efforts of countries to conserve world's megafauna. *Global Ecology and Conservation* **10**, 243-252.

Low, T (2002) 'The new nature.' (Penguin: Camberwell, Victoria).

MacKenzie, DI, Nichols, JD, Royle, JA, Pollock, KH, Bailey, L, Hines, JE (2017) 'Occupancy estimation and modeling: inferring patterns and dynamics of species occurrence.' (Elsevier: San Diego, CA).

Margalida, A, Colomer, MA, Oro, D, Arlettaz, R, Donazar, JA (2015) Assessing the impact of removal scenarios on population viability of a threatened, long-lived avian scavenger. *Scientific Reports* **5**, 16962.

Masters, P, Duka, T, Berris, S, Moss, G (2004) Koalas on Kangaroo Island: from introduction to pest status in less than a century. *Wildlife Research* **31**, 267-272.

McCarthy, DP, Donald, PF, Scharlemann, JPW, Buchanan, GM, Balmford, A, Green, JMH, Bennun, LA, Burgess, ND, Fishpool, LDC, Garnett, ST, Leonard, DL, Maloney, RF, Morling, P, Schaefer, HM, Symes, A, Wiedenfeld, DA, Butchart, SHM (2012) Financial Costs of Meeting Global Biodiversity Conservation Targets: Current Spending and Unmet Needs. *Science* **338**, 946-949.

Metcalf, OC, Ewen, JG, McCready, M, Williams, EM, Rowcliffe, JM, Kurle, C (2019) A novel method for using ecoacoustics to monitor post-translocation behaviour in an endangered passerine. *Methods in Ecology and Evolution* **10**, 626-636.

Miskelly, CM, Powlesland, RG (2013) Conservation translocations of New Zealand birds, 1863–2012. *Notornis* **60**, 3-28.

Morris, SD, Brook, BW, Moseby, KE, Johnson, CN (2021) Factors affecting success of conservation translocations of terrestrial vertebrates: A global systematic review. *Global Ecology and Conservation* **28**, e01630.

Moseby, KE, Blumstein, DT, Letnic, M, West, R (2018) Choice or opportunity: are post-release social groupings influenced by familiarity or reintroduction protocols? *Oryx* **54**, 215-221.

Moseby, KE, Letnic, M, Blumstein, DT, West, R (2018b) Designer prey: Can controlled predation accelerate selection for anti-predator traits in naïve populations? *Biological Conservation* **217**, 213-221.

Nance, AH, Mitchell, W, Clarke, RH, Wilson, M, Brown, SM, MacGregor, NA, Dutson, G, Garnett, ST (2021) Norfolk Island Robin *Petroica multicolor*. In 'The Action Plan for Australian Birds 2020.' (Eds ST Garnett, GB Baker.) pp. 741-744. (CSIRO Publishing: Melbourne).

Parlato, EH, Armstrong, DP (2018) Predicting reintroduction outcomes for highly vulnerable species that do not currently coexist with their key threats. *Conservation Biology* **32**, 1346-1355.

Parlato, EH, Ewen, JG, McCready, M, Parker, KA, Armstrong, DP (2021) A modelling framework for integrating reproduction, survival and count data when projecting the fates of threatened populations. *Oecologia* **195**, 627-640.

- Pierson, JC, Coates, DJ, Oostermeijer, JGB, Beissinger, SR, Bragg, JG, Sunnucks, P, Schumaker, NH, Young, AG (2016) Genetic factors in threatened species recovery plans on three continents. *Frontiers in Ecology and the Environment* **14**, 433-440.
- Rahbek, C (1993) Captive breeding—a useful tool in the preservation of biodiversity? *Biodiversity & Conservation* **2**, 426-437.
- Ramstad, KM, Colbourne, RM, Robertson, HA, Allendorf, FW, Daugherty, CH (2013) Genetic consequences of a century of protection: serial founder events and survival of the little spotted kiwi (*Apteryx owenii*). *Proceedings of the Royal Society B: Biological Sciences* **280**, 20130576.
- Resende, PS, Viana–Junior, AB, Young, RJ, de Azevedo, CS (2020) A global review of animal translocation programs. *Animal Biodiversity and Conservation* **43**, 221-232.
- Richardson, KM, Ewen, JG (2016) Habitat selection in a reintroduced population: social effects differ between natal and post-release dispersal. *Animal Conservation* **19**, 413-421.
- Robert, A (2009) Captive breeding genetics and reintroduction success. *Biological Conservation* **142**, 2915-2922.
- Royle, A, Young, KV (2008) A Hierarchical Model for Spatial Capture-Recapture Data. *Ecology* **89**, 2281-2289.
- Rummel, L, Martínez Abraín, A, Mayol Serra, J, Ruiz Olmo, J, Mañas, F, Jiménez, J, Gómez, JA, Oro de Rivas, D (2016) Use of wild–caught individuals as a key factor for success in vertebrate translocations. *Animal Biodiversity and Conservation* **39**, 207-219.
- Sandbrook, C, Fisher, JA, Holmes, G, Luque-Lora, R, Keane, A (2019) The global conservation movement is diverse but not divided. *Nature Sustainability* **2**, 316-323.
- Seddon, PJ (2010) From Reintroduction to Assisted Colonization: Moving along the Conservation Translocation Spectrum. *Restoration Ecology* **18**, 796-802.
- Seddon, PJ, Griffiths, CJ, Soorae, PS, Armstrong, DP (2014) Reversing defaunation: restoring species in a changing world. *Science* **345**, 406-12.
- Shonfield, J, Bayne, EM (2017) Autonomous recording units in avian ecological research: current use and future applications. *Avian Conservation and Ecology* **12**, 14.
- Sutherland, WJ, Pullin, AS, Dolman, PM, Knight, TM (2004) The need for evidence-based conservation. *Trends in Ecology & Evolution* **19**, 305-308.

Taylor, G, Canessa, S, Clarke, RH, Ingwersen, D, Armstrong, DP, Seddon, PJ, Ewen, JG (2017) Is Reintroduction Biology an Effective Applied Science? *Trends in Ecology & Evolution* **32**, 873-880.

Tetzlaff, SJ, Sperry, JH, DeGregorio, BA (2019) Effects of antipredator training, environmental enrichment, and soft release on wildlife translocations: A review and meta-analysis. *Biological Conservation* **236**, 324-331.

Verdon, SJ, Mitchell, WF, Clarke, MF (2021) Can flexible timing of harvest for translocation reduce the impact on fluctuating source populations? *Wildlife Research* **48**, 458-469.

Verdon, SJ, Watson, SJ, Clarke, MF (2019) Modeling variability in the fire response of an endangered bird to improve fire-management. *Ecological Applications* **29**, e01980.

Verdon, SJ, Watson, SJ, Nimmo, DG, Clarke, MF (2020) Are all fauna associated with the same structural features of the foundation species *Triodia scariosa*? *Austral Ecology* **45**, 773-787.

Walters, JR, Derrickson, SR, Michael Fry, D, Haig, SM, Marzluff, JM, Wunderle, JM (2010) Status of the California Condor (*Gymnogyps californianus*) and Efforts to Achieve Its Recovery. *The Auk* **127**, 969-1001.

Wood, JR, Alcover, JA, Blackburn, TM, Bover, P, Duncan, RP, Hume, JP, Louys, J, Meijer, HJM, Rando, JC, Wilmschurst, JM (2017) Island extinctions: processes, patterns, and potential for ecosystem restoration. *Environmental Conservation* **44**, 348-358.

2. Are we adequately assessing the demographic impacts of harvesting for wild-sourced conservation translocations?

*Mitchell, WF, Boulton, RL, Sunnucks, P, Clarke, RH (2021) Are we adequately assessing the demographic impacts of harvesting for wild-sourced conservation translocations? *Conservation Science and Practice* **4**, e569.

Abstract

Translocation, the human-mediated movement of organisms from one area to another, is a popular tool in conservation management. Wild-caught individuals are more likely to persist following release than those sourced from captive breeding. However, this benefit of obtaining individuals from wild populations must be carefully weighed against the potential harm to the viability of source populations.

In this structured review, we assess the peer-reviewed primary literature that addresses wild-sourced translocation programs. We aim to determine what proportion of studies make *a priori* estimates of the impact of harvesting on source populations, what proportion provide quantitative evidence of demographic trends in source populations following harvest, and which methods are being used to assess impacts of harvesting on source populations.

Of 292 articles reviewed, we identified just 32 instances (11%) where an *a priori* impact on the source population was estimated. The proportion of studies that assess impacts on source populations in a given year has not increased over time. However, studies that make explicit *a priori* comparisons of alternative harvesting strategies are becoming more frequent.

We propose a standardised framework for reporting on management of translocation source populations. Published summaries of wild-sourced translocations should include clear conservation goals, a description of the methods used to assess potential impact, an *a priori* justification based on evidence for the chosen harvesting strategy, an estimated timeline for recovery and a summary of post-removal population trends to assess the efficacy of *a priori* impact assessment. Routinely reporting impacts of harvesting on source populations will inform management when source sustainability is

uncertain, improve transparency and increase the likelihood of successful conservation for many threatened species.

Introduction

Much of biodiversity conservation contributes to one of two fundamental components: the preservation of existing biodiversity assets, or the restoration of those that have been degraded by human activity (Possingham *et al.* 2015). Whilst both approaches are important, preservation is typically considered the higher priority (Dodds *et al.* 2008; Benayas *et al.* 2009; Possingham *et al.* 2015). Restored ecosystems may take years or decades to begin providing desired biodiversity values, require significant financial investment, and yet often still exhibit lower levels of biodiversity than comparable preserved systems (Dodds *et al.* 2008; Benayas *et al.* 2009; Rohr *et al.* 2018). That is not to say that restoration is not important: it is (Lindenmayer *et al.* 2012; De Groot *et al.* 2013; Possingham *et al.* 2015). Rather, conservation practitioners should primarily seek to protect intact biodiversity assets while also engaging in complementary practices framed around restoration and recovery. Defined by the IUCN as '*the human-mediated movement of living organisms from one area, with release in another*', translocation is such a management tool typically employed with goals of restoration or recovery (IUCN/SSC 2013). Translocation is an overarching term that encompasses reintroduction (organisms are returned to an area within their indigenous range but from which they have become extirpated), reinforcement (releases bolster at-risk extant populations), and conservation introduction (organisms are introduced outside their indigenous range for some conservation benefit; IUCN/SSC 2013; Seddon *et al.* 2014). The focal point of any translocation study is invariably the release population, but it is critical that recovery actions are not made at the expense of extant populations from which translocated individuals are sourced (Dimond and Armstrong 2007; Bain and French 2009).

As a popular tool leading to some highly publicised conservation success stories (e.g. Lavery and Moseby 2014; Bolam *et al.* 2020; Greenfield 2020), conservation translocation has received considerable research attention in recent decades (Fischer and Lindenmayer 2000; Taylor *et al.* 2017; Berger-Tal *et al.* 2019; Novak *et al.* 2021). This has led to the establishment and ongoing curation of comprehensive best-practice guidelines. Against such guidelines, we can assess current practices, including those relating to the origin of translocated organisms (IUCN/SSC 2013; Taylor *et al.* 2017). Usually a choice between wild-harvesting or captive breeding, the origin of translocated individuals can influence the success of a translocation as wild-sourced animals typically show higher survival than their captive-bred counterparts (Fischer and Lindenmayer 2000; Rummel *et al.* 2016). Additionally, increasing the size of founder populations can increase the probability of ongoing persistence following release (Fischer and Lindenmayer 2000; Deredec and Courchamp 2007). Accordingly, using larger numbers of individuals from wild sources may be attractive for its likely enhancement of translocation success. Nonetheless, such an approach must be carefully weighed against the potential damage harvesting may cause to wild source populations (Armstrong and Wittmer 2011). For this reason, the

IUCN guidelines for reintroductions and other conservation translocations (2013) explicitly state that *'If removal of individuals or propagules from a source population causes a reduction in its viability in the short term, the translocation objectives should include balancing this with the expected gain in viability of the destination population, so that the species has a greater overall viability than without the translocation, within a stated time period.'* It is also typical that managers must provide regulatory bodies governing translocations in their region with evidence that source populations will not be negatively impacted in the long-term. For example, the Australian state of Victoria's Threatened Fauna Translocation Evaluation Panel (2019) require managers to *'comment on the effect of removing individuals on the source population, including any demographic or genetic effects and whether the removal will affect the viability of the source population.'* Despite these recommendations, a clear framework for assessing demographic impacts on translocation source populations does not appear to be widely used.

Adaptive management is designed to aid decision-making in complex systems while providing an opportunity to increase knowledge of those systems (Williams 2011). Adaptive management of commercially harvested game populations is common (Ramsey *et al.* 2010; Moa *et al.* 2017), but do we apply the same level of rigour to conservation restoration? Under adaptive management, clear goals and quantifiable indicators of success are identified and predictive models are used to inform management actions (Williams 2011; Lacy 2019). The outcomes of management actions are carefully monitored and any knowledge gained is then used to update predictive modelling, in turn, informing future management actions in an iterative process (Williams 2011). Sustainable harvesting models typically rely on the concept of density-dependent vital processes (Pöysä *et al.* 2004; Brook and Bradshaw 2006; Bakker and Doak 2009), whereby a reduction in population density through harvesting can lead to increased fecundity and survival, ultimately resulting in a sustainable yield (Saltz 1998; Brook and Bradshaw 2006). Adaptive management has been applied effectively to the sustainable harvesting of translocation source populations. Dimond and Armstrong (2007) developed *a priori* harvest models, followed by *post hoc* monitoring to quantify and minimise harm to a translocation source population undergoing repeated harvesting. Harvest models were updated with monitoring data prior to any additional harvest events, ensuring the ongoing sustainability of their source population. The adaptive management process, as it applies to the management of wild translocation source populations, is summarised in Fig. 2.1. Adaptive management driven by high-quality ecological data is considered the 'gold standard' when it comes to managing threatened populations (Armstrong *et al.* 2007; Bakker and Doak 2009; Rout *et al.* 2009). However, conservation happens at the coalface. The ecological data necessary for management can take years to collect and for species at the brink of extinction, decisions must frequently be made with imperfect knowledge of the focal system or species (Milner - Gulland *et*

al. 2001). Life history traits, environmental variation, threatening processes and many other factors are also likely to affect the data and analytical requirements to ensure sustainability (Colomer *et al.* 2019; Verdon *et al.* 2021). In light of these realities, it remains unclear to what degree critical analyses of the impact on source populations are implemented during translocation programs.

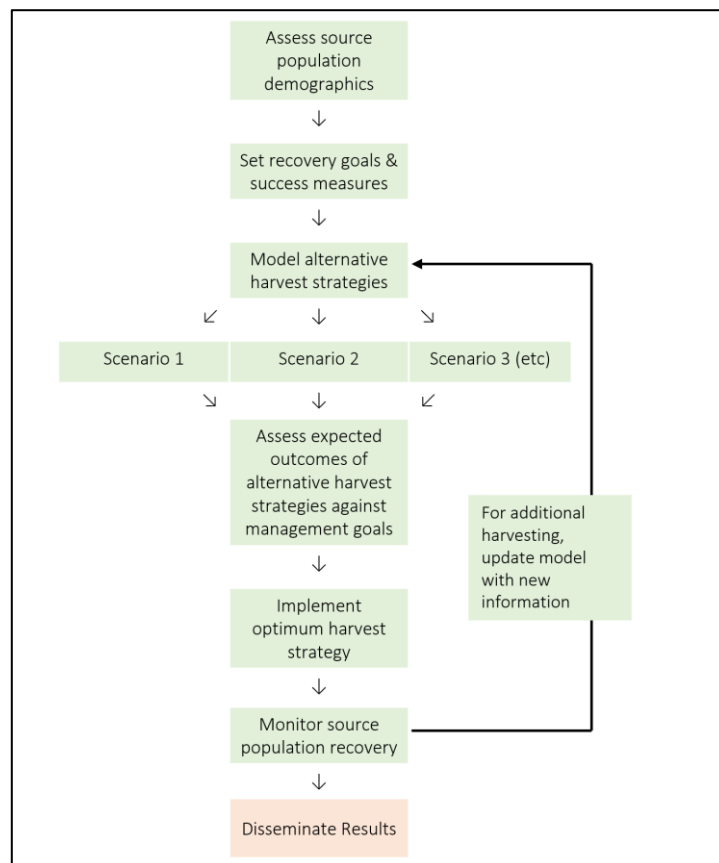


Figure 2.1. A framework for the management of wild populations used as a source in conservation translocation programs. This conceptual model was created by the authors and is based on recommendations highlighted in key literature (Dimond and Armstrong 2007, Williams 2011, Lacy 2019).

Structured reviews are commonly used to aid in objectively assessing practices across a specified timeframe (e.g. Taylor *et al.* 2017; Berger - Tal *et al.* 2019). In this structured review, we assess the peer-reviewed primary literature that addresses wild-sourced translocation programs. We aim to synthesise current practice and determine what proportion of studies make *a priori* estimates of the impact of harvesting. We assess what proportion provide quantitative evidence of population trends following harvest. We seek to determine the realised demographic impacts of harvesting for

translocations on source populations. Finally, we outline a series of recommendations for translocation managers and their advisors, based on our findings.

Methods

Search protocol

We searched for literature within the Web of Science citation search engine's 'Core Collection' and populated the topic field with the search term: "reintroduc* OR translocat*". We limited our search to Web of Science categories 'ecology', 'biodiversity conservation', and 'zoology' for the years 2010–2019 inclusive. We then manually screened all search results for relevance. We included literature with a focus on wild-sourced translocations of terrestrial vertebrate taxa where the motivation for translocation was conservation. Articles that investigated some aspect of a translocation that had already occurred and articles with a key aim of making *a priori* assessments of future translocations were included. Studies that assessed general conservation ecology or genetics of a specific taxon and then suggested translocation as a possible conservation strategy as a concluding remark were not included. To validate the comprehensiveness of our approach, we compiled a list of twenty relevant articles and checked whether they were captured by our search protocol (Table S2.1). All test articles were captured by our search protocol. The distinction between a wild and captive population is not always well defined. For example, fenced wildlife reserves or small intensively managed islands could reasonably fit into either category. In such cases, we deferred to the author's definition of the translocation source. We excluded literature where the focal translocation occurred prior to the year 2000 because our focus was on current best practices. We searched for literature published in the period 2010–2018 on 27th of February 2019 and searched for literature published in 2019 on the 29th of July 2020.

Analyses

Our initial search returned 3,509 publications, excluding duplicates. We read the title and abstract of each study and removed 2,184 studies that did not meet the criteria defined above. Alternative definitions of 'translocation' (e.g. transportation of minerals such as soil or chromosomal translocation), focal taxa that did not meet the inclusion criteria and translocation of captive-reared taxa were common reasons for studies to be removed at this stage of filtering. We then downloaded the full text of the remaining 1,325 publications and assessed each against our inclusion criteria. An additional 1,033 studies were removed. Common reasons for exclusion at this step were, again, a focus on translocations of captive-reared individuals or where the primary motivation was mitigation of human-wildlife conflict. Through this process, we identified 292 relevant peer-reviewed studies for further analysis. We carefully read each article to determine whether and how the potential impact of translocation on

source populations were addressed (Table 2.1). Studies that provided a source population estimate with no additional insight or justification for the potential impact of harvesting were not considered to have assessed source population impact. For each study, we also recorded the journal and year of publication, focal taxa, the focus of the article and the continent where the translocation took place. We used the IUCN Red List of threatened species to determine the threat status of focal species in each study at the time that each study was published (IUCN 2020).

We used binomial regression with a logit link function, year as predictor variable, and the proportion of studies that provide a justification for the impact of harvesting in a given year as response variable to assess how practice has changed over time. We expected that methods used to assess the impact of harvesting would vary between studies but that at least some studies would adopt the best-practice guidelines advocated for in the conservation literature; namely, an explicit comparison of alternative harvesting strategies with potential to inform adaptive management (Fig. 2.1). To assess whether these methods have become more common with time, we used binomial regression with a logit link function, year as predictor variable and the proportion of translocation studies that adopt such methods as response variable. We expected that the proportion of studies that address impacts at the source site would increase with the threat status of the focal species. To test this, we used binomial regression with a logit link function, IUCN threat status as predictor variable and 'whether or not impact at the translocation source site was addressed' as response variable. We compared group means using a *post hoc* Tukey test. We checked assumptions for all generalised linear models using simulated residuals with the 'DHARMA' package and completed all analyses in the statistical environment R (Hartig 2017; R Core Team 2020). The genetic suitability of a source population is another important consideration for translocation managers (Weeks *et al.* 2011; Houde *et al.* 2015). Likewise, it is important that harvesting does not reduce genetic diversity of source populations (Furlan *et al.* 2020). However, in this review we consider only demographic impacts on source populations.

Coverage of the literature

Our dataset included studies of active or planned translocations of 190 unique taxa including 23 reptiles, 75 mammals, 85 birds, and 7 amphibians. Studies originated from all over the world, though there was a clear bias toward wealthy regions with 34% of studies conducted in North America followed by 19% in New Zealand and the Pacific, 14% in western Europe, 12% in Australia and fewer than 10% in each of central and southern America, eastern Europe, Africa and Asia. Studies were published in 73 different peer-reviewed academic journals. Our dataset included studies with a wide range of key areas of focus: 26% investigated factors that may increase translocation success, 23% assessed destination population demographics, 20% made *a priori* assessments of translocation feasibility, 16% assessed

population genetics of taxa that had undergone or were being considered for translocation, 15% assessed behaviour of translocated taxa, 7% focused on assessment of competing management scenarios and fewer than 5% focused on each of physiology or morphology of translocated taxa, impacts of translocated taxa at the destination site, or basic ecology of the focal taxa. While not a systematic review, our structured review approach is consistent with other recent reviews that seek to provide representative insight into current translocation practice (e.g. Taylor *et al.* 2017).

Results

Across 292 peer-reviewed publications documenting conservation translocations of terrestrial vertebrates, we identified only 32 (11%) cases where the impact of harvesting for translocation on the source population was assessed (Fig. 2.2). In an additional 15 cases (5%) animals were 'salvaged' from habitat directly threatened by human impacts. In such cases, no explicit assessment of source population recovery should be expected. In 61 (21%) studies, the size of the source population was reported but any potential impact was not addressed. In 182 (63%) studies, no reference was made to potential impact on, or demographics of, translocation source populations. Two studies reported on reciprocal translocations between populations in attempts to bolster genetic diversity. In total, 52 reintroduction programs were addressed in two or more publications within our dataset. Of these, impact on source population was addressed in at least one publication for 12 (23%) translocation programs (19 publications). The proportion of translocation literature that assessed demographic impact on source populations did not change significantly from 2010 to 2019 ($Z_{1-289} = -0.024$, $p = 0.980$, Fig. 2.2a). However, for studies that explicitly compared alternative harvesting levels to identify an optimum harvesting strategy there was a clear trend for these to be published more recently than those that undertook a more cursory assessment ($Z_{1-289} = -2.164$, $p = 0.031$). We detected a small, non-significant increase in the probability that impact at the source site would be addressed as IUCN threat status of the focal species increased from 'Least Concern' to 'Critically Endangered' (all $Z < 1.446$, all $p > 0.05$; Fig. 2.3).

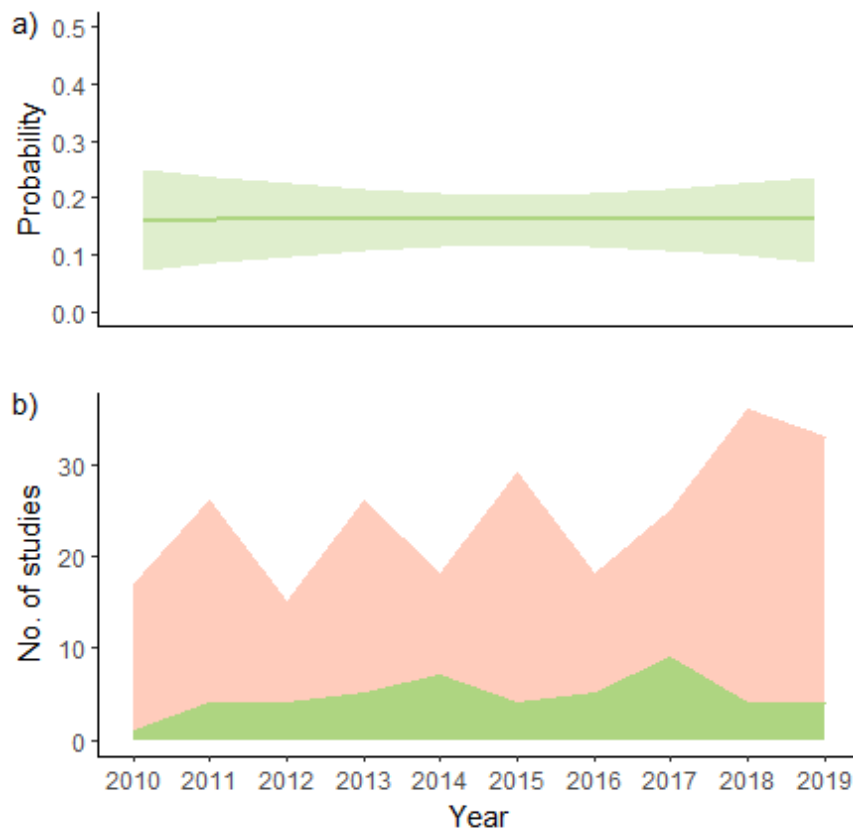


Figure 2.2.a) The mean probability of a study addressing potential impact on translocation source population in a given year, as predicted by logistic regression (the shaded area indicates the 95% CI). b) The number of peer-reviewed papers focusing on wild-sourced, terrestrial, vertebrate translocations published in the years 2010–2019. Green represents those studies that do address the potential impact of harvesting from wild source populations while pink represents those studies that do not. NB: studies that address impact on source populations include cases where individuals were salvaged from a source population at risk of total loss from human impact (e.g. industrial development activities).

Several different rationales were used to justify removing individuals from translocation source populations (Table 2.1). The studies with greatest capacity to influence management used *a priori* population viability (PVA) modelling to assess the potential impact under multiple harvesting strategies. One study took this a step further, adopting an adaptive management approach to harvesting for translocation (see Box 2.1 for summary).



Box 2.1 – A sustainable approach to harvesting the Endangered Apennine yellow-bellied toad (Case Study: Canessa *et al.* 2019, image provided by Dario Ottonello)

The Apennine subspecies of the European yellow-bellied toad - *Bombina variegata pachypus* – is listed as ‘Endangered’ in the IUCN’s red list of threatened species as a result of significant range reduction and population declines over the past 30 years

(Andreone *et al.* 2009). In 2015, a program was initiated with the aim of reintroducing this species to restored habitats within its historic range (Canessa *et al.* 2019). A small and vulnerable source population meant that from the outset this project was carried out with the explicit aim of minimising negative impacts of harvesting. Three translocation strategies were considered: captive breeding, involving the removal of a small number of pairs which would become founders for a captive population and provide a small number of sub-adults seasonally for translocation; ‘head-starting’, involving the removal of eggs from the wild source population to be raised in captivity and then released at the metamorphous stage; and finally, a direct translocation of eggs from the source site to the release site. The authors built a quantitative model of the system and simulated population trajectories at source and release sites under each competing management strategy. Initially, all three strategies were implemented in parallel while monitoring continued across source and release sites. The knowledge gained during the first season of translocations was used to update simulations of future releases. Head-starting was identified as an optimum strategy after two seasons and was adopted for subsequent translocations. The number of juveniles detected at the source population in the two seasons following harvesting events were in the upper range observed since monitoring of this source population began in 2010, suggesting that harvesting was not having a negative impact.

This case study is a comprehensive example of the ideal management of a translocation source population. Canessa *et al.* (2019) explicitly consider the potential impact of harvesting from source populations, compare alternative management strategies using *a priori* modelling and justify their management decisions using quantitative evidence. They provide a detailed summary of their adaptive management process to aid other researchers in adopting a similar approach. Critically, they demonstrate the efficacy of pre-removal impact assessments using monitoring data.

Table 2.1. Justification provided by authors for the harvesting strategy adopted in studies addressing wild-sourced conservation translocations. In total, 292 primary research articles published in the years 2010–2019 were assessed.

Rationale used to justify harvesting for translocation	No. of Studies
<ul style="list-style-type: none"> Quantitative data indicating increase in population size at source site over a period of three or more years prior to the translocation occurring. 	6
<ul style="list-style-type: none"> Authors state that population has reached carrying capacity. In some cases this statement is supported by quantitative data indicating a plateauing demographic trend prior to translocation. In some cases this statement is supported by qualitative observations (e.g. lack of suitable nest sites, available food or breeding territories). 	7
<ul style="list-style-type: none"> Harvesting limited to specified percentage of source population. In such cases the argument is made that harvesting a relatively small proportion of the source population will result in minimal harm but no evidence to support this argument is provided. 	3
<ul style="list-style-type: none"> Explicit modelling, using quantitative demographic data, of impacts to source population under alternative harvesting strategies prior to removal (as illustrated in Fig. 2.1). 	8
<ul style="list-style-type: none"> Subordinate nestlings were removed for translocation from the nest of a species in which siblicide is typical. No additional evidence provided to demonstrate that this approach did not lead to impact on the source population. 	1
<ul style="list-style-type: none"> No <i>a priori</i> estimate of impact but source population is monitored to track population trends post-harvest. 	6
<ul style="list-style-type: none"> Source population managed adaptively with both <i>a priori</i> modelling of impact and <i>post hoc</i> monitoring (Fig. 2.1). 	1
<ul style="list-style-type: none"> Translocated individuals salvaged from area likely to be destroyed or degraded as a result of human impacts. 	15

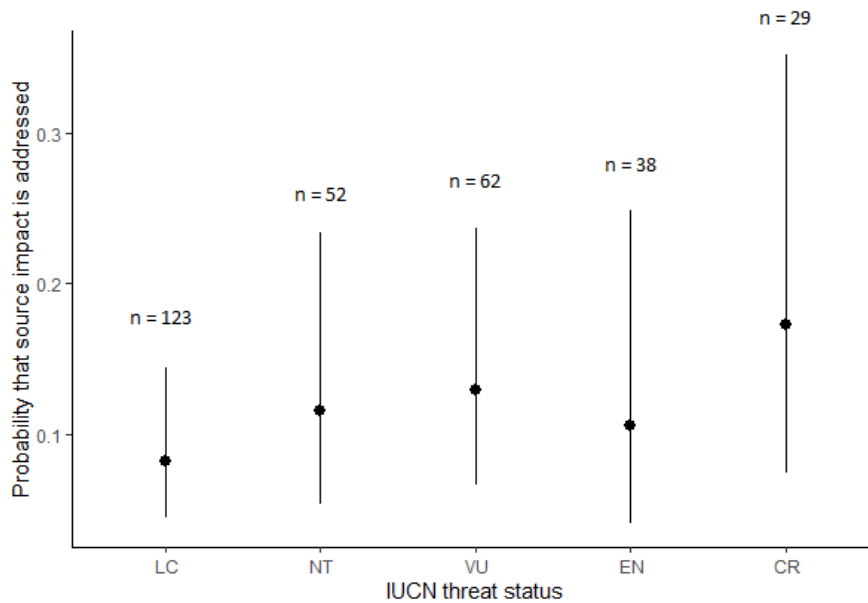


Figure 2.3. The probability (with 95 % CI) that a primary research article focusing on wild-sourced, terrestrial, vertebrate translocations published in the years 2010–2019 will address the potential impact of harvesting on translocation source populations. Studies are grouped by IUCN red list classification of the focal species. LC = Least Concern, NT = Near Threatened, VU = Vulnerable, EN = Endangered, and CR = Critically Endangered.

Discussion

Despite the widespread implementation of translocation as a conservation management tool, we demonstrate that studies providing quantitative evidence of the impact of harvesting from wild source populations remain rare in terrestrial vertebrate translocations. A small subset of studies comprehensively report on population demographics across both source and release populations while providing explicit comparisons of alternative harvesting strategies. Such studies have become more frequent in recent years but still comprise only a small proportion of the translocation literature. Given that protection and restoration are fundamental goals of conservation translocation programs, it is essential that practitioners provide quantitative evidence that such initiatives result in a net positive effect across source and release populations (IUCN/SSC 2013). The inherent risk of ignoring potential harvesting impact has been brought into focus by Margalida *et al.* (2015) who reported that of 57 modelled competing strategies for harvesting of bearded vultures - *Gypaetus barbatus* – for translocation, 77% resulted in source population decline.

The need for conservation management supported by science that explicitly compares alternative management strategies has long been emphasized (Sutherland *et al.* 2004; Taylor *et al.* 2017). In our sample of 292 papers, only the nine studies that adopted an *a priori* modelling approach were able to assess impact under different levels of harvesting. By contrast, 283 of these papers presented no quantitative evidence to suggest that the level of harvesting chosen was the optimum available strategy. As well as allowing managers to identify optimum harvesting strategies and minimise impacts from the outset, harvesting models provide a benchmark for comparison with the results of post-removal monitoring, thus providing the foundations for adaptive management (Armstrong *et al.* 2007; Rout *et al.* 2009).

Some managers have sought to harvest individuals for translocation without any reduction in the natural size of source populations (Ferrer *et al.* 2014). When populations are small, the risks associated with removing individuals for translocation may be exacerbated by inbreeding depression, genetic drift or demographic stochasticity (Norris 2004; Deredec and Courchamp 2007). In such cases, acquiring individuals for translocation with no reduction in source population size may be particularly advantageous. Fecundity may be manipulated by artificially increasing carrying capacity through supplemental feeding (Richardson *et al.* 2013; Ferrer *et al.* 2014; Ferrer *et al.* 2018). This approach may allow harvesting from small populations, while minimising risks associated with the declining population paradigm (Ferrer *et al.* 2014). One study in our dataset suggested that this approach might be a more economically viable source of individuals for translocation than captive breeding, while eliminating many common challenges of captive breeding programs, e.g. expensive infrastructure, adaptation to captivity and loss of predator avoidance behaviour (Ferrer *et al.* 2014). The validity of the data and methods used to reach these conclusions have since been questioned in a critique that nonetheless did not reject the idea that artificially bolstering fecundity may, in some cases, be cheaper than captive breeding as a source for translocations (Margalida *et al.* 2017). While further case studies may be required to demonstrate its effectiveness, artificially bolstering vital rates or carrying capacity of wild source populations may be a useful tool for minimising the impact of harvesting in some translocation programs.

There are many scenarios where the requirement to report on translocation source population demographics may seem overzealous. A translocated species may not itself be of broad conservation concern, with harvesting carried out from large and demographically robust populations. In some scenarios, re-wilding or restoring ecosystem processes may be the primary conservation goal in a translocation program (e.g. Baker *et al.* 2017; Green *et al.* 2018; Perino *et al.* 2019). For example, Elk Island National Park, Canada, has been a source for wapiti - *Cervus canadensis* - reintroductions into various parts of North America for several decades (e.g. Ryckman *et al.* 2010; Muller *et al.* 2018). Wapiti

are abundant in this reserve and number over one million globally (Brook *et al.* 2018). It is unlikely harvesting for translocation poses a serious threat to this species. Similarly, some species have become model examples for studying translocation practice. Island translocations of small passerines in and around New Zealand are routine and managers are among leaders in the field of translocation science. For such species, source and release populations may be small but have been intensively monitored for several decades (e.g. Miskelly and Powlesland 2013; Armstrong *et al.* 2017; Parlato and Armstrong 2018). For those actively involved in management, any impact on source populations would, very reasonably, be considered negligible due to the history of sustainably harvesting from these populations. In both of these examples, a detailed description of harvesting method with rigorous justification for management decisions may not be perceived as beneficial from the perspective of translocation managers on-ground. However, a standard framework around reporting would help capture the confidence in such management strategies while providing transparency and highlighting useful methods for managers working in other systems.

Here we focus solely on the management of translocation source populations. In practice, conservation decisions are made in settings with multiple interacting management goals. Persistence of the release population is typically an overarching goal of any translocation while logistical and financial constraints often influence decision-making (Dimond and Armstrong 2007; McDonald-Madden *et al.* 2011). Increasing the number of founders has been demonstrated to increase the probability of success when establishing new populations through translocation (Fischer and Lindenmayer 2000). When a parallel management goal is to minimise impact associated with obtaining those founders, there is an obvious conflict of objectives. For optimum conservation outcomes, managers must consider the trade-offs between establishing or bolstering destination populations and minimising impacts on source populations while operating within logistical and budgetary limitations.

To ensure the sustainable and transparent management of translocation source populations, we recommend the following approach. Prior to implementing a translocation program, managers should make an initial assessment of the likelihood and magnitude of negatively impacting source populations. If focal taxa are considered 'least concern' by the IUCN red list and translocation managers can provide explicit *prima facie* justification that it is reasonable to expect little impact of harvesting, then additional assessment may not be required. In such cases, managers should provide rationale for this assessment in any published translocation summary. For any taxa that do not meet these two criteria, managers should identify quantifiable goals for minimising impacts on source populations and for measuring recovery following harvesting. Quantitative evidence should be used to make an *a priori* assessment of the impact of removing individuals from wild populations. A range of scenarios should be considered to ensure that the best possible harvesting strategy is identified. Managers should provide a timeline

for recovering populations to return to a pre-removal state. In most cases, such a timeline may be achieved using a population modelling approach (for example, see case study in Box 2.1). Clearly, the demographics of the source population must be well-understood prior to a translocation taking place if they are to be used as a meaningful control against which recovery can be judged. These recommendations largely mirror those made by other active practitioners (Dimond and Armstrong 2007; Taylor *et al.* 2017; Canessa *et al.* 2019; Lacy 2019) and the IUCN (IUCN/SSC 2013). However, we have shown here empirically that the following points are rarely addressed. First, source populations must be monitored following harvest to assess the efficacy of *pre-removal* impact assessments and to demonstrate population recovery. This step is particularly important if populations are to undergo multiple harvesting events, and is a requirement for adaptive management. Second, all publications documenting conservation translocations should address the following with regard to management of source populations:

- a) What quantitative targets have been set to minimise impacts and track recovery?
- b) What proportion of the population is to be harvested (including a breakdown of life-history stages if relevant)?
- c) What methods are being used to assess demographic impact?
- d) Why is the implemented harvesting strategy the most preferred option?
- e) What was the *a priori* projected timeline of recovery for the population undergoing harvest?
- f) Did the population recover from harvesting? How does the rate of recovery compare with pre-removal assessment? (see point e)

In some cases multiple publications investigate different aspects of the same translocation program (e.g. Bennett *et al.* 2012; Bennett *et al.* 2013; Ferrer *et al.* 2014; Ferrer *et al.* 2018). In such cases, at least one study should address the points above in regard to management of source populations, and subsequent publications should reference this.

Conclusion

To reduce risk of overharvesting, we recommend that demographic impacts on translocation source populations be routinely estimated *a priori* and reported. Recovery following harvest should be monitored to ensure the sustainability of the source population and, in scenarios with multiple harvest events, to inform adaptive management. Methods for *a priori* assessment of source populations that formally quantify impact and provide a critical assessment of alternative management options should be prioritised over qualitative or circumstantial estimates of sustainability. Several high-quality case studies have been published illustrating the importance of, and appropriate methods for, sustainable harvesting of translocation source populations. Despite this, just 11% of studies in our sample provided

a justification for removal of individuals from source populations. Routinely reporting impacts of harvesting on source populations will inform management when source sustainability is uncertain, improve transparency and increase the likelihood of ongoing persistence of the increasing numbers of threatened species offered a lifeline through translocation programs.

References

- Andreone, F, Corti, C, Sindaco, R, Romano, A, Giachi, F, Vanni, S, Delfino, G (2009) '*Bombina pachypus* (errata version published in 2016).' Available at <https://dx.doi.org/10.2305/IUCN.UK.2009.RLTS.T54450A11147957.en>. [Accessed 01 March 2021].
- Armstrong, DP, Castro, I, Griffiths, R (2007) Using Adaptive Management to Determine Requirements of Re-Introduced Populations: The Case of the New Zealand Hihi. *Journal of Applied Ecology* **44**, 953-962.
- Armstrong, DP, Le Coeur, C, Thorne, JM, Panfylova, J, Lovegrove, TG, Frost, PGH, Ewen, JG (2017) Using Bayesian mark-recapture modelling to quantify the strength and duration of post-release effects in reintroduced populations. *Biological Conservation* **215**, 39-45.
- Armstrong, DP, Wittmer, HU (2011) Incorporating Allee effects into reintroduction strategies. *Ecological Research* **26**, 687-695.
- Bain, D, French, K (2009) Impacts on a threatened bird population of removals for translocation. *Wildlife Research* **36**, 516-521.
- Baker, CM, Gordon, A, Bode, M (2017) Ensemble ecosystem modeling for predicting ecosystem response to predator reintroduction. *Conservation Biology* **31**, 376-384.
- Bakker, VJ, Doak, DF (2009) Population Viability Management: Ecological Standards to Guide Adaptive Management for Rare Species. *Frontiers in Ecology and the Environment* **7**, 158-165.
- Benayas, JMR, Newton, AC, Diaz, A, Bullock, JM (2009) Enhancement of Biodiversity and Ecosystem Services by Ecological Restoration: A Meta-Analysis. *Science* **325**, 1121-1124.
- Bennett, VA, Doerr, VAJ, Doerr, ED, Manning, AD, Lindenmayer, DB (2012) The anatomy of a failed reintroduction: a case study with the Brown Treecreeper. *Emu - Austral Ornithology* **112**, 298-312.
- Bennett, VA, Doerr, VAJ, Doerr, ED, Manning, AD, Lindenmayer, DB, Yoon, H-J (2013) Causes of reintroduction failure of the brown treecreeper: Implications for ecosystem restoration. *Austral Ecology* **38**, 700-712.

Berger-Tal, O, Blumstein, DT, Swaisgood, RR (2019) Conservation translocations: a review of common difficulties and promising directions. *Animal Conservation* **23**, 121-131.

Bolam, FC, Mair, L, Angelico, M, Brooks, TM, Burgman, M, Hermes, C, Hoffmann, M, Martin, RW, McGowan, PJK, Rodrigues, ASL, Rondinini, C, Westrip, JRS, Wheatley, H, Bedolla-Guzmán, Y, Calzada, J, Child, MF, Cranswick, PA, Dickman, CR, Fessl, B, Fisher, DO, Garnett, ST, Groombridge, JJ, Johnson, CN, Kennerley, RJ, King, SRB, Lamoreux, JF, Lees, AC, Lens, L, Mahood, SP, Mallon, DP, Meijaard, E, Méndez-Sánchez, F, Percequillo, AR, Regan, TJ, Renjifo, LM, Rivers, MC, Roach, NS, Roxburgh, L, Safford, RJ, Salaman, P, Squires, T, Vázquez-Domínguez, E, Visconti, P, Woinarski, JCZ, Young, RP, Butchart, SHM (2020) How many bird and mammal extinctions has recent conservation action prevented? *Conservation Letters* **14**, e12762.

Brook, BW, Bradshaw, CJA (2006) Strength of Evidence for density dependence in abundance time series of 1198 species. *Ecology* **87**, 1445–1451.

Brook, SM, Pluháček, J, Lorenzini, R, Lovari, S, Masseti, M, Pereladova, O, Mattioli, S (2018) *Cervus canadensis* (errata version published in 2019). The IUCN Red List of Threatened Species 2018: e.T55997823A142396828. Available at <https://dx.doi.org/10.2305/IUCN.UK.20182.RLTS.T55997823A142396828.en>. [Accessed 09 June 2021]

Canessa, S, Ottonello, D, Rosa, G, Salvidio, S, Grasselli, E, Oneto, F (2019) Adaptive management of species recovery programs: A real-world application for an endangered amphibian. *Biological Conservation* **236**, 202-210.

Colomer, MÀ, Oliva-Vidal, P, Jiménez, J, Martínez, JM, Margalida, A (2019) Prioritizing among removal scenarios for the reintroduction of endangered species: insights from bearded vulture simulation modeling. *Animal Conservation* **23**, 396-406.

De Groot, R, Blignaut, J, S, VDP, Aronson, J, Elmqvist, T, Farley, J (2013) Benefits of investing in ecosystem restoration. *Conservation Biology* **27**, 1286-93.

Deredec, A, Courchamp, F (2007) Importance of the Allee effect for reintroductions. *Ecoscience* **14**, 440-451.

Dimond, WJ, Armstrong, DP (2007) Adaptive Harvesting of Source Populations for Translocation: A Case Study with New Zealand Robins. *Conservation Biology* **21**, 114-124.

Dodds, WK, Wilson, KC, Rehmeier, RL, Knight, GL, Wiggam, S, Falke, JA, Dalglish, HJ, Bertrand, KN (2008) Comparing ecosystem goods and services provided by restored and native lands. *Bioscience* **58**, 837-845.

Ferrer, M, Morandini, V, Baguena, G, Newton, I, Thompson, D (2018) Reintroducing endangered raptors: A case study of supplementary feeding and removal of nestlings from wild populations. *Journal of Applied Ecology* **55**, 1360-1367.

Ferrer, M, Newton, I, Muriel, R, Báguena, G, Bustamante, J, Martini, M, Morandini, V, Pärt, T (2014) Using manipulation of density-dependent fecundity to recover an endangered species: the bearded vulture *Gypaetus barbatus* as an example. *Journal of Applied Ecology* **51**, 1255-1263.

Fischer, J, Lindenmayer, DB (2000) An assessment of the published results of animal relocations. *Biological Conservation* **96**, 1-11.

Furlan, EM, Gruber, B, Attard, CRM, Wager, RNE, Kerecsy, A, Faulks, LK, Beheregaray, LB, Unmack, PJ (2020) Assessing the benefits and risks of translocations in depauperate species: A theoretical framework with an empirical validation. *Journal of Applied Ecology* **57**, 831 - 841.

Green, DS, Matthews, SM, Swiers, RC, Callas, RL, Scott Yaeger, J, Farber, SL, Schwartz, MK, Powell, RA (2018) Dynamic occupancy modelling reveals a hierarchy of competition among fishers, grey foxes and ringtails. *Journal of Animal Ecology* **87**, 813-824.

Greenfield, P, (2020) 'Up to 48 species saved from extinction by conservation efforts, study finds' *The Guardian*.

Hartig, F (2017) 'DHARMa: residual diagnostics for hierarchical (multi-level/mixed) regression models.' Available at <https://CRAN.R-project.org/package=DHARMa> [Accessed 10 November 2020)].

Houde, ALS, Garner, SR, Neff, BD (2015) Restoring species through reintroductions: strategies for source population selection. *Restoration Ecology* **23**, 746-753.

IUCN (2020) 'The IUCN Red List of Threatened Species.' Available at <https://www.iucnredlist.org>. [Accessed 09 July 2020)].

IUCN/SSC (2013) 'Guidelines for Reintroductions and Other Translocations. Version 1.0.' (IUCN Species Survival Commission: Gland, Switzerland).

Lacy, RC (2019) Lessons from 30 years of population viability analysis of wildlife populations. *Zoo Biology* **38**, 67-77.

Lavery, T, Moseby, K, (2014) 'From the frontline: saving Australia's threatened mammals.' *The Conversation*.

Lindenmayer, DB, Northrop-Mackie, AR, Montague-Drake, R, Crane, M, Michael, D, Okada, S, Gibbons, P (2012) Not all kinds of revegetation are created equal: revegetation type influences bird assemblages in threatened Australian woodland ecosystems. *PLoS One* **7**, e34527.

Margalida, A, Colomer, MA, Oro, D, Arlettaz, R, Donazar, JA (2015) Assessing the impact of removal scenarios on population viability of a threatened, long-lived avian scavenger. *Scientific Reports* **5**, 16962.

Margalida, A, Martínez, JM, Gómez de Segura, A, Colomer, MA, Arlettaz, R, Serrano, D, Pärt, T (2017) Supplementary feeding and young extraction from the wild are not a sensible alternative to captive breeding for reintroducing bearded vultures *Gypaetus barbatus*. *Journal of Applied Ecology* **54**, 334-340.

McDonald-Madden, E, Chades, I, McCarthy, MA, Linkie, M, Possingham, HP (2011) Allocating conservation resources between areas where persistence of a species is uncertain. *Ecological Applications* **21**, 844-858.

Milner-Gulland, E, Shea, K, Possingham, H, Coulson, T, Wilcox, C (2001) Competing harvesting strategies in a simulated population under uncertainty. *Animal Conservation* **4**, 157-167.

Miskelly, CM, Powlesland, RG (2013) Conservation translocations of New Zealand birds, 1863–2012. *Notornis* **60**, 3-28.

Moa, PF, Eriksen, LF, Nilsen, EB (2017) Harvest Regulations and Implementation Uncertainty in Small Game Harvest Management. *Frontiers in Ecology and Evolution* **5**, 1-7.

Muller, LI, Murrow, JL, Lupardus, JL, Clark, JD, Yarkovich, JG, Stiver, WH, Delozier, EK, Slabach, BL, Cox, JJ, Miller, BF (2018) Genetic structure in Elk persists after translocation. *The Journal of Wildlife Management* **82**, 1124-1134.

Norris, K (2004) Managing threatened species: the ecological toolbox, evolutionary theory and declining-population paradigm. *Journal of Applied Ecology* **41**, 413–416.

Novak, BJ, Phelan, R, Weber, M (2021) U.S. conservation translocations: Over a century of intended consequences. *Conservation Science and Practice* **3**, e394.

Parlato, EH, Armstrong, DP (2018) Predicting reintroduction outcomes for highly vulnerable species that do not currently coexist with their key threats. *Conservation Biology* **32**, 1346-1355.

Perino, A, Pereira, HM, Navarro, LM, Fernandez, N, Bullock, JM, Ceausu, S, Cortes-Avizanda, A, van Klink, R, Kuemmerle, T, Lomba, A, Pe'er, G, Plieninger, T, Rey Benayas, JM, Sandom, CJ, Svenning, JC, Wheeler, HC (2019) Rewilding complex ecosystems. *Science* **364**, 1-8.

Possingham, HP, Bode, M, Klein, CJ (2015) Optimal conservation outcomes require both restoration and protection. *PLoS Biology* **13**, e1002052.

Pöysä, H, Elmburg, J, Gunnarson, G, Nummi, P, Sjöberg, K (2004) Ecological basis of sustainable harvesting: is the prevailing paradigm of compensatory mortality still valid? *Oikos* **104**, 612-615.

R Core Team (2020) 'R: A language and environment for statistical computing.' (R Foundation for Statistical Computing: Viena, Austria).

Ramsey, D, Forsyth, DM, Conroy, MJ, Hall, GP, Kingsford, R, Mitchell, G, Roshier, DA, Veltman, CJ, Webb, G, Wintle, B (2010) 'Developing a sustainable harvest model for Victorian waterfowl.' (Arthur Rylah Institute for Environmental Research, Department of Environment, Land, Water and Planning: Heidelberg, Victoria).

Richardson, K, Castro, IC, Brunton, DH, Armstrong, DP (2013) Not so soft? Delayed release reduces long-term survival in a passerine reintroduction. *Oryx* **49**, 535-541.

Rohr, JR, Bernhardt, ES, Cadotte, MW, Clements, WH (2018) The ecology and economics of restoration: when, what, where, and how to restore ecosystems. *Ecology and Society* **23**, 15.

Rout, TM, Hauser, CE, Possingham, HP (2009) Optimal adaptive management for the translocation of a threatened species. *Ecological Applications* **19**, 515-526.

Rummel, L, Martínez Abraín, A, Mayol Serra, J, Ruiz Olmo, J, Mañas, F, Jiménez, J, Gómez, JA, Oro de Rivas, D (2016) Use of wild-caught individuals as a key factor for success in vertebrate translocations. *Animal Biodiversity and Conservation* **39**, 207-219.

Ryckman, MJ, Rosatte, RC, McIntosh, T, Hamr, J, Jenkins, D (2010) Postrelease Dispersal of Reintroduced Elk (*Cervus elaphus*) in Ontario, Canada. *Restoration Ecology* **18**, 173-180.

Saltz, D (1998) A long-term systematic approach to planning reintroductions: the Persian fallow deer and the Arabian oryx in Israel. *Animal Conservation* **1**, 245-252.

Seddon, PJ, Griffiths, CJ, Soorae, PS, Armstrong, DP (2014) Reversing defaunation: restoring species in a changing world. *Science* **345**, 406-12.

Sutherland, WJ, Pullin, AS, Dolman, PM, Knight, TM (2004) The need for evidence-based conservation. *Trends in Ecology & Evolution* **19**, 305-308.

Taylor, G, Canessa, S, Clarke, RH, Ingwersen, D, Armstrong, DP, Seddon, PJ, Ewen, JG (2017) Is Reintroduction Biology an Effective Applied Science? *Trends in Ecology & Evolution* **32**, 873-880.

Translocation Evaluation Panel (2019) 'Threatened Native Fauna. Translocation Proposal Template and Instructions.' Available at <https://www.wildlife.vic.gov.au/managing-wildlife/translocation-of-wildlife> [Accessed 10 November 2020].

Verdon, SJ, Mitchell, WF, Clarke, MF (2021) Can flexible timing of harvest for translocation reduce the impact on fluctuating source populations? *Wildlife Research* **48**, 458-469.

Weeks, AR, Sgro, CM, Young, AG, Frankham, R, Mitchell, NJ, Miller, KA, Byrne, M, Coates, DJ, Eldridge, MD, Sunnucks, P, Breed, MF, James, EA, Hoffmann, AA (2011) Assessing the benefits and risks of translocations in changing environments: a genetic perspective. *Evolutionary Applications* **4**, 709-725.

Williams, BK (2011) Adaptive management of natural resources--framework and issues. *Journal of Environmental Management* **92**, 1346-53.

3. Sustainable harvesting for wild-sourced conservation translocations: A case study using island-endemic passerines

*Mitchell, WF, Nance, A, Clarke, RH (2022) Sustainable harvesting for wild-sourced conservation translocation: A case study using island-endemic passerines – *In review*.

Abstract

Given the frequency with which translocation is implemented as a conservation tool, remarkably little research has assessed the sustainable management of translocation source populations. We sought to quantify population parameters for five endemic island passerines of conservation concern and make an *a priori* estimate of the impact of harvesting from these populations for translocation under multiple scenarios.

Population parameters for our five focal taxa were quantified using distance sampling, based on 297 point surveys conducted in 2019. Intensive nest monitoring data collected between 2018 and 2020 was used to estimate reproductive rates. We used the long-established simulation tool *Vortex* to estimate population viability for all five taxa under a range of alternative harvesting scenarios in forward projections over a 25-year period.

We estimate that Norfolk Island National Park supported 1486 Norfolk robins *Petroica multicolor* (95% CI = 1017–1954), 7184 slender-billed white-eyes *Zosterops tenuirostris* (95% CI = 5817–8551), 2970 Norfolk grey fantails *Rhipidura albiscapa pelzini* (95% CI = 2094–3846), 3676 Norfolk gerygones *Gerygone modesta* (95% CI = 2869–4482), and 1671 Norfolk golden whistlers *Pachycephala pectoralis xanthoprocta* (95% CI = 1084–2259) in 2019. Of 22 harvesting scenarios considered, source population recovery to the level predicted under a ‘no harvest’ setting was projected for 13 scenarios within ten years.

Despite considerable variation in population parameters, we demonstrate all five focal taxa have the potential to sustain harvesting at rates required for future conservation translocations. We provide a clear comparison of differing intensity harvesting strategies for on-ground managers. More broadly, we provide a rare example of an *a priori* assessment of the impact of harvesting for translocation.

Introduction

Conservation translocation refers to the human-facilitated movement of living organisms, from one place to another, for some conservation gain and is a common and effective management tool (IUCN/SSC 2013). The practice has a strong history of aligning research with action and has led to notable success stories over many decades (Fischer and Lindenmayer 2000; Taylor *et al.* 2017; Bolam *et al.* 2020). Despite an impressive track record, a recent review has highlighted that there is room for improvement in the management of populations used as a source for conservation translocations (Mitchell *et al.* 2021; Chapter 2). Of 292 peer-reviewed studies with a focus on wild-harvested conservation translocations, just 11 % presented evidence for an *a priori* assessment of the impact that harvesting for translocation may cause to their focal source population (Mitchell *et al.* 2021; Chapter 2). Recent studies have brought into sharp focus the possible implications of failing to address such impacts. Verdon *et al.* (2021) simulated 48 alternative harvesting scenarios for the endangered mallee emu-wren *Stipiturus mallee* and found that 85 % of scenarios predicted negative impacts on source populations that persisted for five or more years following harvest. Prevailing climatic conditions were a key factor in the ability of source populations to recover following harvest (Verdon *et al.* 2021). Similarly, of 57 simulated scenarios investigating harvesting from bearded vulture *Gypaetus barbatus* source populations, 77 % projected declines (Margalida *et al.* 2015). The International Union for the Conservation of Nature's (IUCN) 'Guidelines for Reintroductions and Other Conservation Translocations' recommend that any reduction in source population viability as a result of harvesting for translocation must be balanced by expected gain for the destination population (IUCN/SSC 2013). For such a goal to be achieved, managers must make some assessment of likely impact and set clear and quantifiable goals around managing such impacts (Lacy 2019).

In the face of uncertainty, effective conservation action is best achieved using structured decision making (Bower *et al.* 2018; Schwartz *et al.* 2018). Structured decision making is a well-established multi-step process that allows empirical assessment of competing management actions in order to address specific goals (Gregory *et al.* 2012). In the context of harvest from wild populations for translocation, management goals should encompass immediate impacts, as well as the capacity of populations to recover from those impacts (Fig. 3.1, Mitchell *et al.* 2021; chapter 2). More specifically, quantitative evidence should be used to assess alternative harvesting strategies, ensuring the strategy chosen is the best option based on available evidence (Mitchell *et al.* 2021; chapter 2). Translocation managers should also formally estimate the extent and duration of recovery following harvest (Mitchell *et al.* 2021; chapter 2). Such predictions are typically achieved within a population viability analysis (PVA) framework (Canessa *et al.* 2019; Lacy 2019; Mitchell *et al.* 2021; chapter 2).

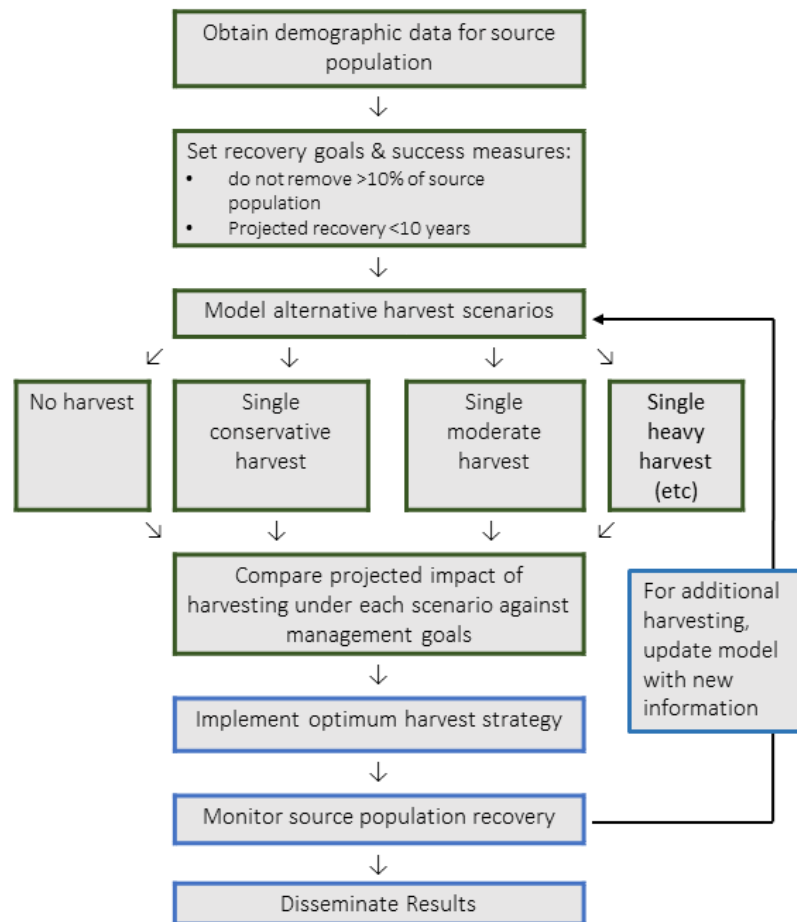


Figure 3.1. A framework for best-practice sustainable harvest of Norfolk Island’s wild endemic passerines for the purpose of conservation translocation. This conceptual model was adapted from Mitchell *et al.* (2021; chapter 2). Boxes outlined in green represent *a priori* steps (i.e. those addressed in this study), while boxes outlined in blue represent post implementation steps.

Population viability analysis refers to a range of modelling approaches that use demographic data to simulate population trajectories into the future (Lacy 2019). PVA has been a key tool to assess multiple conservation management options for several decades (Morris *et al.* 1999; Brook *et al.* 2000; Lacy 2019). PVA requires detailed demographic data to accurately forecast trends (Armstrong and Reynolds 2012; Lacy 2019). Such information is not always available and to obtain comprehensive insight it may be necessary to monitor focal species over several generations (Martin *et al.* 2012; Wolf *et al.* 2015). In the face of immediate threats, conservation decisions must frequently be made with imperfect knowledge of a system (Martin *et al.* 2012). Such uncertainty may reduce the effectiveness of PVA models as a guide for management decisions (Wolf *et al.* 2015). Despite this, PVA often remains the

best tool for assessing the potential outcomes of management interventions (Brook *et al.* 2000; Armstrong and Reynolds 2012; Lacy 2019). To be effective, PVAs should be structured with clear, quantifiable management goals and should explicitly incorporate uncertainty (Lacy 2019).

Island species suffer disproportionately high rates of extinction compared with their mainland counterparts (Johnson and Stattersfield 1990; Caujapé-Castells *et al.* 2010; Kueffer and Kinney 2017). High rates of endemism, small bounded distributions, habitat loss and naivety to introduced predators are common factors contributing to this unfortunate trend (Kier *et al.* 2009; Wood *et al.* 2017). This suite of threats also make translocation a frequently implemented management tool in response to declining island-endemic species (Miskelly and Powlesland 2013; Wood *et al.* 2017). A large number of threatened mainland and island species now have improved conservation outlooks following their translocation to predator-free islands (Miskelly and Powlesland 2013). Newly established island populations may subsequently become a source for further translocations aimed at re-populating areas that have suffered local extinctions (Miskelly and Powlesland 2013). Islands also serve as exemplar model systems for conservation decision making; their reduced size and often simplified ecological structures means formal assessment of alternate management options is an achievable prospect (Kueffer and Kinney 2017).

In this study we sought to estimate population parameters for five endemic island passerines to inform conservation management. We then compared a range of plausible scenarios to estimate how many individuals could be removed from each of our focal populations with a particular focus on the rate at which source populations did or did not recover. We follow the framework for the sustainable management of translocation source populations outlined by Mitchell *et al.* (2021; Chapter 2; Fig. 3.1). We present our approach as a potential exemplar for translocation managers seeking to develop *a priori* predictions on the impact of harvesting using readily accessible tools.

Methods

Study system and taxa

Norfolk Island is an Australian territory located in the western Pacific some ~700 km from the nearest landmass (New Caledonia) and with a land area of 34.6 km² (Fig. 3.2, Parks Australia 2007). High rates of extinction over the last ~200 years (7 avian taxa), mean just five endemic passerine species persist on the island: the Norfolk robin *Petroica multicolor*, slender-billed white-eye *Zosterops tenuirostris*, Norfolk gerygone *Gerygone modesta* and endemic subspecies of golden whistler *Pachycephala pectoralis xanthoprocta* and grey fantail *Rhipidura albiscapa pelzini* (Nance *et al.* 2021a,b,c,d,e). Norfolk Island is populated and has undergone considerable agricultural and residential development. As a

consequence, three of these five threatened birds are largely restricted to the 460 ha Norfolk Island National Park.

Norfolk Island's endemic passerines are threatened by invasive rodents with species persistence likely to be dependent on ongoing rat suppression activities (Nance *et al.* 2021b). The impacts of invasive mammals, especially rodents, was a key driver of previous avian extinctions on Norfolk Island (Garnett and Baker 2021). Conservation translocations present an opportunity to establish the remaining extant taxa on other appropriate islands. Such an approach has been instrumental in the recovery of other critically threatened bird populations (for examples, see Lloyd and Powlesland 1994; Elliott *et al.* 2001; Lee and Jamieson 2001; Kennedy *et al.* 2014). Phillip Island, 6 km south of Norfolk Island, is one potential location where additional populations could be established. Phillip Island, thought to have once been inhabited by a similar bird community to that of Norfolk Island, suffered considerable environmental degradation following the introduction of domestic pigs *Sus scrofa* in 1792 and then goats *Capra hircus* and rabbits *Oryctolagus cuniculus* before 1830 (Coyne 2010). As a result, Phillip Island was completely denuded of vegetation. Since the decline of goats and pigs, the eradication of rabbits by 1988 and concerted revegetation efforts, the island is slowly recovering its indigenous vegetation (Coyne 2010). In fact, restoring a functional songbird community to Phillip Island may have reciprocal benefits for island recovery through the provision of ecosystem services such as pollination, seed dispersal and nutrient cycling (e.g. Halpin *et al.* 2021). Other island groups in the western Pacific may also prove suitable as 'safe harbours' for threatened Norfolk Island passerines. For example a rat eradication program was implemented on Lord Howe Island in 2019 (Wheeler *et al.* 2019) and eradication success there may provide opportunities for Lord Howe Island to host ecological surrogates whilst also conserving species of conservation concern (e.g. the near-threatened Norfolk Island gerygone as an ecological surrogate for the extinct Lord Howe Island gerygone *G. insularis*; Seddon 2010).

Sampling Method

To estimate the population size of our five focal taxa we surveyed at 297 points within Norfolk Island National Park in October 2019 (Fig. 3.2). Norfolk Island National Park is overlaid by a ~50–100 m grid of 'bait lines' traversable on foot that allow access to a network of bait stations used for suppression of invasive rodents. These bait lines often follow natural features such as ridges or valleys and their placement typically involved little to no modification of the natural terrain or vegetation. We placed and accessed survey points using this network of bait lines. At each survey point, an experienced observer recorded the presence and distance from the observer of all individuals of our five focal taxa

that were detected within a five-minute period. Observers began their five-minute survey as soon as they arrived at the point (i.e. no settling period prior to survey, Fig. S3.1, Hutto and Hutto 2020). Distance was recorded at the point of first detection, and birds were excluded if detected > 25 m from the observer. Distance was routinely recorded using a digital range finder but visual obstruction and aural-only detections meant that distance was estimated on occasion.

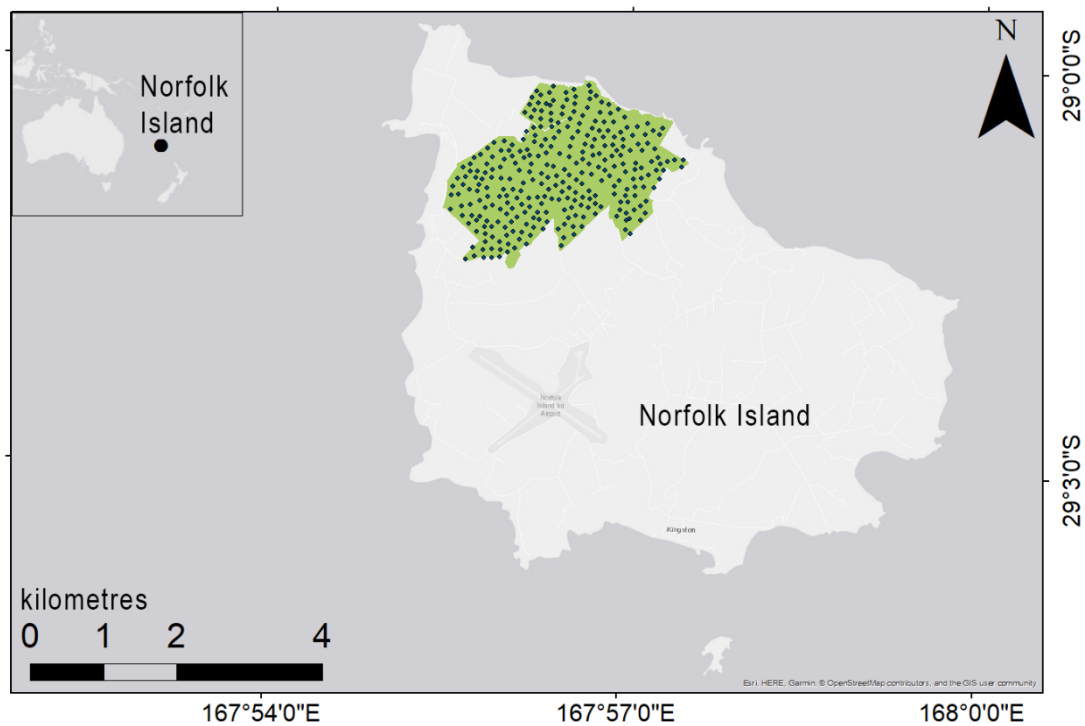


Figure 3.2. Location of all survey points (small dots) for threatened passerine monitoring within Norfolk Island National Park (represented in green). Inset shows location of Norfolk Island in the western Pacific Ocean.

Population Modelling

To estimate population size of our focal species we performed distance-sampling analyses using the package *Distance* in the statistical environment R (Miller *et al.* 2019; R Core Team 2020). Detection probability in *Distance* is modelled using one of three detection functions (termed key functions), i.e., half-normal, hazard-rate, or uniform. A number of adjustment terms can also be added to improve the fit of the base model. To assess if detectability was influenced by external variables we also included combinations of observer, elevation and vegetation class as covariates in distance models for all focal taxa. Following Buckland *et al.* (2012) we selected key function, adjustment terms and the inclusion of covariates based on the Akaike's information criterion (AIC) stopping rule. We assessed model fit using

Q-Q plots and chi-squared goodness-of-fit tests (Buckland *et al.* 2012). Observer was a categorical variable representing one of the two observers that carried out surveys (WFM and AHN). Elevation and vegetation class, a categorical variable with thirteen distinct ground-truthed vegetation classes, were derived from LIDAR data collected in November 2019 (Gallant and Petheram 2021). National Park abundance was calculated for each taxa by multiplying bird density by the size of the national park.

Population Viability and the impact of harvesting

We simulated population trajectories of all five focal taxa over a 25-year period using the software *Vortex10* (Lacy and Pollak 2021). We ran each scenario for 1000 iterations. For each taxon, we parameterised a non-spatial, individual-based population viability model. To assess the suitability of a non-spatial model, we used two binomial generalised linear models assessing the influence of elevation and vegetation class respectively on presence of our five focal taxa. Differences between groups were assessed using a post-hoc Tukey test. We checked assumptions using the package *DHARMA* (Hartig 2017). All models were stochastic, incorporating random variability into simulated population trajectories. Models were structured by age and sex, allowing mate limitation at low population densities, while mortalities and reproduction were modelled to occur yearly.

For each scenario, initial population size was set using results from the 2019 distance sampling described above, while reproductive rate was set using nest survival data collected on Norfolk Island during the period 2018–2020 (Nance *et al.* 2021a,b,c,d,e). During this period, observers carried out regular unstructured, yet intensive, nest searches across Norfolk Island with particular focus on Norfolk Island National Park. The presence, number and life-history status of offspring in any nest detected was recorded and, where possible, a motion-triggered camera was installed to monitor the nest and to capture depredation or fledging events. Nest contents were checked in person every 2–3 days while nests were active. Of those nests with a known outcome, the mean number of offspring fledged per nest and the success rate of nests for each taxon were calculated (Table 3.1).

Despite caution and best practice, population estimates may be influenced by a wide range of biases (MacKenzie *et al.* 2002; Buckland *et al.* 2012; Watson 2017). The threatened bird populations of Norfolk Island are unique and occupy a remarkably small area (Parks Australia 2022). In the face of uncertainty, management decisions should be made conservatively (Johnson 2012). For these reasons, we parameterised simulated population trajectories to begin at the lower 95 % confidence interval for estimated population size (Verdon *et al.* 2021). Carrying capacity for each population was set as the value estimated for population size from distance sampling models described above.

Table 3.1. Parametrisation values for population viability analyses of five endemic passerines in Norfolk Island National Park. The source of the data is also provided for each value.

Taxa	Breeding System	Sex ratio	Breeding years	% Females in breeding pool	Reproductive output per nest attempt (SD)	% nests that result in fledging	Mortality rate (SD)	Max no. broods	Carrying capacity (K) \pm 10 %	Citations
Norfolk gerygone	Monogamous	50:50	1-6 ^A	$= (80 - ((80 - 40) * ((N/K)^2))) * (N / (1 + N))$	1.25 (0.4)	0.57	51.7 ^B (3)	4 ^A	3675	Higgins <i>et al.</i> 2001, Baylis 2017, Nance <i>et al.</i> 2021a.
Norfolk golden whistler	Monogamous	50:50	1-18 ^C	$= (80 - ((80 - 50) * ((N/K)^2))) * (N / (1 + N))$	0.56 (0.18)	0.32	35 ^C (3)	3 ^C	1671	Yom-Tov <i>et al.</i> 1992, Higgins <i>et al.</i> 2001, Nance <i>et al.</i> 2021e.
Norfolk grey fantail	Monogamous	50:50	1-10 ^C	$= (80 - ((80 - 15) * ((N/K)^2))) * (N / (1 + N))$	1.52 (0.22)	0.62	48 ^C (3)	3 ^C	2970	Yom-Tov <i>et al.</i> 1992, Higgins <i>et al.</i> 2001, Nance <i>et al.</i> 2021d.
Norfolk robin	Monogamous	50:50	1-10 ^D	$= (80 - ((80 - 25) * ((N/K)^2))) * (N / (1 + N))$	1.22 (.22)	0.63	42 ^E (3)	3 ^D	1485	Higgins <i>et al.</i> 2001, Baylis 2017, Nance <i>et al.</i> 2021b.
Slender-billed white-eye	Monogamous ^F	50:50	1-19 ^G	$= (80 - ((80 - 54) * ((N/K)^2))) * (N / (1 + N))$	1.11 (0.56)	0.44	55.2 ^G (3)	4 ^F	7184	Higgins <i>et al.</i> 2001, Baylis 2017, Nance <i>et al.</i> 2021c.

^ANew Zealand mainland congeneric *G. igata*

^BAustralian mainland confamilial *Sericornis frontalis*

^CAustralian mainland conspecific

^DAustralian mainland congeneric *P. boodang*

^EAustralian mainland confamilial *Eopsaltria australis*

^FBreeding system of slender-billed white-eye is poorly understood, though cooperative breeding has been recorded. In this model, we assume monogamous reproduction. As population approaches carrying capacity the proportion of breeding females will be reduced (defined by equation 1 in text). Those birds not actively engaging in reproduction may contribute as helpers but no change in fecundity associated with helpers has been included in this model.

^GAustralian mainland congeneric *Z. lateralis*

Vital rate data necessary for model parameterisation were not available for our focal taxa and were estimated based on robust data sourced from closely related species or sub-species (Table 3.1). We assumed that in a single breeding season each taxon would make repeated nest attempts up until the point where they were successful in fledging two independent broods or reached the maximum number of attempts recorded for that species (Gill 1982; van Dongen and Yocom 2005; Debus 2006; Munro 2007). Density-dependent suppression of reproductive output (an individual's reproductive output decreases as population size approaches carrying capacity) is a common phenomenon in natural populations and often forms the basis for sustainable harvest models (Hilborn *et al.* 1995; Pöysä *et al.* 2004). In Vortex, density-dependent suppression of vital rates can be controlled by limiting the percentage of females in the breeding pool $P(N)$ as population size N approaches carrying capacity K using the following default equation where P_0 is the percentage of adult females breeding at low density when there is no suppression of reproductive output, P_k is the percentage of adult females breeding when the population is at carrying capacity, B is a steepness parameter and A is a parameter which determines the strength of Allee effects at low population densities.

$$P(N) = \left(P_0 - \left((P_0 - P_k) * \left(\frac{N}{K} \right)^B \right) \right) * \frac{N}{A + N}$$

For each taxon, we set parameter A and B at default values of 1 and 2 respectively. We set P_0 at 80 % and set P_k such that populations would be stable without any harvest occurring (exponential rate of increase, $r = 0.0 \pm 0.001$, table 3.1).

For each taxon, we assessed the impact of removing individuals for a hypothetical translocation under several alternative harvesting scenarios and compared this with a scenario where no individuals were removed from the population (i.e. 'no harvest'). Each scenario included either a single harvesting event at year one, or a single harvesting event at both years one and two. In each harvesting event either 50, 100 or 150 individuals of even sex ratio were removed from the population, referred to as 'conservative', 'moderate, and 'heavy' harvesting events respectively.

Decision Rules

To minimise impact on Norfolk Island's endemic passerines we set two quantifiable decision rules. First, in any given scenario, the maximum number of individuals removed across harvesting events must not exceed 10% of the total population at the beginning of that scenario. This meant that for some taxa with smaller populations, moderate or heavy harvesting events were not considered. Second, for a harvesting strategy to be considered acceptable, simulated populations must recover in line with the 'No Harvest' scenario within ten years following the final simulated harvesting event. These decision rules were chosen as a point of

reference against which recovery may be measured. Such rules should be established based on expert solicitation where demographic rationale for recovery timelines is not available.

Results

Estimating population size

In total we obtained 783 detections of our five focal species across 297 survey points (Table 3.2). Birds were detected alone or in groups of 2–3 individuals, except for the slender-billed white-eye, which was detected in feeding flocks of up to seven birds. Total estimated population size for our five focal species ranged between 1485 (Norfolk robin) and 7184 (Slender-billed white-eye, Table 3.2). Norfolk gerygone and Norfolk grey fantail have an island-wide distribution and the National Park likely forms part of a meta-population for these taxa. For slender-billed white-eye, Norfolk golden whistler and Norfolk robin, those birds found within the National Park represent the ~global population, with anecdotal observations suggesting fewer than 20 individuals of each of these species occur outside the park and that these individuals likely mostly represent non-breeding dispersers that are largely lost to the population. Neither elevation nor vegetation class were found to be important predictors of detectability for any taxa. Observer was retained as an important predictor of detectability in distance sampling models for Norfolk gerygone and Norfolk grey fantail.

Table 3.2. Population densities of five endemic birds within Norfolk Island National Park. Distance sampling analyses carried out using package *Distance*.

Species	Surveys	Raw Detections	Modelled Detections	Mean group size	Density (birds/Ha)	Total # within National Park	Detection Covariate	Detection function	Previous estimate
Norfolk gerygone	298	185	377.86 ± 42.21	1.24	8.0 ± 0.9	3675.9 (95 % CI = 2869.2- 4482.6)	OBS	Half normal	3800 (Dutson 2012)
Norfolk golden whistler	298	170	170.08 ± 30.5	1.25	3.63 ± 0.65	1671.3 (95 % CI = 1084.1- 2259.3)		Uniform with cosine(1) adjustment	2200 (Dutson 2012)
Norfolk grey fantail	298	197	334.3 ± 50.3	1.13	6.46 ± 0.97	2970.4 (95 % CI = 2094.5- 3846.3)	OBS	Hazard-rate	1600 (Dutson 2012)
Norfolk robin	298	58	149.9 ± 24.15	1.26	3.23 ± 0.52	1485.8 (95 % CI = 1017.0- 1954.6)		Uniform with cosine(1) adjustment	750 (Dawlings 2017)
Slender- billed white- eye	298	173	395.52 ± 38.40	2.31	15.67 ± 1.52	7184.2 (95 % CI = 5817.1- 8551.3)		Uniform with cosine(1) adjustment	4000 (Dutson 2012)

Population viability modelling and the impact of harvesting

We detected no significant influence of vegetation class on the presence of our five focal taxa (all $p > 0.05$, Fig. S3.2). Elevation had a significant influence on presence of Norfolk grey fantail and Norfolk gerygone with more birds occurring at higher elevations (Table S3.1), however, effect size was weak (Fig. S3.3, Table S3.1). Based on these results we concluded that a non-spatial PVA was appropriate for our populations of interest.

Probability of extinction within 25 years in all modelled scenarios remained at 0 (with the caveat that our models assume a stable population in the absence of harvesting, Fig. 3.3). However, the impacts of harvesting for translocation were evident over extended periods of time for some taxa. This was most pronounced for those taxa with the weakest density-dependent reproduction function. Based on the decision rules outlined above, 13 harvesting scenarios of the 22 assessed were considered feasible (Table 3.3). Harvesting of at least 50 individuals was feasible for all five taxa (Table 3.3).

Table 3.3. Number of years required for populations of Norfolk Island passerines to recover from harvesting to a point consistent with the ‘no harvest’ scenario. Acceptable trajectories to recovery (i.e. <10 years) are shown in bold.

Scenario	Norfolk gerygone	Norfolk golden whistler	Norfolk grey fantail	Norfolk robin	Slender-billed white-eye
Single conservative harvest (50 individuals)	5	9	2	5	4
Single moderate harvest (100 individuals)	13	18	5	11	3
Single heavy harvest (150 individuals)	13	-	3	-	5
Two conservative harvests (2 x 50 individuals)	11	>23	1	21	4
Two moderate harvests (2 x 100 individuals)	13	-	4	-	11
Two heavy harvests (2 x 150 individuals)	-	-	-	-	7

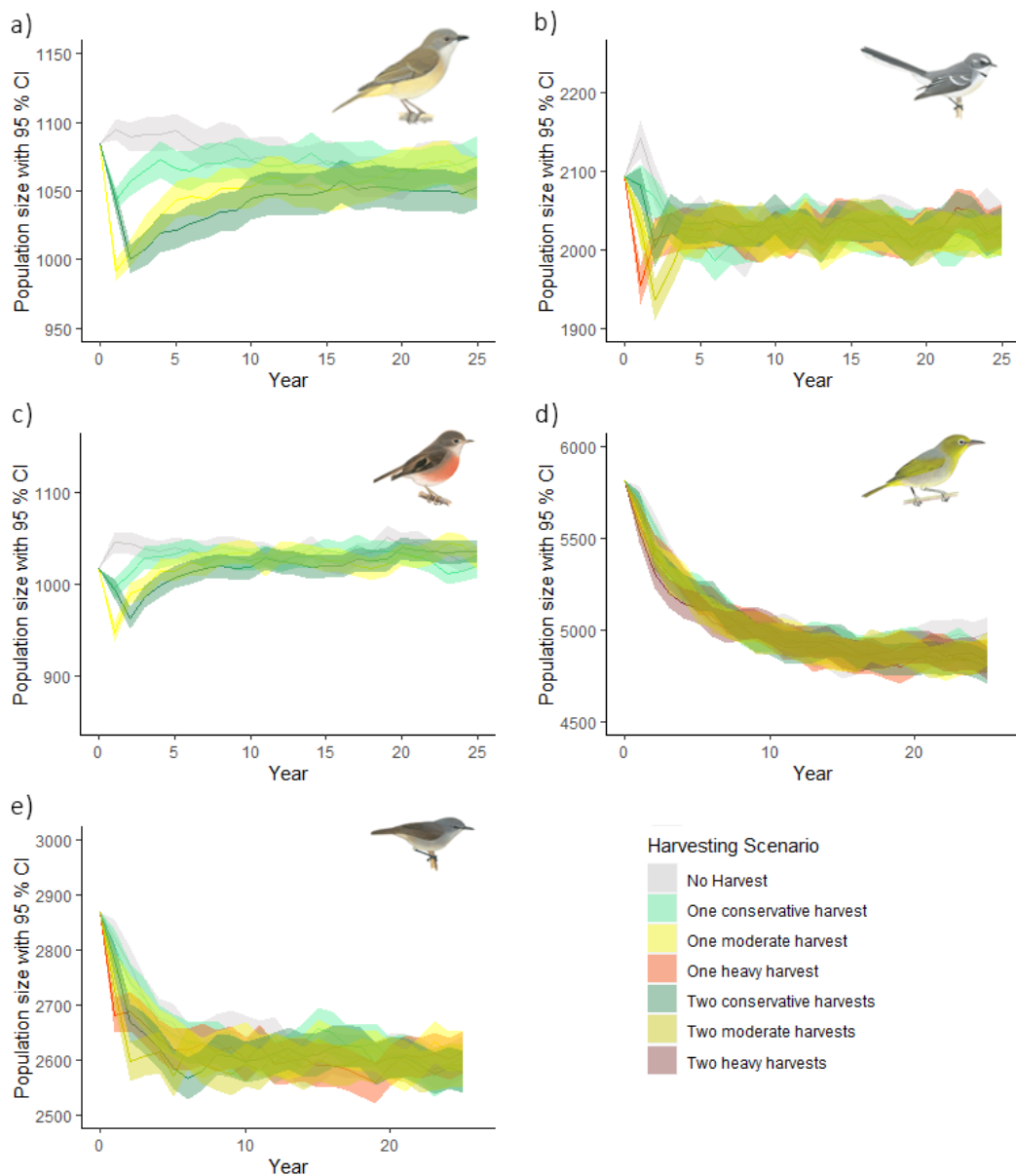


Figure 3.3. Population projections for five endemic passerines in Norfolk Island National Park. Projections for each taxon are modelled under up to seven alternative harvesting scenarios. Owing to our threshold requirement that no more than 10% of the total population be harvested, some species were subjected to a subset of total harvesting scenarios. Harvest scenarios that align with the ‘no harvest’ scenario within ten years of harvest occurring are considered acceptable. Bird images sourced from Menkhorst *et al.* (2017) with permission: a) Norfolk golden whistler *Pachycephala pectoralis xanthoprocta*, b) Norfolk grey fantail *Rhipidura albiscapa pelzelni*, c) Norfolk robin *Petroica multicolor*, d) Slender-billed white-eye *Zosterops tenuirostris*, and e) Norfolk gerygone *Gerygone modesta*.

Discussion

We quantify the demographic impact of harvesting from wild bird populations on Norfolk Island for translocation and provide clear timelines for population recovery. In doing so, we provide a comprehensive example for translocation managers who are seeking to manage translocation source populations sustainably. We also provide an important estimate of population parameters for the remaining endemic passerines on Norfolk Island. By providing examples of populations with varying demographic traits and assessing alternative management scenarios we illustrate how population size, density-dependent reproductive output and scale of harvest can affect the capacity of a population to sustain harvesting. Unfortunately, translocation studies that provide justification for the number of individuals removed from wild populations are rare (Mitchell *et al.* 2021; Chapter 2). Restoration of biodiversity, including through the use of translocations, is a critical component of conservation management but must not come at the expense of maintaining existing intact systems which typically offer greater biodiversity value (Benayas *et al.* 2009; IUCN/SSC 2013; Possingham *et al.* 2015). It is imperative that prior to harvesting for translocation, the demographics of a target population are well understood (Dimond and Armstrong 2007; IUCN/SSC 2013; Verdon *et al.* 2021). If such data is available, then modelling population trends under alternative harvesting scenarios is the necessary and logical next step. Increasing the percentage of *a priori* population assessments for translocations will increase transparency in the field while minimising potential harm to translocation source populations and must become routine in wild-harvested translocation management (Mitchell *et al.* 2021; Chapter 2).

Several factors influenced the number of individuals that could be removed from a population for translocation. We set an *a priori* limit to harvest based on population size but this was not the primary factor that contributed to a population's capacity to recover. Those taxa with the strongest effect of population density on reproductive rate recovered in the shortest period. Density-dependent reproductive rate refers to variability in the number of offspring being produced as a function of population density (Sæther *et al.* 2002; Armstrong *et al.* 2005). This phenomenon acts as the theoretical basis for many sustainable harvesting models (Pöysä *et al.* 2004; Brook and Bradshaw 2006; Bakker and Doak 2009). As population density is reduced by harvesting, compensatory changes in fecundity or mortality result in a sustainable yield (Pöysä *et al.* 2004). This process may be driven by reduced competition for resources such as food or territories (Armstrong *et al.* 2005; Hartmann *et al.* 2017). An understanding of density-dependent processes in a population requires comprehensive data encompassing reproductive output and mortality of individuals across multiple life-history stages and seasons (Abadi *et al.* 2012). Such data can be logistically difficult and expensive to obtain and in this

study, density-dependent processes were estimated based on best-available knowledge. Density-dependent processes have been demonstrated as a common feature across a wide range of taxa (Brook and Bradshaw 2006), and it is reasonable to assume they are an important predictor of reproductive output for the endemic passerines of Norfolk Island. However, density-dependent vital processes are not necessarily associated with compensatory population growth following harvest (Pedersen *et al.* 2004; Cooch *et al.* 2014). *A priori* assumptions about density-dependent processes should be tested experimentally to ensure their accuracy (Pedersen *et al.* 2004; Brouwer *et al.* 2009). Given post-harvest monitoring is a key recommendation for management of source populations, removal of individuals for translocations provides a suitable foundation for exclusion experiments aimed at assessing changes in reproductive vital rates as a function of population density (Mitchell *et al.* 2021; Chapter 2). Any knowledge gained from such an approach may be used to update sustainable harvest models for additional translocations within an adaptive management framework (Canessa *et al.* 2019; Mitchell *et al.* 2021; Chapter 2). Monitoring at the translocation destination population also has capacity to provide important insight into density-dependent vital rates of focal species (Armstrong *et al.* 2005). Following establishment of a new population, and in the absence of significant threats, one may expect an initial rapid rate of population growth associated with high fecundity and survival, followed by a decline as that population approaches carrying capacity. This response has been demonstrated in several reintroduced bird populations including North Island saddleback *Philesturnus rufusater*, takahe *Porphyrio hochstetteri* and Seychelles warbler *Acrocephalus sechellensis* (Armstrong *et al.* 2005; Brouwer *et al.* 2009; Grueber *et al.* 2012). Key factors that make investigating density-dependent processes more tractable within a newly established population in comparison to a source population are that individuals are typically marked for identification and there is reduced potential for immigration influencing population density. Translocations of Norfolk Island passerines must incorporate an assessment of density-dependent vital rates across destination and source populations following removal. This will provide key insight into the processes regulating population growth of Norfolk's threatened passerines and ensure that any future harvesting for translocation of these taxa remains sustainable.

We provide a timely update on the status of Norfolk Island's endemic passerine populations. Surveys of Norfolk Island's bird populations have occurred intermittently since the 1980s (Robinson 1988, 1997; Dutson 2012). Stochastic environmental variation, Allee effects and depredation from invasive rodents all have potential to cause rapid population decline of the Island's birds (Towns *et al.* 2006; Courchamp *et al.* 2008; Dawlings 2017). To inform management and ensure the ongoing persistence of these taxa,

current demographic data is critically important. This is particularly true for the Norfolk robin, slender-billed white-eye and Norfolk golden whistler, as the ~global population of these taxa is restricted to the Norfolk Island National Park. 95 % confidence intervals around our population estimates encompass previous population estimates for Norfolk gerygone and Norfolk golden whistler, indicating populations for these taxa are similar in size to when last surveyed (Dutson 2012). Our estimates for the remaining three taxa indicate net population growth over the last decade (Dutson 2012). Yearly mean rainfall on Norfolk Island during this period varied between 778 mm and 1765 mm (Bureau of Meteorology 2021). Seasonal variation in the size of Norfolk Island's bird populations as a result of climatic variation is likely, and may have contributed to differences in population estimates between surveys. However, without yearly monitoring of population trends little can be inferred about the magnitude of variations in population size caused by climate. Considerable conservation efforts have been expended to realise biodiversity gains on Norfolk Island since the 2007 management plan was implemented and it is probable that these actions have also facilitated population growth (Parks Australia 2007). Parts of NI National Park have been revegetated, while a comprehensive rat suppression program has been ongoing in some form since 1992 with further review and ongoing program improvements in the period 2015-2021 (Robinson 1997; Dutson 2012; Parks Australia 2022). Finally, bias is an ever-present component of ecological modelling which, despite best efforts, cannot be entirely eliminated (Buckland *et al.* 2012). Our estimates for slender-billed white-eye are nearly double that of previous studies, or any other single taxa within the park. Noting the marked departure from previous estimates, the present estimate should be treated with caution. It is possible that the true population size of the slender-billed white-eye may be closer to the lower 95 % confidence interval for this species.

One important limitation in this study was that we had little insight concerning the relationship between the invasive rodent population dynamics and our focal bird population dynamics. A recent study conducted in Norfolk Island National Park compared nest survival of Norfolk robins in areas that were either under active rodent suppression or not (Dawlings 2017). A twofold increase in density of invasive rodents was associated with fecundity that was 20 times lower for Norfolk robins. It was estimated that, in the absence of rodent suppression, Norfolk Island's robin population would be driven to extinction by nest depredation in as little as six years (Dawlings 2017). The population dynamics of invasive rodents clearly have a strong influence on vital rates of endemic passerines. Variation in rodent density, either as a result of seasonal variation, or changes in suppression management should be incorporated into population trajectories for species of conservation concern. To achieve this, future monitoring efforts

should seek to quantify density of both rodents and focal passerines across appropriate time intervals representative of seasonal variation.

Translocation managers in many parts of the world have sought to artificially increase carrying capacity, allowing removal of individuals for translocation with minimal reduction in the natural size of translocation source populations (eg. Richardson *et al.* 2013; Ferrer *et al.* 2014; Ferrer *et al.* 2018). This is often achieved through provision of nest-boxes or supplementary feeding (Ferrer *et al.* 2014). On Norfolk Island, invasive rodents have been demonstrated to suppress fecundity of threatened passerines (Dawlings 2017). Enhancing rodent suppression efforts for a period surrounding a harvesting event may provide surplus individuals (relative to pre-rodent control levels) for translocation with minimal impact on natural source population levels. Such actions would also be expected to hasten population recovery following harvest by removing predation pressure.

Conclusion

We implement a framework for the sustainable management of translocation source populations and, in doing so, provide a real-world example of an *a priori* assessment of the demographic impacts that may arise from harvesting from wild populations for translocation. We estimate that the Norfolk Island populations of Norfolk Gerygone, golden whistler and robin could sustain a single harvest of 50 individuals, the Norfolk grey fantail population could sustain up to two harvests of 100 individuals and the slender-billed white-eye population could sustain two harvests of 150 individuals. Population size and harvest intensity must be considered when assessing the capacity of a population to sustain harvesting but the most important factor influencing rate of recovery is density-dependence of vital rates. Measuring this phenomenon is difficult, but estimates based on best available data still offer insight while providing a foundation for adaptive management of source populations. Assessing the impact of harvesting is vital to ensure the ongoing persistence of source populations and must become standard practice in translocation management. Norfolk Island's remaining endemic forest birds have persisted in spite of the ever-present threat of invasive rodents. However, translocation remains an attractive and feasible option to establish insurance populations against future catastrophe for the five passerines endemic to Norfolk Island.

References

Abadi, F, Gimenez, O, Jakober, H, Stauber, W, Arlettaz, R, Schaub, M (2012) Estimating the strength of density dependence in the presence of observation errors using integrated population models. *Ecological Modelling* **242**, 1-9.

Armstrong, DP, Davidson, RS, Perrott, JK, Roygard, JON, Buchanan, LEN (2005) Density-dependent population growth in a reintroduced population of North Island saddlebacks. *Journal of Animal Ecology* **74**, 160-170.

Armstrong, DP, Reynolds, MH (2012) Modelling Reintroduced Populations: The State of the Art and Future Directions. In 'Reintroduction Biology.' (Eds JG Ewen, DP Armstrong, KA Parker, PJ Seddon.) pp. 165-222. (Wiley-Blackwell: Oxford, UK).

Bakker, VJ, Doak, DF (2009) Population Viability Management: Ecological Standards to Guide Adaptive Management for Rare Species. *Frontiers in Ecology and the Environment* **7**, 158-165.

Baylis, SM (2017) Planting the seeds of a Tree of Death: A new approach, supporting information, test cases, and a national-scale study of population mortality structures from animal-marking records. Doctor of Philosophy thesis, Monash University.

Benayas, JMR, Newton, AC, Diaz, A, Bullock, JM (2009) Enhancement of Biodiversity and Ecosystem Services by Ecological Restoration: A Meta-Analysis. *Science* **325**, 1121-1124.

Bolam, FC, Mair, L, Angelico, M, Brooks, TM, Burgman, M, Hermes, C, Hoffmann, M, Martin, RW, McGowan, PJK, Rodrigues, ASL, Rondinini, C, Westrip, JRS, Wheatley, H, Bedolla-Guzmán, Y, Calzada, J, Child, MF, Cranswick, PA, Dickman, CR, Fessl, B, Fisher, DO, Garnett, ST, Groombridge, JJ, Johnson, CN, Kennerley, RJ, King, SRB, Lamoreux, JF, Lees, AC, Lens, L, Mahood, SP, Mallon, DP, Meijaard, E, Méndez-Sánchez, F, Percequillo, AR, Regan, TJ, Renjifo, LM, Rivers, MC, Roach, NS, Roxburgh, L, Safford, RJ, Salaman, P, Squires, T, Vázquez-Domínguez, E, Visconti, P, Woinarski, JCZ, Young, RP, Butchart, SHM (2020) How many bird and mammal extinctions has recent conservation action prevented? *Conservation Letters* **14**, e12762.

Bower, SD, Brownscombe, JW, Birnie-Gauvin, K, Ford, MI, Moraga, AD, Pusiak, RJP, Turenne, ED, Zolderdo, AJ, Cooke, SJ, Bennett, JR (2018) Making Tough Choices: Picking the Appropriate Conservation Decision-Making Tool. *Conservation Letters* **11**, e12418.

Brook, BW, Bradshaw, CJA (2006) Strength of Evidence for density dependence in abundance time series of 1198 species. *Ecology* **87**, 1445–1451.

Brook, BW, O'Grady, JJ, Chapman, AP, Burgman, MA, Akcakaya, HR, Frankham, R (2000) Predictive accuracy of population viability analysis in conservation biology. *Nature* **404**, 385-387.

- Brouwer, L, Tinbergen, JM, Both, C, Bristol, R, Richardson, DS, Komdeur, J (2009) Experimental evidence for density-dependent reproduction in a cooperatively breeding passerine. *Ecology* **90**, 729-741.
- Buckland, ST, Anderson, DR, Burnham, KP, Laake, JL (2012) 'Distance sampling: estimating abundance of biological populations.' (Springer Science & Business Media: Berlin, Germany).
- Bureau of Meteorology (2021) 'Climate Data Online: Monthly Rainfall, Norfolk island Aero.' Available at <http://www.bom.gov.au/climate/data/> [Accessed 09 August 2021].
- Canessa, S, Ottonello, D, Rosa, G, Salvidio, S, Grasselli, E, Oneto, F (2019) Adaptive management of species recovery programs: A real-world application for an endangered amphibian. *Biological Conservation* **236**, 202-210.
- Caujapé-Castells, J, Tye, A, Crawford, DJ, Santos-Guerra, A, Sakai, A, Beaver, K, Lobin, W, Vincent Florens, FB, Moura, M, Jardim, R (2010) Conservation of oceanic island floras: Present and future global challenges. *Perspectives in Plant Ecology, Evolution and Systematics* **12**, 107-129.
- Cooch, EG, Guillemain, M, Boomer, GS, Lebreton, J-D, Nichols, JD (2014) The effects of harvest on waterfowl populations. *Wildfowl Special Issue* **4**, 220-276.
- Courchamp, F, Berec, L, Gascoigne, J (2008) 'Allee effects in ecology and conservation.' (Oxford University Press: New York).
- Coyne, P (2010) Ecological rebound on Phillip Island, South Pacific. *Ecological Management & Restoration* **11**, 4-15.
- Dawlings, F (2017) Threats of introduced predators to an endemic island passerine during nesting. Honours thesis, Monash University.
- Debus, S, J., S. (2006) Breeding biology and behaviour of the scarlet robin *Petroica multicolor* and eastern yellow robin *Eopsaltria australis* in remnant woodland near Armidale, New South Wales. *Corella* **30**, 59-65.
- Dimond, WJ, Armstrong, DP (2007) Adaptive Harvesting of Source Populations for Translocation: A Case Study with New Zealand Robins. *Conservation Biology* **21**, 114-124.
- Dutson, G (2012) Population densities and conservation status of Norfolk Island forest birds. *Bird Conservation International* **23**, 271-282.

Elliott, GP, Merton, DV, Jansen, PW (2001) Intensive management of a critically endangered species: the kakapo. *Biological Conservation* **99**, 121-133.

Ferrer, M, Morandini, V, Baguena, G, Newton, I, Thompson, D (2018) Reintroducing endangered raptors: A case study of supplementary feeding and removal of nestlings from wild populations. *Journal of Applied Ecology* **55**, 1360-1367.

Ferrer, M, Newton, I, Muriel, R, Báguena, G, Bustamante, J, Martini, M, Morandini, V, Pärt, T (2014) Using manipulation of density-dependent fecundity to recover an endangered species: the bearded vulture *Gypaetus barbatus* as an example. *Journal of Applied Ecology* **51**, 1255-1263.

Fischer, J, Lindenmayer, DB (2000) An assessment of the published results of animal relocations. *Biological Conservation* **96**, 1-11.

Gallant, J, Petheram, C (2021) 'Norfolk Island lidar. v1. CSIRO Data Collection.' Available at <https://data.csiro.au/collections/collection/CI43016>

Garnett, ST, Baker, GB (2021) 'The Action Plan for Australian Birds 2020.' (CSIRO publishing: Melbourne, Australia).

Gill, BJ (1982) Breeding of the grey warbler *Gerygone igata* at Kaikoura, New Zealand. *Ibis* **124**, 123-147.

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: Oxford, UK).

Grueber, CE, Maxwell, JM, Jamieson, IG (2012) Are introduced takahe populations on offshore islands at carrying capacity? Implications for genetic management. *New Zealand Journal of Ecology* **36**, 223-227.

Halpin, LR, Terrington, DI, Jones, HP, Mott, R, Wong, WW, Dow, DC, Carlile, N, Clarke, RH (2021) Arthropod Predation of Vertebrates Structures Trophic Dynamics in Island Ecosystems. *American Naturalist* **198**, 540-550.

Hartig, F (2017) 'DHARMa: residual diagnostics for hierarchical (multi-level/mixed) regression models.' Available at <https://CRAN.R-project.org/package=DHARMa> [Accessed 10 November 2020)].

Hartmann, SA, Oppel, S, Segelbacher, G, Juina, ME, Schaefer, HM (2017) Decline in territory size and fecundity as a response to carrying capacity in an endangered songbird. *Oecologia* **183**, 597-606.

Higgins, PJ, Peter, JM, Steele, WK (2001) 'Handbook of Australian, New Zealand and Antarctic Birds.' (Oxford University Press: Melbourne).

Hilborn, R, Walters, CJ, Ludwig, D (1995) Sustainable Exploitation of Renewable Resources. *Annual Review of Ecology and Systematics* **26**, 45-67.

Hutto, RL, Hutto, RR (2020) Does the presence of an observer affect a bird's occurrence rate or singing rate during a point count? *Journal of Field Ornithology* **91**, 214-223.

IUCN/SSC (2013) 'Guidelines for Reintroductions and Other Translocations. Version 1.0.' (IUCN Species Survival Commission: Gland, Switzerland)

Johnson, AR (2012) Avoiding Environmental Catastrophes: Varieties of Principled Precaution. *Ecology and Society* **17**, 9.

Johnson, T, Stattersfield, A (1990) A global review of island endemic birds. *Ibis* **132**, 167-180.

Kennedy, ES, Grueber, CE, Duncan, RP, Jamieson, IG (2014) Severe inbreeding depression and no evidence of purging in an extremely inbred wild species—the Chatham Island black robin. *Evolution* **68**, 987-95.

Kier, G, Kreft, H, Lee, TM, Jetz, W, Ibisch, PL, Nowicki, C, Mutke, J, Barthlott, W (2009) A global assessment of endemism and species richness across island and mainland regions. *Proceedings of the National Academy of Sciences* **106**, 9322-9327.

Kueffer, C, Kinney, K (2017) What is the importance of islands to environmental conservation? *Environmental Conservation* **44**, 311-322.

Lacy, RC (2019) Lessons from 30 years of population viability analysis of wildlife populations. *Zoo Biology* **38**, 67-77.

Lacy, RC, Pollak, JP (2021) 'Vortex: A stochastic simulation of the extinction process.' (Chicago Zoological Society: Brookfield, Illinois, USA).

Lee, WG, Jamieson, IG (2001) 'The takahe: fifty years of conservation management and research.' (University of Otago Press: Otago, New Zealand).

Lloyd, B, Powlesland, R (1994) The decline of kakapo *Strigops habroptilus* and attempts at conservation by translocation. *Biological Conservation* **69**, 75-85.

- MacKenzie, DI, Nichols, JD, Lachman, GB, Droege, S, Royle, JA, Langtimm, CA (2002) Estimating Site Occupancy Rates When Detection Probabilities Are Less Than One. *Ecology* **83**, 2248-2255.
- Margalida, A, Colomer, MA, Oro, D, Arlettaz, R, Donazar, JA (2015) Assessing the impact of removal scenarios on population viability of a threatened, long-lived avian scavenger. *Scientific Reports* **5**, 16962.
- Martin, TG, Nally, S, Burbidge, AA, Arnall, S, Garnett, ST, Hayward, MW, Lumsden, LF, Menkhorst, P, McDonald-Madden, E, Possingham, HP (2012) Acting fast helps avoid extinction. *Conservation Letters* **5**, 274-280.
- Menkhorst, P, Rogers, DI, Clarke, R (2017) 'The Australian bird guide.' (CSIRO Publishing: Melbourne, Victoria).
- Miller, DL, Rexstad, E, Thomas, L, Marshall, L, Laake, JL (2019) Distance Sampling in R. *Journal of Statistical Software* **89**, 1-28.
- Miskelly, CM, Powlesland, RG (2013) Conservation translocations of New Zealand birds, 1863–2012. *Notornis* **60**, 3-28.
- Mitchell, WF, Boulton, RL, Sunnucks, P, Clarke, RH (2021) Are we adequately assessing the demographic impacts of harvesting for wild-sourced conservation translocations? *Conservation Science and Practice* **4**, e569.
- Morris, W, Doak, D, Groom, M, Kareiva, P, Fieberg, J, Gerber, L, Murphy, P, Thomson, D (1999) A practical handbook for population viability analysis. (The Nature Conservancy: Arlington, Virginia).
- Munro, K (2007) Breeding behaviour and ecology of the grey fantail (*Rhipidura albiscapa*). *Australian Journal of Zoology* **55**, 257-265.
- Nance, AH, Mitchell, W, Brown, SM, Clarke, RH, MacGregor, NA, Ward, R, Garnett, ST (2021a) Norfolk Island Gerygone *Gerygone modesta*. In 'The Action Plan for Australian Birds 2020.' (Eds ST Garnett, GB Baker.) pp. 651-653. (CSIRO Publishing: Melbourne).
- Nance, AH, Mitchell, W, Clarke, RH, Wilson, M, Brown, SM, MacGregor, NA, Dutson, G, Garnett, ST (2021b) Norfolk Island Robin *Petroica multicolor*. In 'The Action Plan for Australian Birds 2020.' (Eds ST Garnett, GB Baker.) pp. 741-744. (CSIRO Publishing: Melbourne).

Nance, AH, Mitchell, W, Clarke, RH, Wilson, M, Brown, SM, MacGregor, NA, Dutson, G, Garnett, ST (2021c) Slender-billed White-eye *Zosterops tenuirostris*. In 'The Action Plan for Australian Birds 2020.' (Eds ST Garnett, GB Baker.) pp. 763-765. (CSIRO Publishing: Melbourne).

Nance, AH, Mitchell, W, Wilson, M, Brown, SM, Clarke, RH, MacGregor, NA, Garnett, ST (2021d) Norfolk Island Grey Fantail *Rhipidura albiscapa pelzelni*. In 'The Action Plan for Australian Birds 2020.' (Eds ST Garnett, GB Baker.) pp. 734-736. (CSIRO Publishing: Melbourne).

Nance, AH, Mitchell, W, Wilson, M, Brown, SM, Clarke, RH, MacGregor, NA, Ward, R, Garnett, ST (2021e) Norfolk Island Golden Whistler *Pachycephala pectoralis xanthoprocta*. In 'The Action Plan for Australian Birds 2020.' (Eds ST Garnett, GB Baker.) pp. 709-710. (CSIRO Publishing: Melbourne).

Parks Australia (2007) Norfolk Island National Park and Norfolk Island Botanic Garden Management Plan 2008-2018. Canberra, Australia.

Parks Australia (2022) Norfolk Island Region Threatened Species Recovery Plan. Canberra, Australia.

Pedersen, HC, Steen, H, Kastdalen, L, Broseth, H, Ims, RA, Svendsen, W, Yoccoz, NG (2004) Weak compensation of harvest despite strong density-dependent growth in willow ptarmigan. *Proceedings: Biological Sciences* **271**, 381-5.

Possingham, HP, Bode, M, Klein, CJ (2015) Optimal conservation outcomes require both restoration and protection. *PLoS Biology* **13**, e1002052.

Pöysä, H, Elmburg, J, Gunnarson, G, Nummi, P, Sjöberg, K (2004) Ecological basis of sustainable harvesting: is the prevailing paradigm of compensatory mortality still valid? *Oikos* **104**, 612-615.

R Core Team (2020) 'R: A language and environment for statistical computing.' (R Foundation for Statistical Computing: Viena, Austria).

Richardson, K, Castro, IC, Brunton, DH, Armstrong, DP (2013) Not so soft? Delayed release reduces long-term survival in a passerine reintroduction. *Oryx* **49**, 535-541.

Robinson, D (1988) 'Ecology and management of the Scarlet Robin, White-breasted White-eye and Long-billed White-eye on Norfolk Island.' (Department of Zoology, Monash University: Clayton, Australia).

Robinson, D (1997) 'An evaluation of the status of the Norfolk island Robin following rat-control and weed-control works in the Norfolk island National Park.' (D. Robinson: Department of Zoology, Monash University: Clayton, Australia).

Sæther, B-E, Engen, S, Matthysen, E (2002) Demographic Characteristics and Population Dynamical Patterns of Solitary Birds. *Science* **295**, 2070.

Schwartz, MW, Cook, CN, Pressey, RL, Pullin, AS, Runge, MC, Salafsky, N, Sutherland, WJ, Williamson, MA (2018) Decision Support Frameworks and Tools for Conservation. *Conservation Letters* **11**, e12385.

Seddon, PJ (2010) From Reintroduction to Assisted Colonization: Moving along the Conservation Translocation Spectrum. *Restoration Ecology* **18**, 796-802.

Taylor, G, Canessa, S, Clarke, RH, Ingwersen, D, Armstrong, DP, Seddon, PJ, Ewen, JG (2017) Is Reintroduction Biology an Effective Applied Science? *Trends in Ecology & Evolution* **32**, 873-880.

Towns, DR, Atkinson, IAE, Daugherty, CH (2006) Have the Harmful Effects of Introduced Rats on Islands been Exaggerated? *Biological Invasions* **8**, 863-891.

van Dongen, WF, Yocom, LL (2005) Breeding biology of a migratory Australian passerine, the golden whistler (*Pachycephala pectoralis*). *Australian Journal of Zoology* **53**, 213-220.

Verdon, SJ, Mitchell, WF, Clarke, MF (2021) Can flexible timing of harvest for translocation reduce the impact on fluctuating source populations? *Wildlife Research* **48**, 458-469.

Watson, DM (2017) Sampling effort determination in bird surveys: do current norms meet best-practice recommendations? *Wildlife Research* **44**, 183-193.

Wheeler, R, Priddel, D, O'Dwyer, T, Carlile, N, Portelli, D, Wilkinson, I (2019) Evaluating the susceptibility of invasive black rats (*Rattus rattus*) and house mice (*Mus musculus*) to brodifacoum as a prelude to rodent eradication on Lord Howe Island. *Biological Invasions* **21**, 833-845.

Wolf, S, Hartl, B, Carroll, C, Neel, MC, Greenwald, DN (2015) Beyond PVA: Why Recovery under the Endangered Species Act Is More than Population Viability. *Bioscience* **65**, 200-207.

Wood, JR, Alcover, JA, Blackburn, TM, Bover, P, Duncan, RP, Hume, JP, Louys, J, Meijer, HJM, Rando, JC, Wilmshurst, JM (2017) Island extinctions: processes, patterns, and potential for ecosystem restoration. *Environmental Conservation* **44**, 348-358.

4. Using experimental trials to improve translocation protocols for a cryptic, endangered passerine

*Mitchell, WF, Boulton, RL, Ireland, L, Hunt, TJ, Verdon, SJ, Olds, LGM, Hedger, C, Clarke, RH (2021) Using experimental trials to improve translocation protocols for a cryptic, endangered passerine. *Pacific conservation biology* – online early.

Abstract

When key ecological information is lacking, conservation translocations should be conducted within an adaptive, experimental framework to maximise knowledge gained, and to increase the probability of success. Here, we investigated whether timing of release or composition of release groups influenced indices of success during a trial reintroduction of the mallee emu-wren *Stipiturus mallee* to Ngarkat Conservation Park, South Australia.

We translocated cohorts of 40 and 38 birds in the Austral autumn and spring of 2018 respectively. We released individuals in small groups, comprising either familiar or unfamiliar birds, and intensively monitored all treatments for two weeks post-release to quantify short-term survival and dispersal. We used occupancy modelling to assess persistence of the translocated population for two years following releases. We also monitored source populations to assess the impact of removals.

Mallee emu-wrens released in spring were more likely to remain at the release site and attempt breeding. Familiarity within a release group did not influence short-term survival. Mallee emu-wren occupancy at the release sites declined following releases and by July 2019 (12–15 months after releases), we could no longer detect any emu-wrens. Density at source populations was lower 12 months after removal compared with pre-harvest levels, though these differences were not significant.

Despite the failure to establish a population, we gained valuable management insights regarding both the focal species, and translocation practice more broadly. Timing of release can influence short-term indices of success. Spring releases should be considered priority actions in future mallee emu-wren translocations.

Introduction

The translocation of threatened species to establish new populations or augment existing populations is frequently employed to conserve species (Fischer and Lindenmayer 2000; Taylor *et al.* 2017). Despite notable successes, translocations have historically been subject to a high failure rate (Taylor *et al.* 2017; Berger–Tal *et al.* 2019). Funding is often a limiting factor in conservation management, and when dealing with vulnerable species, it is critical to maximise positive conservation outcomes (IUCN/SSC 2013). In this light, factors that may influence the success of conservation translocations, including husbandry, social interactions, habitat suitability, number of founders, and genetic diversity, have received considerable research attention (Griffith *et al.* 1989; Dickens *et al.* 2010; Jamieson 2011; Mihoub *et al.* 2011; Parker *et al.* 2012; Tetzlaff *et al.* 2019). For social animals, an ability to form new group associations may increase probability of survival following translocation (Franks *et al.* 2020). In ecosystems susceptible to variable or harsh environmental conditions, timing releases such that they occur when conditions are favourable may increase the likelihood of successful population establishment (Bright and Morris 1994; Hellstedt and Kallio 2005). For efficient resource allocation, managers require a thorough understanding of how these factors will influence their target species (Armstrong *et al.* 2007). Where uncertainty exists, translocations should be designed within an adaptive experimental framework, as far as practicable, to inform future management (Armstrong *et al.* 2007; Taylor *et al.* 2017).

An increase in the use of translocations as a conservation management tool has led to improvements in practices and outcomes for species (Taylor *et al.* 2017). However, several areas have been highlighted where translocation practice and theory can be further aligned. One such example is that long-term persistence following translocation is rarely included as a component of success in the translocation literature (Taylor *et al.* 2017). Research should also more often provide explicit comparisons of alternative management strategies to aid on-ground decision-making (Taylor *et al.* 2017). Managers must also ensure that harvesting for translocation does not negatively impact source populations (Stevens and Goodson 1993; Dimond and Armstrong 2007; Bain and French 2009; Easton *et al.* 2019). This is of particular concern for management of threatened species where source populations are often small and harvesting individuals for translocation may exacerbate threatening processes. Publication bias may also distort perceptions of the effectiveness of translocations as success stories are more likely to be published than failures (Møller and Jennions 2001; Miller *et al.* 2014).

Here, we report on the trial reintroduction of the mallee emu-wren to Ngarkat Conservation Park, South Australia. We investigate whether the timing of release and familiarity of release groups influenced the probability of successful population establishment as these are considered important elements of translocation success (Bright and Morris 1994; Franks *et al.* 2020). As this was the first translocation of the

mallee emu-wren, significant logistical challenges due to the ecological characteristics of the species (e.g. crypsis and evasiveness) also needed to be overcome. We framed the reintroduction in two distinct phases. In 'phase one' (this study), our aim was to trial and optimise capture, transfer and release protocols for mallee emu-wrens, whilst also seeking to establish the foundations of a new population if possible. The management insights gained during this first phase will inform a larger scale 'phase two' translocation, where the overarching goal is to re-establishing a population of mallee emu-wrens in South Australia. In phase one we adopted an experimental approach where mallee emu-wrens were translocated in one of two distinct seasonal cohorts to determine whether timing of release would affect post-release dispersal, survival or the probability of successful reproduction. Release groups comprised either familiar or unfamiliar individuals to determine whether sociality would increase the probability of successful population establishment in future releases. We monitored the translocated population to track population trends and assess the outcomes of the different treatments. In parallel, we monitored the source population trends to assess the impact of harvesting birds for translocation.

Methods

Study Species and system

Endemic to mallee habitats south of the Murray River in South Australia and Victoria, the Endangered mallee emu-wren is a diminutive, hummock grass *Triodia scariosa* specialist, though the species has historically also been found in *Xanthorrhoea* sp. dominated habitats (Fig. 4.1; Brown *et al.* 2009; Paton *et al.* 2009; Verdon *et al.* 2019). Mallee emu-wrens are found in small social groups and are secretive, often only detectable by their high pitched call (Menkhorst *et al.* 2017). Breeding is thought to occur between late August and November (though likely varies with environmental conditions) and females lay clutches of two to three eggs (Higgins *et al.* 2001). Nests are invariably obscured from view within a *Triodia* hummock (Higgins *et al.* 2001). Breeding ecology of mallee emu-wrens remains poorly known, though it is likely similar to that of other emu-wrens (e.g. Maguire and Mulder 2004). Low to moderate levels of genetic diversity have been recorded across mallee emu-wren populations with some evidence of gene flow across the species' range (Brown *et al.* 2013). For management purposes the mallee emu-wren can be considered a single genetic unit (Brown *et al.* 2013, also Chapter 5). In recent decades the global population of the species has declined due to habitat loss, drought, and a series of catastrophic wildfires (Brown *et al.* 2009). By 2014, it was considered extinct in South Australia and all remaining populations were confined to a network of Victorian reserves comprising Murray-Sunset National Park, Hattah-Kulkyne National Park, Wyperfeld National Park, and Nowingi State Forest (hereafter

Murray-Sunset, Hattah, Wyperfeld and Nowingi; Verdon *et al.* 2019; Fig. 4.1). In today's fragmented landscapes, mallee emu-wrens have no capacity to naturally recolonise most areas of suitable habitat following local extinctions due to reserve-scale wildfire. Additionally, the ever-present threat of catastrophic wildfire in currently occupied habitat jeopardises the long-term persistence of the mallee emu-wren (Department of Environment, Land, Water and Planning 2016). A successful translocation would increase the global population of the species, while providing an insurance population against further wildfires in currently occupied habitat. As such, translocation was highlighted as a potential conservation strategy in the national recovery plan for the mallee emu-wren (Department of Environment, Land, Water and Planning 2016). In 2018, we implemented a trial reintroduction of mallee emu-wrens to Ngarkat Conservation Park (hereafter Ngarkat), South Australia.

Emu Springs Track in Ngarkat was chosen as the release site due to the presence of suitable *Triodia* heath habitat, and because it was formerly occupied by mallee emu-wrens, prior to their extirpation by wildfires in 2006 (Paton *et al.* 2009; Fig. 4.1). To mitigate the threat of wildfire at the release site, fuel reduction burns were undertaken by South Australia's Department of Environment, Water and Natural Resources north of Emu Springs Track prior to the translocation to establish a protective fire-break. Additionally, the release site was listed as an environmental asset to be prioritised for protection in the event of wildfire in the area. Mallee emu-wren populations in western Murray-Sunset, Hattah and Nowingi were chosen as sources for translocation. Although mallee emu-wrens occupy *Triodia* mallee habitats at these sites, which is structurally different to the *Triodia* heath dominated habitat at the release site, these source sites were selected for their high density of emu-wrens, accessibility by road, relatively high levels of genetic diversity compared with other populations and because areas of *Triodia* heath habitat with sufficient mallee emu-wrens to sustain harvesting no longer exist (Brown *et al.* 2013; Boulton and Hedger 2018). The number of mallee emu-wrens in the Victorian reserve network was estimated to be ~16,000 for the period 1999–2006 (Brown *et al.* 2009; Boulton and Lau 2015), though a more recent study (conducted after the translocation) estimated the population to number 6,449 (95 % CI: 1,923–12,013) individuals in 2019 (Verdon *et al.* 2021).

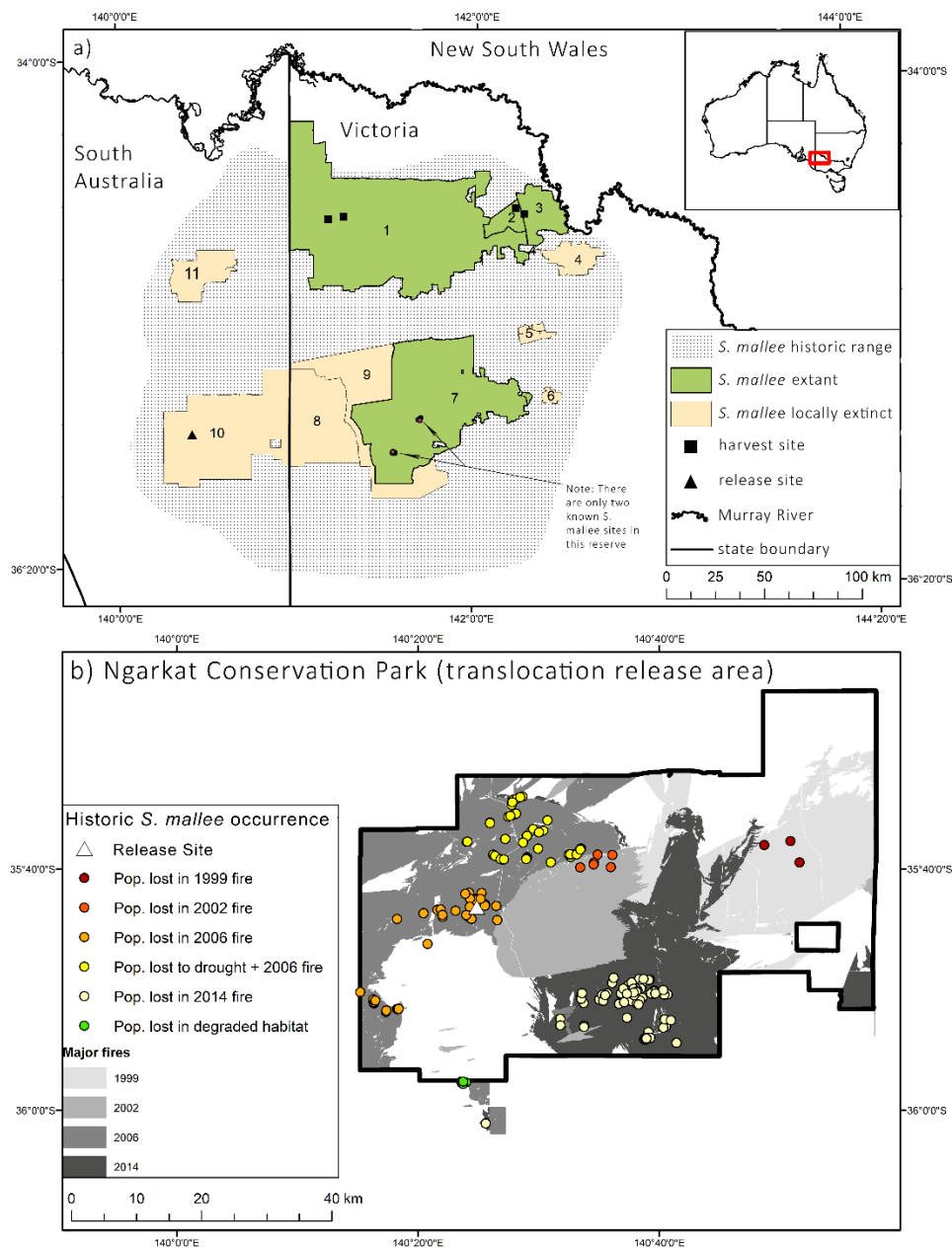


Figure 4.1. a) Early 20th century range of the mallee emu-wren *Stipiturus mallee* with contemporary reserve network overlaid. Reserves depicted are Murray-Sunset National park (1), Nowingi State Forest (2), Hattah-Kulkyne National Park (3), Annuello Flora and Fauna Reserve (4), Bronzewing Flora and Fauna Reserve (5), Wathe Flora and Fauna Reserve (6), Wyperfeld National Park (7), Big Desert State Forest (8), Big Desert Wilderness Park (9), Ngarkat Conservation Park (10), and Billiatt Wilderness Protection Area (11). b) Vegetation age since major fires in Ngarkat Conservation Park with translocation release site and historic records of mallee emu-wrens *S. mallee* overlaid.

Capture and transport

Within their contemporary distribution, mallee emu-wrens have a strong association with *Triodia scariosa*; a dense, interwoven hummock-forming grass (hereafter *Triodia*; Howe 1910; Verdon *et al.* 2020). Mallee emu-wrens have adapted to move ‘rodent-like’ through this complex vegetation and are consequently adept at avoiding capture in mist-nets. For this reason, mallee emu-wrens were captured using a weighted throw-net that was placed over a *Triodia* hummock in which birds were observed to be sheltering (Brown 2011). Each bird was uniquely marked with a combination of two colours. Given an initial concern that leg-bands or VHF transmitters (Hill and Elphick 2011) may cause birds to become snared by *Triodia* spines, individuals released in autumn were marked by painting the 5–10 mm terminal tip of the central two tail feathers with unique combinations of nail polish (Fig. 4.2a). These tail-markings remained for approximately two weeks but were difficult to discern due to degradation of colours and visual obstruction from vegetation. As a result, identification during post-release monitoring was challenging. After a captive trial with rufous-crowned emu-wrens *S. ruficeps*, leg bands were approved for birds released in spring. For this cohort, each bird was marked with a single Australian Bird and Bat Banding Scheme (ABBBS) metal band to which two bands of coloured tape were affixed before a protective epoxy coating was applied (males = right leg, females = left leg; Koronkiewicz *et al.* 2005, Fig. 4.2b). Following capture, mallee emu-wrens were held, singly or in pairs, in custom-made transport boxes approximately 300 mm x 150 mm x 150 mm. Each box had slide access-doors on both ends and a full length soft fly-wire mesh-covered opening at the side, with a ventilated sliding cover for airflow and to allow birds to be observed if required (e.g. during transfer). They were provisioned with live food (mini meal-worms and crickets), and driven to Ngarkat (190 km by road from Murray-Sunset and 270 km from Hattah/Nowingi, Fig. 4.1). The distance between catch and release sites meant that birds were held overnight for approximately 24 hours before release. At the point of release, birds were held for a 30 minute period within transport boxes where the mesh window was positioned to face *Triodia* vegetation (allowing the birds to gain at least some familiarity with their immediate surroundings), but otherwise the protocol was a ‘hard’ release with no supplementary food or shelter. Each group was released in a patch of dense *Triodia* habitat that was at least 400 m distant from any other release group. This density approximated that found within the source population. Mallee emu-wrens from the spring cohort were released in the same general area as the autumn cohort but all spring releases were at least two kilometres from any autumn-released birds that were known to remain at that time.

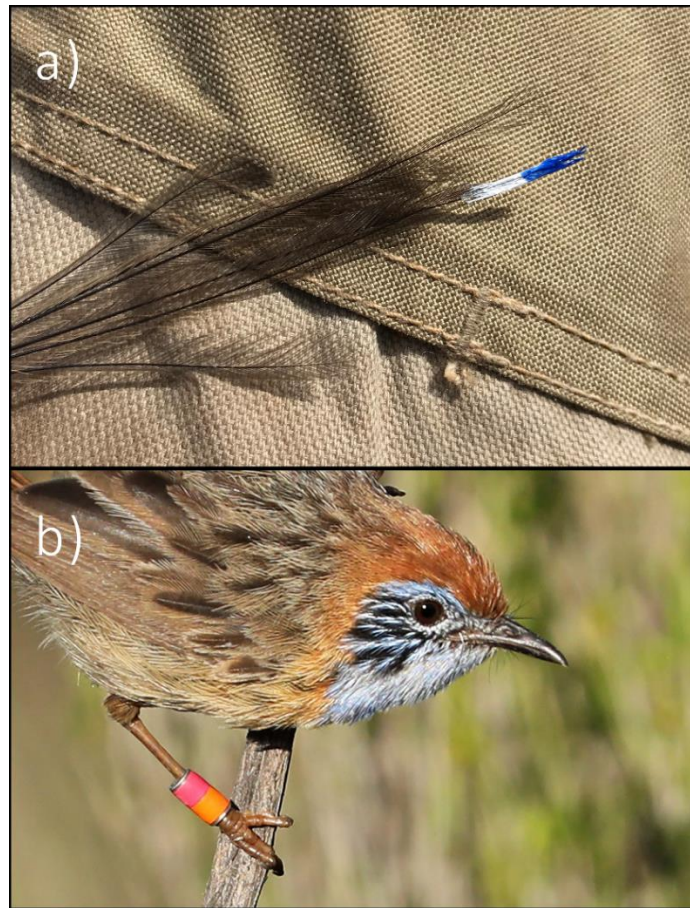


Figure 4.2. Marking methods used to identify translocated mallee emu-wrens in Ngarkat Conservation Park, South Australia. Birds released in Austral autumn were marked using a) a two-colour combination of nail polish on the terminal tip of the central tail feather. This method proved difficult to discern in the field and, consequently, birds released the following spring were marked with a single ABBBS metal band with a two-colour tape, and covered by a protective epoxy coating. Photographs provided by Thomas Hunt.

Timing of release

During autumn, mallee emu-wrens form social groups of up to eight birds and territories are only loosely maintained. As spring approaches, these groups divide into pairs (though sometimes supported by one or more helpers) and establish fixed territories (W. Mitchell; unpublished data). Greater dispersal in autumn may increase the probability that mallee emu-wrens move away from the release site and, in doing so, fail to form a cohesive population (Ward and Schlossberg 2004). Translocation closer to the breeding season may reduce dispersal probability but the stress associated with capture and handling at a time when individuals could already be reproductively active may reduce breeding opportunities immediately after release (Dickens *et al.*

2010). Translocated individuals may suffer elevated mortality compared with the first generation of offspring born at the release site (Armstrong *et al.* 2017). Therefore, it is essential that managers maximise reproductive output in the first breeding season following release. To determine the optimum timing for release, this translocation involved both April (hereafter ‘Austral autumn’) and August (hereafter ‘Austral spring’) release cohorts.

Familiarity of release groups

Maintaining intact social groupings through the capture and transport phases of a translocation may reduce dispersal distances and stress experienced by individuals following release as a result of reduced aggression between individuals (though case studies have shown that this is often not the case; Armstrong 1995; Armstrong and Craig 1995; Franks *et al.* 2020). This protocol requires additional time and labour for effective implementation. Unplanned events, such as mortality during holding, may also necessitate the release of group members that do not have prior familiarity. As such, there is value in understanding how separation from a cohesive social unit will influence an individual’s probability of post-release survival. To test this, release groups within each seasonal cohort contained either ‘familiar’ or ‘unfamiliar’ individuals based on association at capture. Mallee emu-wren groups are typically distributed sparsely and birds within a group forage close to one another. When separate groups do intercept, males and females engage in territorial behaviour, often perching in prominent locations and singing loudly (W. Mitchell; pers. obs.). During such displays it is not unusual for group members perceived by the observer to be subordinate or young to remain quiet and hidden until rival birds have moved away. Given these distinctive behaviours, it is unlikely that mallee emu-wrens from separate groups could be confused for familiar individuals during capture for translocation.

Establishment and persistence at the release site

Monitoring of translocated mallee emu-wrens in Ngarkat followed two distinct protocols: short-term intensive monitoring (10–18 days following final release) and longer-term occupancy monitoring (~2 and ~12 months post release). Short-term intensive monitoring commenced immediately following the first release of each cohort. Experienced observers conducted exhaustive area searches on a daily basis in habitat surrounding release points. The search area encompassed all *Triodia* habitat with 2000 ha of release points. For the autumn release, searches began on 17th April and finished 3rd May. For the spring release, searches began on 23rd August and finished 8th September. Searching began at ~dawn each day and continued until ~midday or until conditions became unsuitable for searching (e.g. high winds, temperatures exceeding 35 C). Searches were also conducted in the late afternoon when conditions were typically cooler and bird activity increased. Birds meeting the criteria for ‘short-term survival’ were those known to be present at the conclusion of the short-

term monitoring period. This assessment did not account for imperfect detectability, however, search effort per unit area was far higher than typical surveys. During these monitoring periods, over 1,200 'person hours' were invested in comprehensively searching suitable habitat surrounding release sites. We defined dispersal as the distance between point of release and last known position for all unique individuals that could be positively identified. For the reasons mentioned above, fewer birds from the autumn cohort were able to be identified. We tested for differences in dispersal between autumn and spring cohorts using linear regression with season as sole predictor variable and dispersal as response variable. We also used linear regression to test for differences in dispersal between familiar and unfamiliar groups from the spring cohort with familiarity as predictor and dispersal as response. We examined diagnostics plots to ensure that our data did not violate assumptions of linear models. We assessed group cohesion between familiar and unfamiliar groups using Fisher's exact test (Fisher 1992). We used a binomial generalised linear model with a logit link function and no additional covariates to assess differences in short-term survival between familiar and unfamiliar groups. We checked assumptions using simulated residuals (no. iterations = 1000) in the 'DHARMA' package (Hartig 2017). All analyses were performed in the statistical environment R (R Core Team 2020).

During the longer-term monitoring we assessed persistence of the translocated population using occupancy modelling based on repeated call-broadcast surveys at 122 key habitat points surrounding the release area. Surveys of fauna populations can be biased when individuals that are present remain undetected (MacKenzie *et al.* 2017). Occupancy modelling uses detection histories from repeated visits at multiple survey points to estimate the probability of detection (p) and occupancy (ψ) at each point (MacKenzie *et al.* 2017). Occupancy modelling relies on the assumption of 'closure', or that the occupancy state (whether the target species is present or absent) at each survey point remains consistent between repeated visits (MacKenzie *et al.* 2017). During July surveys, at least one group of birds was suspected of moving between survey points, hence estimated occupancy for this period may represent an upper estimate. The purpose of occupancy surveys was to assess the long-term persistence of the entire translocated population including both seasonal cohorts. To observe colour markings on a mallee emu-wren leg band, one must typically invest a significant amount of time in careful stalking. This was not feasible during occupancy surveys and, consequently, no attempt was made to differentiate between seasonal cohorts during occupancy modelling. Analyses were carried out using the package 'unmarked' in R (Fiske and Chandler 2011). Ngarkat is characterised by semi-arid heath interspersed with patches of *Triodia* that form at the base of dunes on the south-eastern face. In this habitat mallee emu-wrens move through heath vegetation but are dependent on *Triodia*, and territories typically incorporate these *Triodia* patches. All such patches within a ~2,000 ha area surrounding release points were identified using a combination of topographic data, satellite imagery and ground-truthing. Any two survey

points were separated by at least 150 m. At each point, an observer played a 30 sec recording of mallee emu-wren contact calls at a volume that approximated free-ranging emu-wren calls, and then listened and watched for 30 sec. This survey protocol was repeated once if no birds were detected. Experienced observers visited each point daily for 4 days between July 25th–28th, 2018; October 16th–20th, 2018; April 9th–13th, 2019; and July 30th–August 3rd, 2019. The time period between releases and follow-up surveys varied between the two cohorts due to logistical constraints.

Impact of harvesting at source sites

We conducted power analyses following Guillera-Arroita and Lahoz-Monfort (2012) to assess the feasibility of using occupancy modelling to quantify the impact of harvesting on source populations. The statistical power required to detect a change in occupancy between seasons is influenced by ψ , p , the number of occupancy sites being surveyed (s), and the number of visits to each site (k). Increasing s , to obtain a reasonable confidence (0.8) of detecting a change in occupancy across seasons, diluted the size of the effect we were trying to detect. This was because the number of birds being harvested did not change despite the increase in survey area. Given this inverse relationship between sampling area and relative effect size, we found that occupancy modelling would not be informative in this scenario.

Mallee emu-wrens are highly cryptic and detectability can vary between days. However, during spring, territories typically remain fixed. Therefore, the true abundance of mallee emu-wrens in any area is unlikely to change significantly over 1-5 days. Prior to the removal of mallee emu-wrens that made up the spring cohort, the primary harvest sites in Murray-Sunset and Nowingi were surveyed to establish baseline emu-wren density. Birds sourced for the spring translocation were not removed from any sites used as a source during the autumn translocation. We established 50 survey points, encompassing 200 ha and spaced at 200 m intervals, in a grid at each primary harvest site. Experienced observers visited each point daily for three days and played a 30 sec recording of mallee emu-wren contact calls, followed by a 30 sec period in which the observer listened carefully and scanned for any responding individuals. If no birds were detected this protocol was repeated once (this method mirrored that used during occupancy surveys described above). Where a group was detected, observers approached the group and carefully counted the number of individuals present. Following Bain and French (2009), the survey with the largest number of detections was designated as being closest to the 'true' abundance. Control sites, which were anticipated to support a similar density of mallee emu-wrens, were surveyed using the same method. Each capture site was paired with a 'distant control' at least 2 km from the treatment. A further control site was established adjacent to the treatment site in Nowingi, but this did not occur at the Murray-Sunset site as a patch of suitable habitat of approximately

equal size was not available adjacent to the harvest site. These surveys were repeated 12 months after the translocation (August 2019) to assess the impact of removing birds for translocation, and are ongoing. Here, we report results of monitoring that was undertaken 12 months post-removal. Differences in abundance of mallee emu-wrens between years and treatments at each site were assessed with negative binomial generalised linear models with log link functions using the R package 'MASS' (equation = emu-wren detections $\sim 1 + \text{year} * \text{treatment}$, family = poisson, link-function = log; Venables and Ripley 2002). Interactions between groups were assessed using a post-hoc Tukey test. Assumptions were checked using simulated residuals (no. iterations = 1000) in the 'DHARMa' package.

Results

The autumn cohort of mallee emu-wrens were released in Ngarkat between the 17th and 22nd of April 2018. Twenty-four birds (captured from eight groups) were sourced from Murray-Sunset and 16 (captured from four groups) were sourced from Hattah. The autumn cohort comprised seven 'familiar' groups and two 'unfamiliar' (3–7 birds per group). Spring releases took place between the 23rd and 28th of August 2018. Twenty-two birds (captured from 13 groups) were sourced from Murray-Sunset and 16 birds (captured from eight groups) were sourced from Nowingi. The cohort comprised eight 'familiar' groups and nine 'unfamiliar' groups (2–3 birds per group). All birds within a group were captured at the same reserve. During autumn two individuals died in transit, and a third was injured during the catching process, resulting in mortality. Five mallee emu-wren mortalities occurred during transit in spring. Aside from the individual injured during capture, histopathology and gross necropsy examinations revealed no obvious cause of death for the other seven individuals. However, it was likely that stress relating to the capture and translocation process was responsible for the deaths of at least some individuals. In total, 85 mallee emu-wrens were harvested from source populations.

Measures of success

Of the 40 birds released in autumn, 14–17 individuals distributed across 4–5 groups were known to be present at the conclusion of short-term intensive area searches on May 3rd 2018. Painted-tail markings had been difficult to read throughout this monitoring period due to cryptic behaviour and frequent, rapid tail movements. Difficulties were exacerbated by tail-moult and further deterioration of markings, leading to uncertainty of the number of individuals remaining. Of the 38 birds released in spring, at least 27 individuals distributed across 15 groups persisted until the conclusion of intensive short-term monitoring on September 8th 2018. This included an additional individual from this cohort that was subsequently identified at this site in October 2018.

Birds released in spring were more likely to remain close to their release site when compared with autumn releases, and many exhibited behaviour indicative of breeding within two weeks of release (Fig. 4.3). By contrast, known dispersal was significantly higher in autumn when compared with spring ($F_{1,59} = 44.2$, $p < 0.001$, Fig. 4.3). Values presented here relating to short-term survival, dispersal and reproductive output relate only to birds of known fate. Several birds were never resighted following release and this may have resulted from any combination of cryptic behaviour, mortality or dispersal. However, the highest concentration of suitable mallee emu-wren habitat in Ngarkat occurs in the immediate area surrounding release sites. This area was comprehensively surveyed throughout the post-release monitoring period and birds dispersing beyond this area can reasonably be considered lost from the population, as any chance of renewed contact was unlikely, whilst a decline in suitable *Triodia* habitat beyond this area further reduced the probability of long-term persistence.

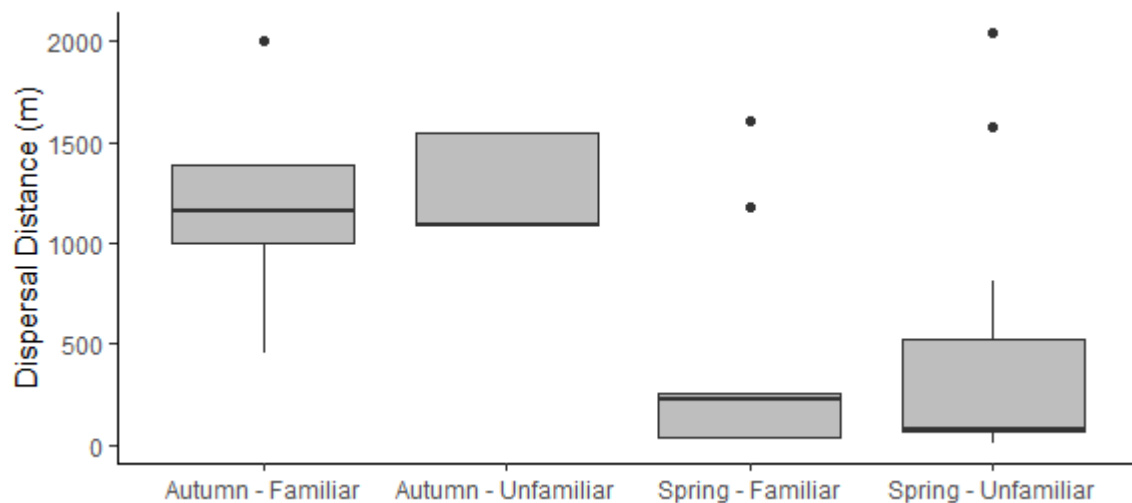


Figure 4.3. Mean dispersal of mallee emu-wrens that could be re-detected following release in Ngarkat Conservation Park, South Australia. Austral autumn and spring cohorts comprised 40 and 38 birds respectively. Each cohort was further divided into small groups containing either familiar or unfamiliar birds based on association at capture.

The challenge of identifying birds from the autumn cohort meant that it was not possible to assess how familiarity between release group members influenced group cohesion, dispersal, and persistence at the release site. By contrast, with colour-banded individuals in the spring release, individual identifications were more readily obtained. Of those spring cohort birds present at the release site at the conclusion of monitoring, 82 % of birds released in familiar groups maintained group fidelity compared with 38 % released with unfamiliar birds ($p = 0.047$, Table 4.1). There was no significant difference in known survival ($z_{1,37} = 1.19$, $p =$

0.232) between birds released with either familiar (probability of survival = 0.65, 95 % CI = 0.40–0.83) or unfamiliar conspecifics (probability of survival = 0.76, 95 % CI = 0.54–0.90). Similarly, dispersal did not differ significantly between familiar and unfamiliar groups ($F_{1-19} = 0.06$, $p = 0.817$, Fig. 4.3).

For longer-term success mallee emu-wren occupancy in Ngarkat declined steadily following releases until August 2019, after which point we no longer detected any birds (Fig. 4.4).

Table 4.1. Summary of mallee emu-wren translocation to Ngarkat Conservation Park, South Australia. Mallee emu-wrens were released in 2018, as part of either an Austral autumn or spring cohort. Each cohort was further separated into small groups comprising either familiar or unfamiliar birds based on their association at capture.

	No. released	Mortalities during holding	Presence at release site 12 days after final release (n, %)	Proportion to stay with release group (n, %)	Surviving to breeding attempt**
Autumn*	40	2	n = 14-17 (35-42.5 %)	NA	3
Spring	38	5	n = 27 (71%)		9
-familiar			n = 11 (64%)	n = 9 (82%)	4
-unfamiliar			n = 16 (76%)	n = 6 (38%)	5

*Identification of mallee emu-wrens released in autumn was hindered by deterioration of identifying colour marks

** Three additional individuals were detected in breeding groups but could not be assigned to a seasonal cohort.

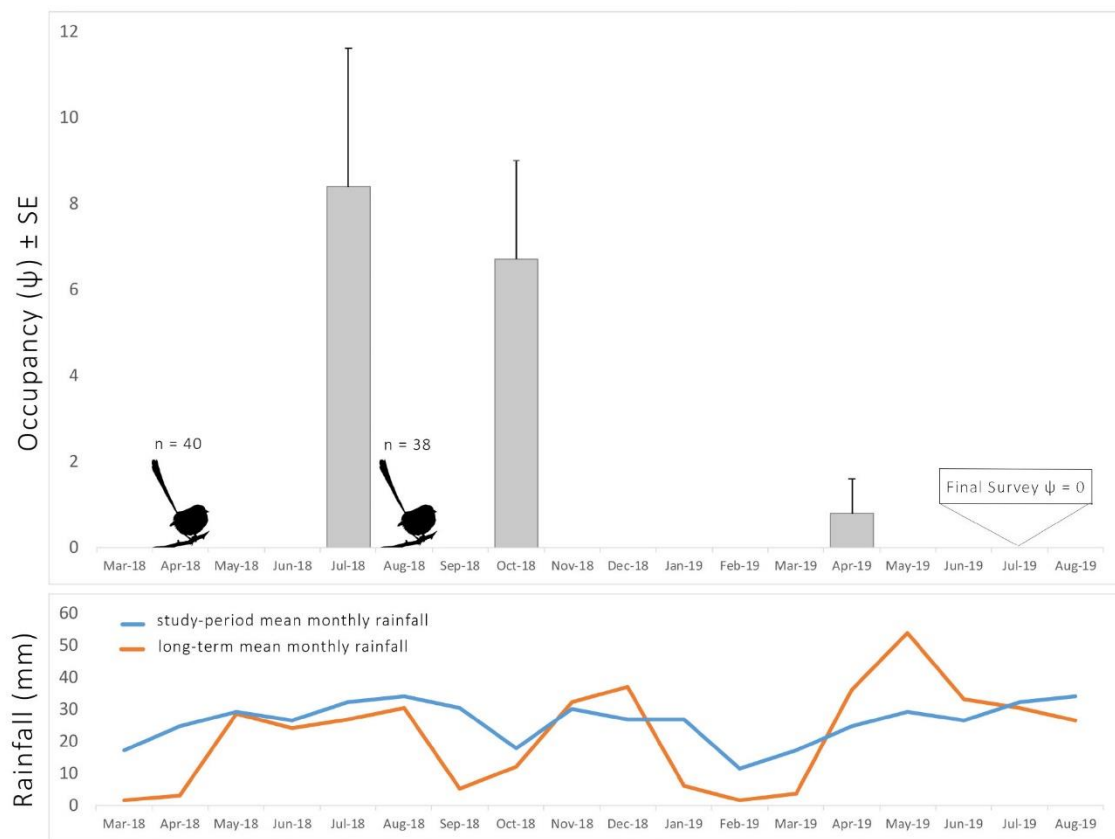


Figure 4.4. Timeline illustrating population change following mallee emu-wren translocations to Ngarkat Conservation Park, South Australia and monthly rainfall over the same time period. Emu-wren silhouettes represent releases of 40 and 38 birds respectively. Bars depict mallee emu-wren occupancy (ψ) \pm standard error based on repeated playback surveys at 122 key habitat points surrounding release sites. Occupancy surveys occurred in July 2018, October 2018, April 2019 and July 2019.

Reproduction at the release site

During occupancy surveys at Ngarkat in October 2018 and additional unstructured searches in December 2018, breeding behaviour was observed on multiple occasions. Ultimately, 15 birds from seven distinct groups were confirmed to have contributed to a nesting attempt (based on discoveries of nests containing eggs/chicks or the presence of fledglings with adults). Of the 12 birds that could be identified, 9 were from the spring release cohort (Table 4.1). Of the three unidentified birds, in two cases a parent had disappeared prior to discovery of the nest and was therefore not identified, while for one female the presence or absence of a band could not be confirmed due to cryptic behaviour. We observed some indication of attempted breeding (e.g. courtship displays, distraction displays indicative of active nests) in an additional three pairs (two spring vs one autumn group), but breeding was not confirmed.

Impact of harvest on the source population

At Nowingi, inter-annual variation (i.e. the factor 'year') was an important predictor of mallee emu-wren abundance with greater numbers estimated pre-harvest compared with post-harvest ($z_{1-299} = 2.291$, $p = 0.022$; Fig. 4.5a). Treatment was not an important predictor of emu-wren abundance, indicating that the effect of year was not due to the impact of harvest. At Murray-Sunset, abundance of mallee emu-wrens did not significantly differ by year or treatment ($z_{1-199} = 0.480$, $p = 0.631$, Fig. 4.5b). At both Murray-Sunset and Nowingi the difference in population size between years was greater at harvest and adjacent control sites when compared to distant controls, though these differences were non-significant (all $z < 2.515$; all p -values > 0.05). We detected no significant interaction between year and treatment at either site.

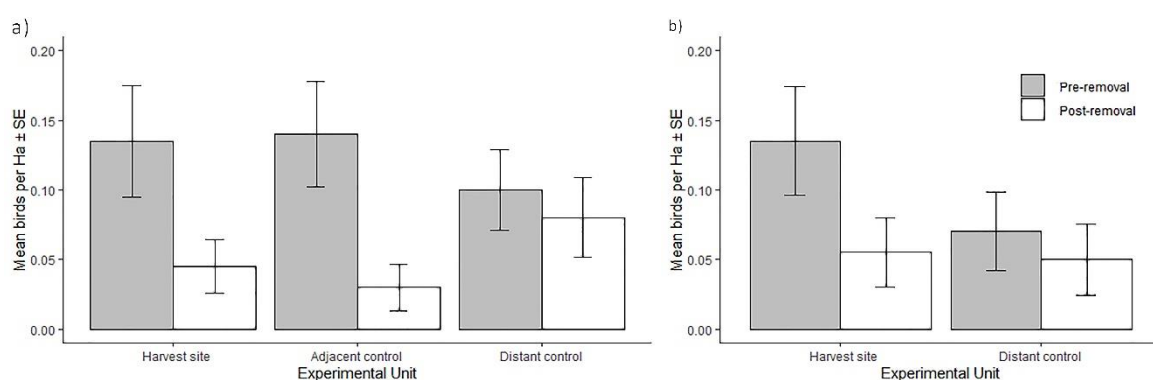


Figure 4.5. Maximum abundance of mallee emu-wrens before and 12 months after birds were removed for translocation at source and control sites in a) Nowingi State Forest and b) Murray-Sunset National Park. Surveys took place in the Austral spring of 2018 and 2019. Distant control surveys took place at least 2 km from harvest sites in similar habitat. An adjacent control survey took place in similar habitat that abutted the source site in Nowingi but not Murray-Sunset.

Discussion

Here we document the first conservation translocations of the Endangered mallee emu-wren. These actions serve as a key step in a recovery process that seeks to implement larger-scale translocations as a conservation tool. We gained valuable insights regarding both the mallee emu-wren specifically and translocation in a broader context. Familiarity of release groups and timing of release can influence post-release behaviour and persistence at release sites. Despite cryptic behaviour, we were able to capture an adequate number of mallee emu-wrens in this first phase for future large-scale translocations to be considered feasible. Individuals persisted at the release site for at least 12 months and a number of translocated individuals formed or

maintained pairs and were able to successfully fledge young. Ultimately though, the reintroduced population did not persist and we explore possible reasons for this below.

Release in autumn or spring?

The season in which release occurred had a measurable impact on post-release behaviour, persistence at the release site and likelihood of producing offspring. Birds released in autumn dispersed further and were less likely to survive in the short-term than those released in spring, though reduced dispersal and higher incidences of territorial behaviour associated with breeding may have positively biased estimates of persistence for the spring cohort. Additionally, smaller group size during autumn may have been a source of bias to estimates of abundance. While small group size meant there were more groups available to be detected during this period, this smaller group size may have decreased detectability when compared with the autumn cohort. However, given exhaustive survey coverage during short-term intensive area searches, we believe that we were able to detect the majority of birds that remained within the release area. Few of the mallee emu-wrens released in autumn were known to have persisted at the release site by spring, and consequently few birds from this cohort were available to integrate with the spring cohort or to breed. Maximising reproductive output of translocated populations is critical for ongoing persistence (Sigg *et al.* 2005; Batson *et al.* 2015). Selecting the most beneficial season of release is one way that translocation managers might influence post-release behaviour, increase survival and increase reproductive opportunities. In light of our findings, any future mallee emu-wren translocations should prioritise spring releases.

Changes in animal behaviour between time periods is a near-universal phenomenon (Sutherland 1998). In semi-arid systems, behavioural variation occurs both seasonally (e.g. breeding versus non-breeding seasons), and over decadal timescales (e.g. breeding events triggered by periods of above-average rainfall; Verdon-Kidd and Kiem 2009). In this translocation, season of release influenced post-release dispersal, survival, and reproduction. Aligning translocations with favourable longer-term climatic events (e.g. during periods of above-average rainfall as forecast by La Niña climate cycles in southern Australia), may also increase the probability of long-term persistence of translocated populations (Letnic *et al.* 2005; Chen *et al.* 2020).

Familiar or unfamiliar?

Translocating cohesive social groups increased the likelihood of post-release group fidelity but had no detectable effect on known dispersal or survival in spring. Release protocols have been found to influence post-release group cohesion in other translocated species (Armstrong 1995; Armstrong and Craig 1995; Anstee and Armstrong 2001; Clarke *et al.* 2002; Bennett *et al.* 2012; Moseby *et al.* 2018; Franks *et al.* 2020). Whether or not this has led to improved survival rates appears to have been largely species-dependent. In

translocated juvenile hihi *Notiomystis cincta*, a positive association was found between the number of associates gained during a period of experimental social mixing and post-release survival (Franks *et al.* 2020). A similar mechanism may have been operating amongst mallee emu-wren groups released in Ngarkat. Slightly more mallee emu-wrens survived when they were released with unfamiliar individuals, though this difference was not significant. For translocation managers, increased post-release group cohesion represents a potential trade-off against increased capture effort and potential for stress in focal individuals. For cryptic species it may not always be possible to capture an intact group. Similarly, mortality during transit may leave managers with an isolated individual. In such a scenario it is advantageous to know the probability of survival of a release group comprising unfamiliar birds compared with that of an intact social group. The precautionary principle still applies and wherever possible mallee emu-wren social groups should be kept intact. An additional justification for capture of intact social groups is that fewer groups within the source population may be impacted by harvesting (remove fewer complete groups in comparison with partial removal of a larger number of groups). As yet, the impact of interrupting group social dynamics is unknown within source populations. However, in future translocations, managers may be able to further limit capture stress in birds during harvest, by avoiding extended pursuits of cryptic individuals if all members of a social unit are not required for translocation.

Impact of harvest on the source population

Whilst there was a trend towards larger declines at harvest sites, indicative of an impact of harvesting, this was not significant. However, given small sample size it is likely that removal of mallee emu-wrens did have a negative impact on source populations. The recorded decrease in population exceeded the number of mallee emu-wrens removed for translocation, and detections were also lower at distant control sites 12 months after pre-removal surveys, indicating that the removal of birds was not the sole cause of population decrease. Managers must account for abiotic factors that might influence sustainable harvest rates of source populations where possible. Little is known about mallee emu-wren recruitment, but it is possible that below average rainfall in the 12 months following harvesting contributed to the significantly lower abundance across both treatment and control sites at Nowingi. Ongoing monitoring at these sites will improve our understanding of mallee emu-wren recruitment and the long-term sustainability of current populations as a source for future translocations.

Despite repeated calls to routinely investigate impacts of harvesting on source populations the reporting of outcomes on this aspect of translocation practice remains rare (e.g. Stevens and Goodson 1993; Dimond and Armstrong 2007; IUCN/SSC 2013; Furlan *et al.* 2020). In contrast to our results, no significant reduction in

abundance was detected following harvest of 44 eastern bristlebirds *Dasyornis brachypterus*, another small cryptic passerine (Bain and French 2009). It is essential that source populations are managed conservatively in settings where the impact of harvest is uncertain (Dimond and Armstrong 2007).

Population Decline

A key measure of success in any translocation program is long-term persistence of the translocated population (Taylor *et al.* 2017). Our explicit focus lay in developing protocols for effective transport and establishment. However, understanding population decline during this early stage is crucial for planning future releases. Several factors may have contributed to the decline in mallee emu-wren occupancy following release. Allee effects, the suppression of population vital rates at low density, have been detected in translocated populations (Courchamp *et al.* 2008; Armstrong and Wittmer 2011). Little is known about mallee emu-wren vital rates, however, naturally high mortality has been reported in the closely related southern emu-wren *S. malachurus* with few birds surviving beyond two breeding seasons (Maguire and Mulder 2004). High mortality may have been exacerbated at low density through several mechanisms including reduced social cohesion or greater susceptibility to harsh environmental conditions, e.g. if mallee emu-wrens rely on huddling for thermal protection during cold nights (Gilbert *et al.* 2010). Emu-wrens may suffer increased susceptibility to mortality following death of a group member, particularly if opportunities to find new associates are rare. Harvest and release sites suffered below average rainfall and higher than average temperatures in the 12 months following release (Fig. 4.4, Bureau of Meteorology 2020). Mallee emu-wrens are adapted to semi-arid environments and variable conditions, but populations typically contract in dry years, as evidenced by reduced abundance at source sites over this same period (Connell 2019). Adverse conditions culminated in an extended period of low rainfall in early 2019, which may have severely limited available resources for mallee emu-wrens in Ngarkat. Days of extreme heat can also have a significant effect on passerine mortality in semi-arid systems. Sharpe *et al.* (2019) found that mortality of jacky winter *Microeca fascians* increased by a factor of three during extreme climatic events. Further inference here is limited by a lack of data on the effect of environmental conditions on mallee emu-wrens.

Post-release dispersal behaviour may also have affected long-term persistence (Berger-Tal *et al.* 2019). Though source and release sites both contained abundant *Triodia*, Ngarkat differs in vegetation structure to source sites (Brown *et al.* 2009). Previously occupied habitat is not necessarily an indicator of suitable habitat and it is difficult to identify all requirements for a translocated population (Osborne and Seddon 2012). Mallee emu-wrens may have dispersed from the release area seeking habitat more similar to that in which they were captured. We found that releasing birds immediately prior to the breeding season significantly reduced

dispersal compared to those released in autumn, but this may have been related to biological cues driving birds to reproduce. At the conclusion of the breeding season groups may have continued to disperse seeking natal habitat. Finally, it is possible that habitat in Ngarkat may become better suited for mallee emu-wren releases with more time. Verdon *et al.* (2019) found that mallee emu-wren time window of occurrence peaked at 20–40 years since fire for lower productivity *Triodia mallee* habitat. In this study, mallee emu-wrens were translocated into vegetation 12 years post-fire. Despite this relatively short time since fire, *Triodia* vegetation in Ngarkat was considered high quality prior to releases based on expert appraisal.

Financial Accountability

Disclosure of the financial details of conservation actions serves as a valuable guide for other researchers and managers in the planning and funding phases of translocation actions (Fischer and Lindenmayer 2000). In addition to formal funding and in-kind support from partner organisations, dedicated volunteers provided hundreds of person-hours of in-kind labour during this project. In total, the phase one translocation of mallee emu-wrens to Ngarkat Conservation Park cost \$538,882 AUD, comprising \$287,958 AUD of funding and \$250,924 AUD of in-kind support (Table S4.1).

Conclusion

In threatened species research, sample sizes are invariably small, and disentangling the many factors that may influence conservation outcomes is a common hurdle. Despite such limitations, insight can be gained when explicit trials are incorporated into conservation management. Season of release can have a significant impact on dispersal, persistence in the short term and reproductive output of translocated individuals. Translocating socially cohesive units can increase post-release group fidelity but, in this case, did not affect survival or dispersal. The mallee emu-wren remains vulnerable to catastrophic wildfire in currently occupied habitat. Given a demonstrated inability to halt many wildfires (Boer *et al.* 2020), translocation remains an important tool to mitigate this threat. Any future mallee emu-wren translocations should prioritise release immediately prior to the breeding season. Capture and transport of socially cohesive groups should be pursued but is not here considered essential when scarce resources might be better spent. Harvesting mallee emu-wrens for translocation impacted source populations and additional research should focus on population demographics at source sites to ensure that harvesting for translocation is sustainable. To improve the likelihood of success in future conservation measures for mallee emu-wrens, further studies that investigate factors that contribute to longer-term population decline are warranted. Despite not establishing a self-sustaining population, the outcomes of this study provide insight for future translocation programs and valuable learnings for the ongoing conservation of the mallee emu-wren.

References

- Anstee, S, Armstrong, K (2001) The effect of familiarity and mound condition in translocations of the western pebble-mound mouse, *Pseudomys chapmani*, in the Pilbara region of Western Australia. *Wildlife Research* **28**, 135-140.
- Armstrong, DP (1995) Effects of familiarity on the outcome of translocations, II. A test using New Zealand robins. *Biological Conservation* **71**, 281-288.
- Armstrong, DP, Castro, I, Griffiths, R (2007) Using adaptive management to determine requirements of re-introduced populations: the case of the New Zealand hihi. *Journal of Applied Ecology* **44**, 953-962.
- Armstrong, DP, Craig, JL (1995) Effects of familiarity on the outcome of translocations, I. A test using saddlebacks *Philesturnus carunculatus rufusater*. *Biological Conservation* **71**, 133-141.
- Armstrong, DP, Le Coeur, C, Thorne, JM, Panfylova, J, Lovegrove, TG, Frost, PGH, Ewen, JG (2017) Using Bayesian mark-recapture modelling to quantify the strength and duration of post-release effects in reintroduced populations. *Biological Conservation* **215**, 39-45.
- Armstrong, DP, Wittmer, HU (2011) Incorporating Allee effects into reintroduction strategies. *Ecological Research* **26**, 687-695.
- Bain, D, French, K (2009) Impacts on a threatened bird population of removals for translocation. *Wildlife Research* **36**, 516-521.
- Batson, W, Abbott, R, Richardson, KM (2015) Release strategies for fauna reintroductions: theory and tests. In 'Advances in reintroduction biology of Australian and New Zealand Fauna'. (Eds D.P. Armstrong, M.W. Hayward, D. Moro, and P.J. Seddon.). pp 7–16. (CSIRO Publishing: Clayton South, Australia).
- Bennett, VA, Doerr, VAJ, Doerr, ED, Manning, AD, Lindenmayer, DB (2012) The anatomy of a failed reintroduction: a case study with the Brown Treecreeper. *Emu - Austral Ornithology* **112**, 298-312.
- Berger-Tal, O, Blumstein, DT, Swaisgood, RR (2019) Conservation translocations: a review of common difficulties and promising directions. *Animal Conservation* **23**, 121-131.
- Boer, MM, de Dios, VR, Bradstock, RA (2020) Unprecedented burn area of Australian mega forest fires. *Nature Climate Change* **10**, 171-172.

- Boulton, RL, Hedger, C (2018) Reintroduction of the mallee emu-wren *Stipiturus mallee* to Ngarkat Conservation Park, Phase 1. Report to Fauna Translocation Evaluation Panel, Department of Environment, Land, Water and Planning.
- Boulton, RL, Lau, J (2015) Threatened Mallee Birds Conservation Action Plan, Report June 2015. Birdlife Australia Report to the Threatened Mallee Birds Implementation Team.
- Bright, PW, Morris, PA (1994) Animal translocation for conservation: Performance of dormice in relation to release methods, origin and season. *Journal of Applied Ecology* **31**, 699-708.
- Brown, S (2011) Mallee emu-wren (*Stipiturus mallee*): Multi-scale habitat requirements and population structure. PhD thesis, Deakin University Melbourne.
- Brown, S, Clarke, M, Clarke, RH (2009) Fire is a key element in the landscape-scale habitat requirements and global population status of a threatened bird: The mallee emu-wren (*Stipiturus mallee*). *Biological Conservation* **142**, 432-445.
- Brown, SM, Harrison, KA, Clarke, RH, Bennett, AF, Sunnucks, P (2013) Limited population structure, genetic drift and bottlenecks characterise an endangered bird species in a dynamic, fire-prone ecosystem. *PLoS One* **8**, e59732.
- Bureau Of Meteorology [online] (2020) Lameroo (Austin Plains) Weather Station: monthly mean temperature. Available at <http://www.bom.gov.au/climate/data/> [Accessed 1 January 2020].
- Chen, HC, Tseng, YH, Hu, ZZ, Ding, R (2020) Enhancing the ENSO Predictability beyond the Spring Barrier. *Scientific Reports* **10**, 984.
- Clarke, RH, Boulton, RL, Clarke, MF (2002) Translocation of the socially complex Black-eared Miner *Manorina melanotis*: a trial using hard and soft release techniques. *Pacific Conservation Biology* **8**, 223-234.
- Connell, J (2019) Fire and rain: Investigating how major ecological drivers shape a semi-arid bird community over space and time. PhD Thesis, Department of Ecology, Environment and Evolution, School of Life Sciences, La Trobe University.
- Courchamp, F, Berec, L, Gascoigne, J (2008) 'Allee effects in ecology and conservation.' (Oxford University Press: Oxford).

Department of Environment, Land, Water and Planning (2016) National Recovery Plan for the mallee emu-wren *Stipiturus mallee*, red-lored whistler *Pachycephala rufogularis* and western whipbird *Psophodes nigrogularis leucogaster*. (Australian Government: Canberra).

Dickens, MJ, Delehanty, DJ, Romero, LM (2010) Stress: An inevitable component of animal translocation. *Biological Conservation* **143**, 1329-1341.

Dimond, WJ, Armstrong, DP (2007) Adaptive harvesting of source populations for translocation: A case study with New Zealand robins. *Conservation Biology* **21**, 114-124.

Easton, LJ, Bishop, PJ, Whigham, PA (2019) Balancing act: modelling sustainable release numbers for translocations. *Animal Conservation* **23**, 434-442.

Fischer, J, Lindenmayer, DB (2000) An assessment of the published results of animal relocations. *Biological Conservation* **96**, 1-11.

Fisher, RA (1992) Statistical methods for research workers. In 'Breakthroughs in statistics'. (Eds S. Kotz and N.L. Johnson) pp. 66-70. (Springer. Verlag: New York).

Fiske, I, Chandler, RB (2011) unmarked: An R Package for Fitting Hierarchical Models of Wildlife Occurrence and Abundance. *Journal of Statistical Software* **43**, 1-23.

Furlan, EM, Gruber, B, Attard, CRM, Wager, RNE, Kerezszy, A, Faulks, LK, Beheregaray, LB, Unmack, PJ (2020) Assessing the benefits and risks of translocations in depauperate species: A theoretical framework with an empirical validation. *Journal of Applied Ecology* **57**, 831-841.

Guillera-Aroita, G, Lahoz-Monfort, JJ (2012) Designing studies to detect differences in species occupancy: power analysis under imperfect detection. *Methods in Ecology and Evolution* **3**, 860-869.

Franks, VR, Andrews, CE, Ewen, JG, McCready, M, Parker, KA, Thorogood, R (2020) Changes in social groups across reintroductions and effects on post-release survival. *Animal Conservation* **23**, 443-454.

Gilbert, C, McCafferty, D, Le Maho, Y, Martrette, JM, Giroud, S, Blanc, S, Ancel, A (2010) One for all and all for one: the energetic benefits of huddling in endotherms. *Biological Reviews* **85**, 545-569.

Griffith, B, Scott, JM, Carpenter, JW, Reed, C (1989) Translocation as a species conservation tool: Status and strategy. *Science* **245**, 477-480.

Hartig, F (2017) DHARMA: residual diagnostics for hierarchical (multi-level/mixed) regression models. *R package version 0.1*, 5.

- Hellstedt, P, Kallio, ER (2005) Survival and behaviour of captive-born weasels (*Mustela nivalis nivalis*) released in nature. *Journal of Zoology* **266**, 37-44.
- Higgins, PJ, Peter, JM, and Steele, WK (2001) 'Handbook of Australian, New Zealand & Antarctic Birds, Volume 5: Tyrant-flycatchers to Chats.' (Oxford University Press: Melbourne).
- Hill, JM, Elphick, CS (2011) Are grassland passerines especially susceptible to negative transmitter impacts? *Wildlife Society Bulletin* **35**, 362-367.
- Howe, F (1910) Notes on the mallee emu-wren. *Emu – Austral Ornithology* **10**, 336-337.
- IUCN/SSC (2013) Guidelines for reintroductions and other translocations. Version 1.0. (IUCN Species Survival Commission: Gland, Switzerland.)
- Jamieson, IG (2011) Founder effects, inbreeding, and loss of genetic diversity in four avian reintroduction programs. *Conservation Biology* **25**, 115-123.
- Koronkiewicz, TJ, Paxton, EH, Sogge, MK (2005) A technique to produce aluminum color bands for avian research. *Journal of Field Ornithology* **76**, 94-97.
- Letnic, M, Tamayo, B, Dickman, CR (2005) The responses of mammals to La Niña (El Niño Southern Oscillation)–associated rainfall, predation, and wildfire in central Australia. *Journal of Mammalogy* **86**, 689-703.
- MacKenzie, DI, Nichols, JD, Royle, JA, Pollock, KH, Bailey, L, Hines, JE (2017) 'Occupancy estimation and modeling: inferring patterns and dynamics of species occurrence'. (Elsevier: Amsterdam).
- Maguire, GS, Mulder, RA (2004) Breeding biology and demography of the southern emu-wren (*Stipiturus malachurus*). *Australian Journal of Zoology* **52**, 583-604.
- Menkhorst, P, Rogers, DI, Clarke, R (2017) 'The Australian bird guide'. (CSIRO Publishing: Melbourne, Victoria).
- Mihoub, JB, Robert, A, Le Gouar, P, Sarrazin, F. (2011) Post-release dispersal in animal translocations: Social attraction and the "vacuum effect". *PLoS One* **6**, e27453.
- Miller, KA, Bell, TP, Germano, JM (2014) Understanding publication bias in reintroduction biology by assessing translocations of New Zealand's herpetofauna. *Conservation Biology* **28**, 1045-1056.
- Møller, AP, Jennions, MD (2001) Testing and adjusting for publication bias. *Trends in Ecology & Evolution* **16**, 580-586.

- Moseby, KE, Blumstein, DT, Letnic, M, West, R (2018) Choice or opportunity: Are post-release social groupings influenced by familiarity or reintroduction protocols? *Oryx* **54**, 215-221.
- Osborne, PE, and Seddon, PJ (2012) Selecting suitable habitats for reintroductions: variation, change and the role of species distribution modelling. In '*Reintroduction biology: integrating science and management*'. (Eds JG Ewen, DP Armstrong, KA Parker, PJ Seddon.) pp. 73–104: (Wiley-Blackwell: Oxford).
- Parker, KA, Dickens, MJ, Clarke, RH, Lovegrove, TG, Ewen, J, Armstrong, D (2012). The theory and practice of catching, holding, moving and releasing animals. In '*Reintroduction biology: integrating science and management*'. (Eds JG Ewen, DP Armstrong, KA Parker, PJ Seddon.) pp. 73–104: (Wiley-Blackwell: Oxford).
- Paton, DC, Rogers, DJ, Cale, P, Willoughby, N, Gates, JA (2009) Birds. In '*Natural History of the Riverland and Murraylands*'. (Ed JT Jennings.) pp. 371-396. (Royal Society of South Australia Inc.: Adelaide).
- Sharpe, L, Cale, B, Gardner, JL (2019) Weighing the cost: the impact of serial heatwaves on body mass in a small Australian passerine. *Journal of Avian Biology* **50**, 1-9.
- Sigg, D, Goldizen, A, Pople, A (2005) The importance of mating system in translocation programs: reproductive success of released male bridled nailtail wallabies. *Biological Conservation* **123**, 289-300.
- Stevens, DR, Goodson, NJ (1993) Assessing effects of removals for transplanting on a high-elevation bighorn sheep population. *Conservation Biology* **7**, 908-915.
- Stoinski, T, Beck, B, Bloomsmith, M, Maple, T (2003) A behavioral comparison of captive-born, reintroduced golden lion tamarins and their wild-born offspring. *Behaviour* **140**, 137-160.
- Sutherland, WJ (1998) The importance of behavioural studies in conservation biology. *Animal Behaviour* **56**, 801-809.
- Taylor, G, Canessa, S, Clarke, RH, Ingwersen, D, Armstrong, DP, Seddon, PJ, Ewen, JG (2017) Is reintroduction biology an effective applied science? *Trends in Ecology & Evolution* **32**, 873-880.
- Tetzlaff, SJ, Sperry, JH, DeGregorio, BA (2019) Effects of antipredator training, environmental enrichment, and soft release on wildlife translocations: A review and meta-analysis. *Biological Conservation* **236**, 324-331.
- Venables, WN, Ripley, B.D. (2002) '*Modern Applied Statistics with S*'. 4th Edn. (Springer, New York).
- Verdon-Kidd, DC, Kiem, AS (2009) Nature and causes of protracted droughts in southeast Australia: Comparison between the Federation, WWII, and Big Dry droughts. *Geophysical Research Letters* **36**, 22.

Verdon, SJ, Watson, SJ, Clarke, MF (2019) Modeling variability in the fire response of an endangered bird to improve fire-management. *Ecological Applications* **29**, e01980.

Verdon, SJ, Watson, SJ, Nimmo, DG, Clarke, MF (2020) Are all fauna associated with the same structural features of the foundation species *Triodia scariosa*? *Austral Ecology* **45**, 773-787.

Verdon, SJ, Mitchell, WF, and Clarke, MF (2021) Can flexible timing of harvest for translocation reduce the impact on a fluctuating donor population? *Wildlife Research* **48**, 458-469.

Ward, MP, Schlossberg, S (2004) Conspecific attraction and the conservation of territorial songbirds. *Conservation Biology* **18**, 519-525.

5. Prioritising genetic diversity of founders in translocation planning for an endangered semi-arid passerine

*Mitchell, WF, Pavlova, A, Clarke, RH, Sunnucks, P (2022) Prioritising genetic diversity of founders in translocation planning for an endangered semi-arid passerine – in preparation for submission

Abstract

Genetic diversity underpins all biological diversity and is essential for the ongoing persistence and future adaptation of species. Despite this, genetic management of focal taxa has been poorly implemented in many threatened species conservation programs. Here, we characterise genetic structure and diversity across the global population of the Endangered mallee emu-wren and use this information to identify conservation management priorities for the species. Specifically, we seek to identify optimum source populations to maximise genetic diversity in future mallee emu-wren translocations.

Using a genome-wide SNP dataset comprising 14,107 loci, we assessed range-wide genetic structure, population genetic diversity and differentiation among seven sampling locations across three geographic regions encompassing the contemporary range of the mallee emu-wren and one location from which the species has become extinct.

We found weak structure and consistently low heterozygosity across all populations. Mean kinship and Weir and Cockerham pairwise F_{ST} indicated that differentiation between sampling locations was weak but significant.

Our results, based on thousands of genomewide genetic markers, add to previous research suggesting that the global mallee emu-wren population may be considered a single genetic unit for management purposes. To maximise genetic diversity in newly established populations, managers should prioritise gene-pool mixing with founders sourced from all three remnant regions inhabited by mallee emu-wrens: Wyperfeld, Murray-Sunset and Hattah-Kulkyne. Little is known about population dynamics of mallee emu-wren in Wyperfeld. A comprehensive assessment of the demographics of that population will be a crucial step in assessing the feasibility of its use as a source for gene-pool mixing.

Introduction

It is widely acknowledged that our planet is in the midst of a human-driven extinction crisis (Chapin *et al.* 2000; Ceballos *et al.* 2015). Threatening processes such as anthropogenic climate change, habitat loss and degradation, and over-exploitation of natural resources have resulted in a hundred-fold increase in global extinction rates when compared with background levels (Ceballos *et al.* 2015; Newbold *et al.* 2015). Translocation (the human-facilitated movement of living organisms from one area to another) is increasingly employed as a management tool to combat extinction (Fischer and Lindenmayer 2000; IUCN/SSC 2013; Berger-Tal *et al.* 2019; Langridge *et al.* 2021).

Common conservation goals that may be addressed by conservation translocations include the movement of individuals to broaden their distribution (either to areas previously occupied, i.e. reintroduction, or outside the historic range of the focal taxa, i.e. conservation introduction), to bolster genetic diversity or demographics of existing populations (i.e. reinforcement), or into reserves where threatening processes are actively managed as insurance against future losses of extant populations (i.e. ex-situ management, IUCN/SSC 2013; Tanentzap and Lloyd 2017; Morris *et al.* 2021). One key factor that underpins the viability of any conservation initiative, including translocation, is the genetic diversity of individuals undergoing management (Weeks *et al.* 2011; DeWoody *et al.* 2021). Despite its significance, genetic diversity of focal species has been poorly incorporated into conservation management (Laikre *et al.* 2010; Pierson *et al.* 2016; Cook and Sgro 2017). In recent years, a number of active conservation practitioners have advocated for ‘evolutionarily enlightened’ conservation management (Cook and Sgro 2017; Ralls *et al.* 2018), including in the context of conservation translocations (Weeks *et al.* 2011; He *et al.* 2016; Liddell *et al.* 2021).

Populations that are small and fragmented—traits typical of threatened species—are susceptible to strong genetic drift and increased likelihood of inbreeding (Courchamp *et al.* 2008; Weeks *et al.* 2016; Frankham *et al.* 2017; Schlaepfer *et al.* 2018). These processes erode genetic diversity (reducing the capacity of a population to adapt to environmental change), reduce fitness (i.e. inbreeding depression) and can lead to the accumulation of deleterious alleles (Lande 1995; Saccheri *et al.* 1998; Crnokrak and Roff 1999; Binks *et al.* 2007). These processes, if left unmanaged, may result in a feedback loop of accelerated population decline, ultimately leading to extinction (Saccheri *et al.* 1998; Keller and Waller 2002).

Depending on the context, conservation translocation may act as either a driver of, or a means to address, reduced genetic diversity and inbreeding depression. Translocations that establish new populations are invariably founded from a subset of individuals, and hence a subset of the genetic diversity, available from a source populations (He *et al.* 2016). This ‘founder effect’ places an upper limit on the genetic diversity that a

population may contain at establishment (Nei *et al.* 1975; Hundertmark and Van Daele 2010; Andersen *et al.* 2014). Newly established populations are also typically small (Langridge *et al.* 2021), rendering them susceptible to the processes described above that may erode genetic diversity and fitness (Andersen *et al.* 2014). For these reasons, it is essential that translocation managers seek to optimise genetic diversity through careful selection of founders based on quantitative assessment of genetic richness of source populations (He *et al.* 2016; Malone *et al.* 2018). Translocations may also be used to augment gene flow for small, isolated populations, providing a source of novel genetic material (Grueber *et al.* 2017). By introducing individuals from larger, more diverse populations, or conducting reciprocal translocations from multiple small populations, managers may alleviate the effects of inbreeding, bolster fitness and improve the adaptive potential of populations (Binks *et al.* 2007; Heber *et al.* 2013; Frankham 2015). Gene flow augmentation, referred to as genetic rescue, can greatly improve the likelihood of ongoing persistence for populations suffering low genetic variation (Frankham 2015), but does pose a risk of reduced fitness (i.e. outbreeding depression) in some circumstances. This is especially true of scenarios where the individuals that are being mixed have been exposed to opposing selective pressures (Frankham *et al.* 2011). While this potential outcome must be considered, the weight of evidence indicates that the risk of outbreeding depression is typically small compared to the potential conservation benefits of genetic rescue or the risk of doing nothing (Ralls *et al.* 2020; Liddell *et al.* 2021).

Here we consider genetic diversity in the global population of the Endangered mallee emu-wren *Stipiturus mallee*. The mallee emu-wren is a small passerine endemic to the semi-arid mallee region of north-western Victoria and eastern South Australia (Higgins *et al.* 2001). This species has a strong association with the hummock-forming grass *Triodia scariosa* and is rarely found in areas where *Triodia* is absent (Verdon *et al.* 2020). Historic clearing of vegetation for agriculture, successive landscape-scale wildfires, and senescence of *Triodia* have led to considerable range reduction and population decline of the mallee emu-wren. An estimated <6,500 individuals remain, distributed in several fragmented sub-populations (for a map displaying mallee emu-wren density across the northern part of its range, see Verdon *et al.* 2021).

Extant mallee emu-wren populations exhibit characteristics that are cause for conservation concern. Mallee emu-wrens are confined to just three contiguous tracts of remnant native vegetation (referred to here as ‘regions’) in north-western Victoria: Hattah-Kulkyne National Park and contiguous reserves (Hattah-Kulkyne region); Murray-Sunset National Park (Murray-Sunset region); and the more southerly network of reserves comprising Ngarkat Conservation Park, Big Desert Wilderness Area and Wyperfeld National Park (southern mallee region)(Verdon *et al.* 2021).

Fewer than 200 mallee emu-wrens are estimated to remain in the southern mallee region. Across the species range, reserve-scale wildfires have led to the extirpation of mallee emu-wren from many remnants they once occupied (Brown *et al.* 2009). The mallee emu-wren is a poor flyer. Natural immigration, and therefore gene flow, is not feasible across the agricultural matrix that separates the remaining remnants occupied by the species. As a result, mallee emu-wrens are unable to naturally recolonise many areas burnt by wildfire despite subsequent recovery of suitable habitat. Within large remnants, population trajectories for this species are dynamic and influenced by prevailing climatic conditions and the time since fire (Brown *et al.* 2009; Connell *et al.* 2017; Verdon *et al.* 2019; Connell *et al.* 2021). Wildfire is an ever-present feature of the semi-arid Australian bushland and *Triodia* habitat takes at least fifteen years following fire to be suitable for occupation by mallee emu-wren (Brown *et al.* 2009). In sub-optimal habitat (elevation 55–98 m), emu-wren have an occurrence window ~20–40 years post fire (Verdon *et al.* 2019). However, in core habitat (elevation 28–55 m), mallee emu-wren occurrence does not decline with time since fire and is likely more resilient to periods of unfavourable climatic conditions. This interaction between fire-age of vegetation communities and recent climate history results in temporally and spatially variable connectivity and gene flow (Brown *et al.* 2013). It is possible that the high quality habitat, at elevations 28–55 m, serves as a source for re-colonisation events within remnant tracts of vegetation following repeated local extinctions caused by habitat senescence or wildfire. Wildfire poses a great risk in this system. Long-unburnt areas of high-quality habitat have disproportionately high occurrence of mallee emu-wrens (Verdon *et al.* 2019). A reserve-scale wildfire encompassing this lower-elevation core habitat would have devastating implications for the global persistence of the mallee emu-wren (Brown *et al.* 2009).

Translocation may present as a tool to address many of the threats that the mallee emu-wren faces (Brown *et al.* 2009). Indeed, translocations were listed as a priority conservation action for this species, and this recommendation led to the 2018 trial reintroduction into Ngarkat Conservation Park in South Australia (Boulton and Lau 2015; Mitchell *et al.* 2021a; Chapter 4). That trial sought to optimise translocation protocols for the mallee emu-wren whilst laying the theoretical groundwork for future translocations which may include:

- Release of mallee emu-wrens into areas of suitable habitat that were burnt by fire but have since recovered, thereby increasing the global distribution of the species and providing wild insurance populations against future wildfire.
- Movement to a captive, managed population to act as insurance against wildfire and to provide a captive-bred source for future translocations.
- Transfers between small isolated sub-populations to bolster size and genetic diversity, thereby improving the probability of the ongoing persistence of at-risk populations.

Previous research using eleven microsatellite markers characterised genetic diversity across mallee emu-wren populations as low to moderate with evidence of bottlenecks and genetic drift (Brown *et al.* 2013). Spatial population genetic structure was found to be weak, leading to the conclusion that at least some gene flow was maintained during periods of habitat connectivity associated with climatic conditions and fire-history (Brown *et al.* 2013). Subsequent to that study, a small and isolated population of mallee emu-wrens was discovered in Wyperfeld National Park (southern region), while populations in Ngarkat Conservation Park became extinct due to wildfire (southern mallee region, Mitchell *et al.* 2021a; Chapter 4). In addition, high-throughput sequencing now feasibly allows analytical power at orders of magnitude higher than that provided by microsatellite markers (Reuter *et al.* 2015).

In this study we use a dataset of 14,107 single nucleotide polymorphism (SNP) loci to assess the genetic diversity and structure of the mallee emu-wren across its entire distribution. We aim to:

1. assess range-wide genetic structure and quantify levels of genetic differentiation among sampling locations;
2. assess levels of genetic diversity within sampling locations;
3. identify populations at risk of inbreeding depression that may benefit from gene flow augmentation;
4. identify optimum sources of founders for future translocation or captive breeding programs that will maximise genetic diversity in future generations.

Methods

Sample collection and genotyping

A 2018 trial reintroduction of the mallee emu-wren provided a unique opportunity to increase our understanding of the genetic characteristics of this Endangered species. In April and August of 2018, 85 mallee emu-wrens were captured for translocation in Nowingi State Forest and Hattah-Kulkyne and Murray-Sunset National Parks (Mitchell *et al.* 2021a; Chapter 4). Two or three pin-feathers were removed from each bird for sequencing. To supplement this dataset we obtained an additional 72 DNA samples from Museums Victoria, collected between 2006 and 2008 (Brown *et al.* 2013). A small and isolated mallee emu-wren population exists in Wyperfeld National Park. In September 2019 we captured three mallee emu-wrens from this population following the approach outlined by Mitchell *et al.* (2021; chapter 4). Up to 24 µl of blood was drawn from the brachial vein of each bird using a heparinised capillary tube and then transferred to a solution of ethanol. DNA

was extracted from these samples using DNeasy Blood and Tissue Kits following Qiagen's (the manufacturer) instructions.

The terminal tip of each pin-feather collected during the 2018 mallee emu-wren translocation was sent to Diversity Arrays Technology (Pty Ltd) for DNA extraction and genotyping (85 samples). We also sent an additional plate containing DNA samples collected in Wyperfeld NP (three samples) and DNA samples obtained from Museums Victoria (72 samples) for sequencing only. Unfortunately, following shipping from Monash University, the genetic material collected during the translocation (85 feather samples) was lost. Three museum samples contained insufficient DNA for sequencing. For the remaining samples, codominant, genome-wide, biallelic single nucleotide polymorphism markers were generated by Diversity Arrays Technology Pty. Ltd. using their DArTseq™ platform (Kilian *et al.* 2012, see appendix 4).

In all, genetic data were generated for 72 individuals comprising 27,727 codominant bi-allelic SNPs. These samples represent all three continuous tracts of remnant vegetation inhabited by mallee emu-wrens and were collected at six sampling locations currently occupied by mallee emu-wrens and one sampling location from which the species has been locally extirpated (Ngarkat Conservation park, southern mallee region, Table 5.1, Fig. 5.1).

Table 5.1. The number of genotyped samples obtained from each sampling location (excluding those that were not included in analyses). Extant mallee emu-wren range encompasses three continuous tracts of remnant vegetation, here referred to as ‘regions’.

Sampling location name	Sampling location	Region	No. of individuals (Female:Male)	Status	Sampling date	Max. distance between individuals
HK	Hattah-Kulkyne National Park + Nowingi State Forest	Hattah Kulkyne and contiguous reserves	31 (11:20)	Extant	2006-2008	23.1 km
MSW	Murray-Sunset National Park (west)	Murray-Sunset	11 (5:6)	Extant	2006-2008	13.4 km
MSC	Murray-Sunset National Park (central)	Murray-Sunset	8 (4:4)	Extant	2006-2008	18.1 km
MSE	Murray-Sunset National Park (East)	Murray-Sunset	8 (4:4)	Extant	2006-2008	8.7 km
MSS	Murray-Sunset National Park (South)	Murray-Sunset	5 (2:3)	Extant	2006-2008	4.6 km
WYP	Wyperfeld National Park	Southern mallee	3 (0:3)	Extant	2019	22.4 km
NGA	Ngarkat Conservation Park	Southern mallee	4 (3:1)	<i>Extinct</i>	2006-2008	1.5 km

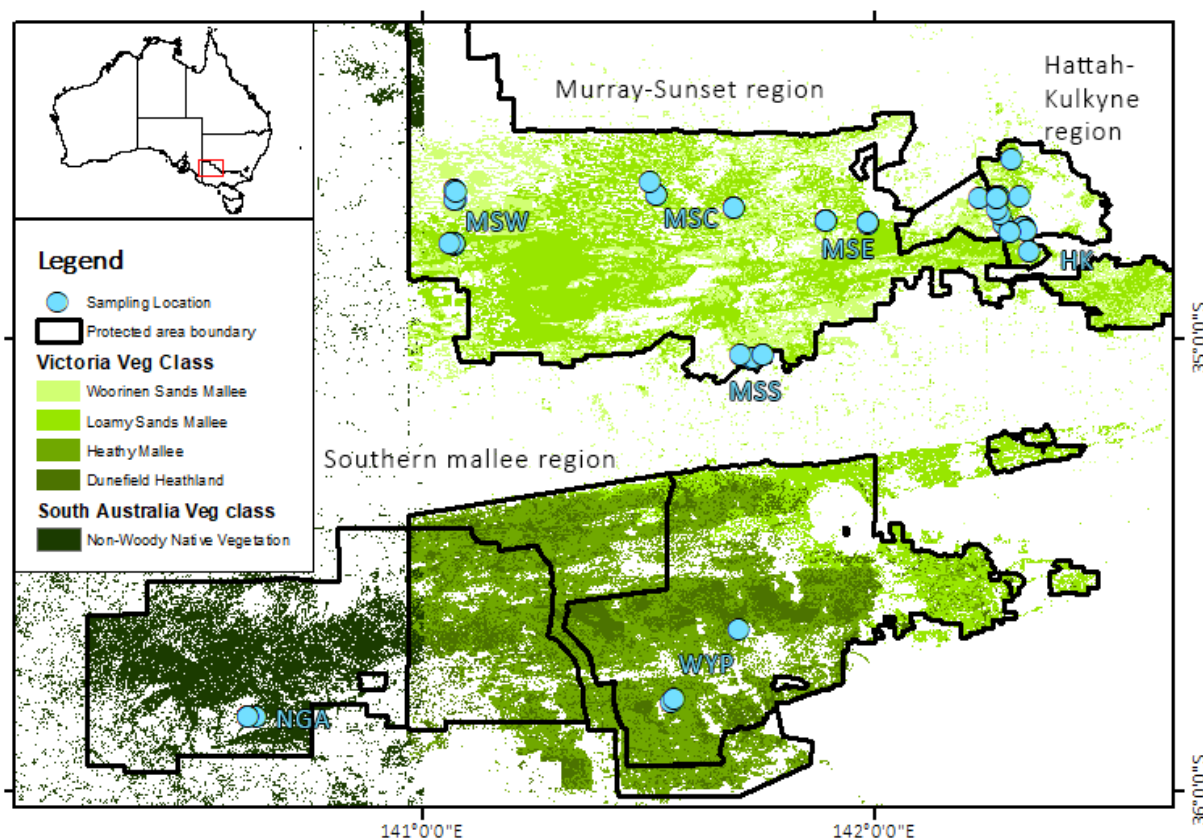


Figure 5.1. Collection points (blue circles) of mallee emu-wren genetic material, grouped by sampling location (Table 5.1). Vegetation classes that potentially contain mallee emu-wren habitat are shown in shades of green. The actual suitability of habitat at any given time will be dependent on several factors including time since fire and climatic conditions during preceding years. For a detailed study of the factors influencing mallee emu-wren occurrence, see Verdon *et al.* (2019). State governing bodies use different vegetation categories which is reflected on this map. State borders have been removed to improve clarity.

Data filtering

We performed filtering of genomic data generated from 72 mallee emu-wren samples using the R package *DartR* (Gruber *et al.* 2018). We removed 7,555 loci that were not 100% reproducible. Repeatability is determined during the genotyping step with each locus being given a repeatability score using technical replicates for 25% of all samples. Because missing data may be a source of considerable bias during analyses of large genomic datasets (Yi and Latch 2021), we removed 3,816 loci with more than 25% missing data. Two individuals with >15% of data missing were removed. After these filters, we searched for monomorphic loci and removed all eight. We retained only one SNP per sequenced fragment, which necessitated removal of an

additional 1,779 loci. Finally, we filtered out loci with patterns of genotypes indicative of sex-linkage using the function `gl.sexlinkage` in the package *dartR*. ZW gametologs (i.e. loci that are heterozygous in all females and homozygous in all males) were detected using `t.hom=0, t.het=0, system=ZW`. Z-linked loci (e.g. loci heterozygous in >10% of males but homozygous- or rather hemizygous- in all females) were detected using `t.hom=0.9, t.het=0, system=XY`. One ZW gametolog and 461 Z-linked loci were removed.

Our final filtered autosomal data set comprised 70 individuals from seven sampling locations and included 14,107 binary SNPs with overall 3.35% missing data. We did not filter out loci that were potentially under selection because in small, bottlenecked populations such as the present ones, genetic drift will cause many false positives, and there was no obvious potential driver of selection to focus on. Even genuine candidate loci under selection are expected to be relatively few, and highly correlated with neutral variation (Fernandez-Fournier *et al.* 2021).

Analyses

Population structure was inferred using *STRUCTURE* v2.3.4. Ten replicate runs were performed for K values of 2–10 (i.e. hypothesized genetic clusters). Each cluster had a burn in of 10,000 followed by 50,000 Markov chain Monte Carlo (MCMC) iterations. We used the *STRUCTURE* parameter settings admixture model without prior population information. We used CLUMPAK software (Kopelman *et al.* 2015) to estimate best K using both the Evanno Delta K method (Evanno *et al.* 2005) and $\ln \Pr(X|K)$ method (Pritchard *et al.* 2000). In addition, we assessed population genetic structure using principal coordinate analysis (PCoA) using the function `gl.pcoa` in the R package *dartR*. We tested for isolation by distance using the function `gl.ibd` in the package *dartR* which performs a mantel test (1000 permutations) between genetic distance (population based pairwise $F_{ST}/1 - F_{ST}$) and log Euclidean geographic distance between pairs of samples.

We estimated pairwise Weir and Cockerham F_{ST} using the R package *StAMPP* (Weir and Cockerham 1984; Pembleton *et al.* 2013). We used 1000 bootstrap replicates, resampling a subset of loci, to calculate statistical significance and 95 % confidence intervals. F_{ST} is a frequently used measure of genetic differentiation between geographic groups of organisms. However, mean kinship (MK) has been suggested as a preferable choice for characterising genetic variation of groups of conservation concern (Frankham *et al.* 2017). An individual's mean kinship is the average co-ancestry it shares with every other individuals in a population, including itself (Robledo-Ruiz *et al.* 2022). We calculated pairwise kinship between each individual in the dataset using the *beta.dosage* function in the R package *hierfstat* (Goudet 2005). We then manually averaged these values for all pairwise comparisons between each population to calculate MK between sampling locations.

We used the R package *hierfstat* to calculate observed (H_o) and expected (H_s) heterozygosity, allelic richness (AR) and the inbreeding coefficient F_{IS} for each population, to test for strong deviations from neutral expectations such as might be driven by local population substructure.

Results

A low level of genetic differentiation between birds sampled from different tracts of remnant vegetation was supported by principal coordinate and *STRUCTURE* analyses (Figs 5.2 and 5.3). The first PCoA axis, explaining 4.6% of variance in the dataset, showed a distinction between HK and all other populations (Fig. 5.2). Individuals from the southern mallee region were clustered with individuals from the northern Murray-Sunset region, despite considerable geographic separation. On axis 2 (3.5% variance), little separation was evident except for three individuals from MSW and one individual from HK (Fig. 5.2). No clear population level differentiation was evident on subsequent axes (Fig. S5.3). Low levels of population structure were apparent among sampling locations that occupy the three regions of contiguous remnant emu-wren habitat (Fig. 5.3). The optimal value of k (indicating the number of genetically distinct groups within a sample) for *STRUCTURE* analysis was determined to be six using the Delta K method, while the $\ln \Pr(X|k)$ method identified seven as the best-supported k (Fig. S5.5). Small numbers of individuals were identified by *STRUCTURE* as belonging to a unique cluster in comparison to other individuals from the same sampling location (Fig. 5.3). Within sampling locations, these outlying individuals were found to have a high degree of co-ancestry and were sampled within close proximity to one another (Table S5.2). We found significant isolation by distance among all populations ($r = 0.735$, $p = 0.007$, Fig. 5.4).

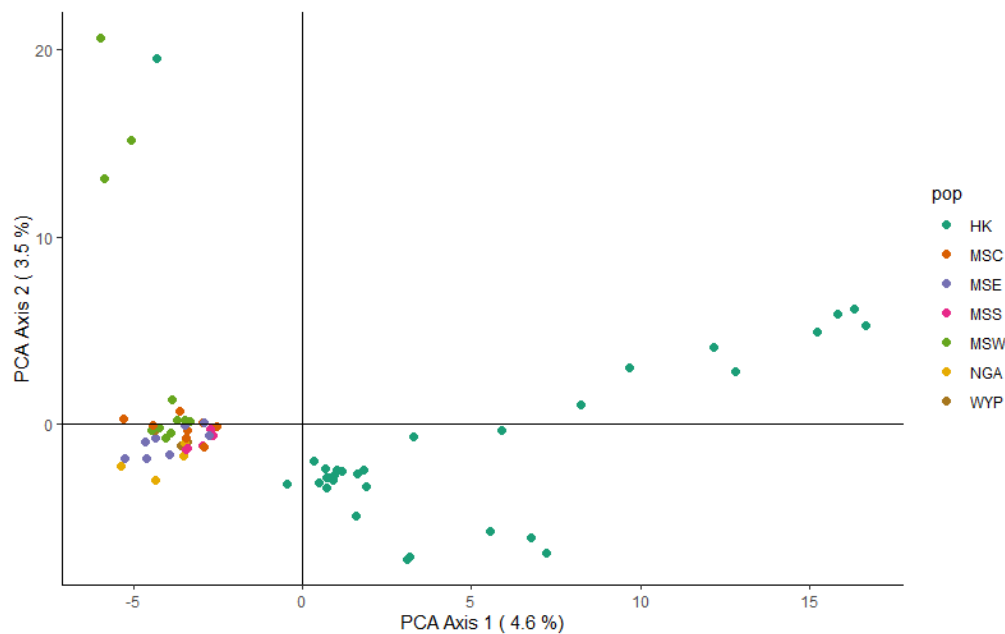


Figure 5.2. Ordinance plot displaying principal coordinate analysis results for 70 mallee emu-wrens sampled across the contemporary range of the species and location from which they have become extinct (NGA). HK = Hattah Kulkyne, MSC = Murray-Sunset central, MSE = Murray-Sunset east, MSS = Murray-Sunset south, MSW = Murray-Sunset west, NGA = Ngarkat, WYP = Wyperfeld.

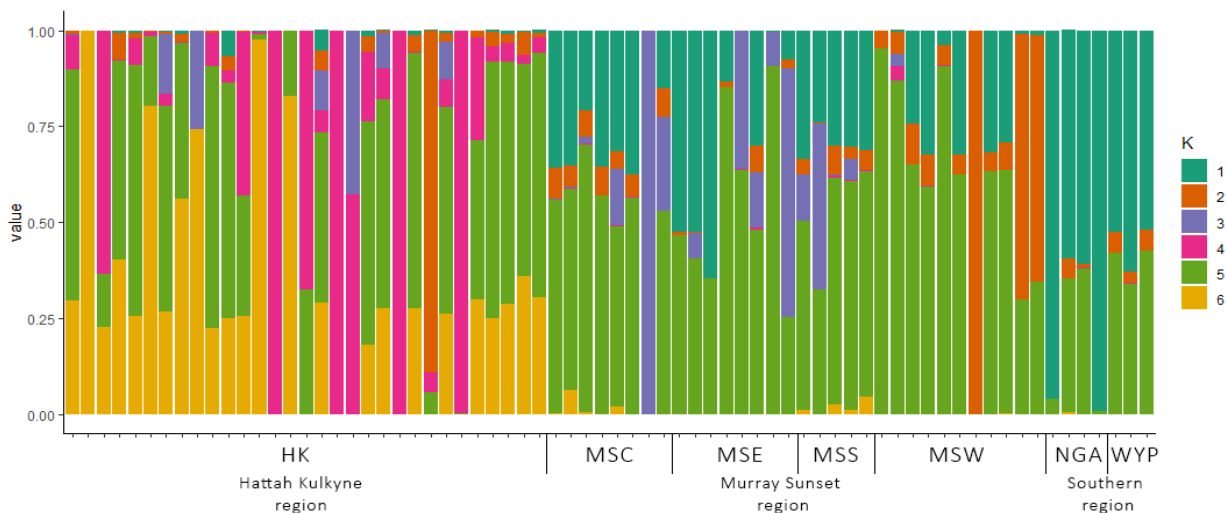


Figure. 5.3. Barplot displaying results of k=6 structure across 70 mallee emu-wrens sampled across the contemporary range of the species. Best K determined using the Evanno Delta K method. HK = Hattah Kulkyne, MSC = Murray-Sunset central, MSE = Murray-Sunset east, MSS = Murray-Sunset south, MSW = Murray-Sunset west, NGA = Ngarkat, WYP = Wyperfeld.

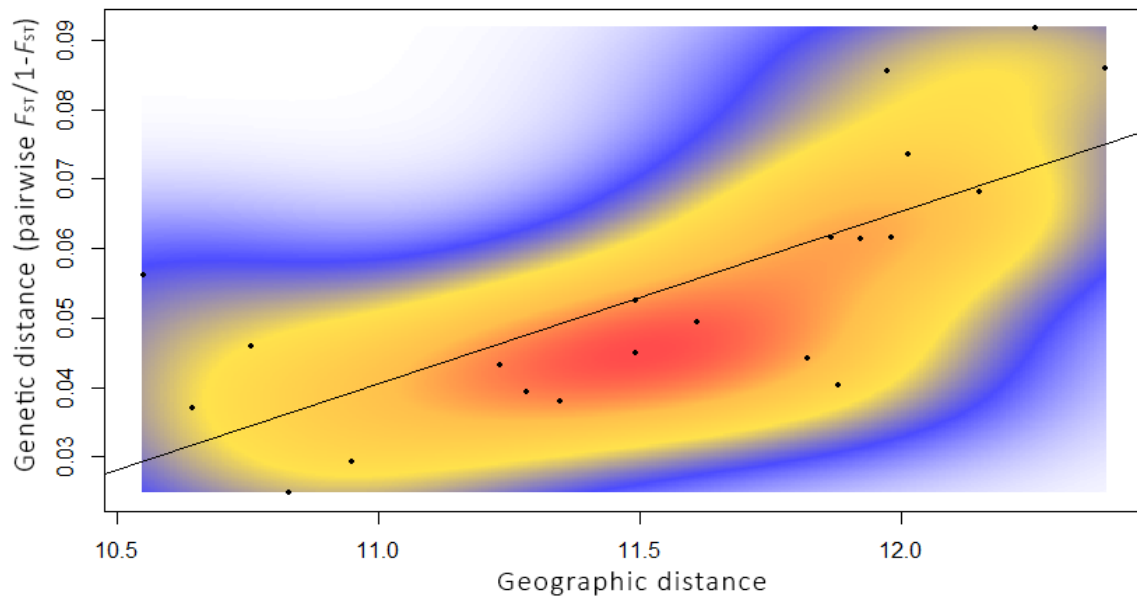


Figure 5.4. Isolation by distance (genetic distance against log Euclidian geographic distance) for 70 mallee emu-wrens from six sampling locations across the contemporary range of the species and one location from which mallee emu-wrens have become extinct.

The results of pairwise F_{ST} and MK broadly aligned, though there were some exceptions. A high level of differentiation was found between NGA and all other sampling locations (Table 5.2). NGA differed most from MSC using both F_{ST} and MK. Despite both sampling locations being located in the southern mallee region, relatively high differentiation was found between NGA and WYP using both F_{ST} and MK (Table 5.2). Between extant populations, WYP had a high level of differentiation from all other sampling locations, in particular HK, MSE, and MSS. MK indicated that the greatest differentiation of WYP was with MSC but F_{ST} indicated that WYP was most different from HK. The pairs of sampling locations with the highest level of co-ancestry were all found within the Murray-Sunset region (pairwise combinations of MSW, MSC, MSS and MSE; Table 5.2). Mean kinship, but not F_{ST} , indicated a moderately high level of co-ancestry between MSW and HK. One other notable exception between the two methods was that MK revealed moderate co-ancestry between WYP and MSW, in comparison to other populations in the Murray-Sunset region, which were shown to have low co-ancestry with WYP (Table 5.2).

Genetic diversity was consistently low across all sampling locations. The now extinct Ngarkat Conservation Park mallee emu-wren population, NGA, exhibited the highest heterozygosity of all sampling locations (Table 5.3). Of extant populations, the Murray-Sunset central population, MSC, had greatest heterozygosity, though there was little variation between sampling locations overall (Table 5.3).

Table 5.2. Genetic differentiation between sampling locations. Weir and Cockerham pairwise F_{ST} with bootstrap estimates of 95% CI (bottom left semi-matrix) and mean kinship with 2*SE (top right semi-matrix). Mean kinship is scaled such that 0 = global average. All F_{ST} values were significant (P value <0.001). = high differentiation between pairwise sampling locations (top 25% of range), = moderate differentiation (value within 25-75% of range), = low differentiation (bottom 25% of range).

	WYP	HKNP	MSW	MSC	MSE	NGA	MSS
WYP		-0.038 (0.004)	-0.0001 (0.011)	-0.043 (0.007)	-0.040 (0.008)	-0.037 (0.007)	-0.039 (0.007)
HKNP	0.058 (0.053– 0.064)		0.022 (0.005)	-0.022 (0.003)	-0.021 (0.003)	-0.050 (0.004)	-0.015 (0.003)
MSW	0.057 (0.050– 0.063)	0.043 (0.040– 0.045)		0.019 (0.007)	0.014 (0.007)	-0.014 (0.009)	0.022 (0.008)
MSC	0.040 (0.034– 0.046)	0.039 (0.036– 0.041)	0.029 (0.025– 0.032)		-0.023 (0.005)	-0.057 (0.005)	-0.019 (0.004)
MSE	0.057 (0.051– 0.065)	0.053 (0.050– 0.056)	0.050 (0.046– 0.054)	0.036 (0.032– 0.040)		-0.057 (0.005)	-0.021 (0.005)
NGA	0.048 (0.040– 0.055)	0.079 (0.073– 0.084)	0.078 (0.072– 0.083)	0.063 (0.058– 0.069)	0.083 (0.077– 0.089)		-0.047 (0.004)
MSS	0.043 (0.036– 0.050)	0.041 (0.037– 0.044)	0.036 (0.032– 0.040)	0.024 (0.020– 0.028)	0.043 (0.038– 0.048)	0.066 (0.060– 0.073)	

Table 5.3. Observed heterozygosity (H_o), expected heterozygosity (H_s) the inbreeding coefficient F_{IS} and allelic richness (AR) for 70 mallee emu-wrens from six sampling locations across the contemporary range of the species and one location from which mallee emu-wrens have become extinct.

Sampling location	H_o	H_s	F_{IS}	AR
HK	0.139	0.173	0.163	1.26
MSC	0.145	0.180	0.140	1.27
MSE	0.142	0.174	0.133	1.26
MSS	0.143	0.177	0.124	1.26
MSW	0.130	0.163	0.154	1.24
NGA	0.151	0.176	0.076	1.26
WYP	0.145	0.182	0.104	1.27

Discussion

We assessed genetic diversity and structure in the global mallee emu-wren population using genetic markers from 70 individuals across three contiguous tracts of remnant vegetation within the contemporary range of the species and one location from which they have become extinct. We found weak genetic structure among regions despite considerable geographic barriers and perceived low dispersal capability. Genetic diversity was similar between populations despite considerable variation in population size and connectivity. Metrics of differentiation between sampling locations, pairwise F_{ST} and MK, broadly aligned. To maximise genetic diversity in mallee emu-wren translocations, founders should be sourced from those populations with greatest differentiation. However, given the small size and vulnerability of some populations, the risk of demographic impact may outweigh the potential benefit of using small populations as a source for translocation. Similarly, reciprocal translocations between geographically isolated mallee emu-wren populations will likely improve genetic diversity and enhance fitness. However, given similar heterozygosity and low differentiation between sampling locations and the risks inherent to translocated individuals, the potential costs and benefits of reciprocal translocations must be carefully weighed.

Genetic Structure

We found evidence of very weak genetic structure among individuals sampled from the three continuous tracts of remnant vegetation that are still inhabited by mallee emu-wrens. Hattah-Kulkyne had the greatest difference from all other sampling locations, while structure separating the Murray-Sunset and southern mallee regions was subtle following *STRUCTURE* and not supported by PCoA. This result contrasts that provided by Brown *et al.* (2013) who, using microsatellite markers, found evidence for a genetic cluster comprising Ngarkat and another cluster comprising populations in western, central and southern Murray-Sunset as well as Hattah-Kulkyne. The genetic distinction of Hattah-Kulkyne may be explained by the ~400 km² Raak Plain, which lies between Murray-Sunset and Hattah-Kulkyne. This geological feature is more saline than surrounding land and is predominantly vegetated by chenopod shrubs and samphire (Department of Environment Land Water and Planning 2021). These conditions are not suitable for *Triodia* growth and, consequently, mallee emu-wrens are unlikely to have persisted in Raak Plain during at least the last several thousand years. Gene flow between mallee emu-wrens in the Murray-Sunset and Hattah-Kulkyne regions has only been feasible through the southern portion of Hattah-Kulkyne, south of Raak Plain. The low level of genetic difference between the southern mallee and Murray-Sunset regions is more difficult to explain. These regions have been separated by a broad expanse of agricultural land since at least the 1950s (Clarke *et al.* 2001). Consequently, gene flow between these regions cannot have occurred for >80 years due to the poor dispersal capability of mallee emu-wrens outside of *Triodia* vegetation. Prior to widespread land clearing, the

intervening landscape would have been characterised by a matrix of Woorinen sands mallee and loamy sands mallee that cycled through phases of suitability for mallee emu-wrens depending on prevailing climate and fire history (Brown *et al.* 2013; Department of the Environment 2014). The lack of structure evident in this study may indicate relatively little drift in the decades since separation between the southern mallee and Murray-Sunset regions, though this is unlikely based on life history and small population size of mallee emu-wrens in the southern mallee region. Sample size in this study was small, especially for the southern region (due to the low number of mallee emu-wrens in this population). Increased efforts to collect genetic material from this population would increase the power to detect genetic differences across regions.

The inclusion of closely related individuals in *STRUCTURE* analyses can lead to strong support for population structure even when no structure is present (Anderson and Dunham 2008). This problem is exacerbated when datasets include large numbers of loci (as is this case in this study). We found high co-ancestry (indicating first-degree relatives) among several pairs of mallee emu-wrens that exhibited structure profiles indicative of a unique population (compared with other individuals sampled at the same location). Mallee emu-wrens are sparsely distributed, exist in small groups of related individuals and are difficult to find and capture (Mitchell *et al.* 2021a; Chapter 4). These factors increase the likelihood of closely related individuals being sampled. Capturing all members of a social group is more efficient than capturing one individual and ignoring other individuals within that group before beginning a search for another group, which may take considerable time. It is likely that the inclusion of closely related individuals in this dataset resulted in an inflated estimate of *k* (or the number of unique genetic clusters represented in the dataset, Anderson and Dunham 2008). Despite this, we found little structure among sampling locations within regions. This result suggests that, within regions, mallee emu-wrens disperse sufficiently to maintain at least some gene flow. This conclusion supports Brown *et al.* (2013) who inferred that genetic connectivity of mallee emu-wrens is likely maintained by movement across spatially and temporally variable habitat.

Genetic diversity across sampling locations and regions

Heterozygosity and allelic richness differed little between mallee emu-wren populations despite considerable variation in population size and connectivity (for density and distribution of mallee emu-wren, see Verdon *et al.* 2021). This was in contrast to results presented by Brown *et al.* (2013), who found comparable levels of heterozygosity between sampling locations but lower levels of allelic richness in NGA and MSE compared with other sampling locations. Smaller populations are at greater risk of losing genetic diversity through drift than are larger ones (Bouzat 2010; Furlan *et al.* 2012). Only one area in the southern mallee region, WYP, is confirmed to be inhabited by mallee emu-wrens (Mitchell *et al.* 2021a; Chapter 4). Little is known about this

population but it is thought to be severely isolated and to number < 200 birds. Mallee emu-wren occurrence is influenced significantly by climatic conditions (Connell *et al.* 2021). Vital rates will increase and decrease in line with rainfall and time since fire. Further, mortality is likely to be high. A reproductive study of a population of the closely related southern emu-wren *S. malachurus* revealed that adults rarely survive beyond three years (Maguire and Mulder 2004). These characteristics (small population size, high mortality and periodic population decline) suggest a high likelihood that WYP has experienced genetic drift and, consequently, suffers low diversity (Allendorf 1986). Compounding this, isolation of the southern mallee region means that there is no capacity for genetic diversity to be restored through natural gene flow from other known mallee emu-wren populations. Based on these characteristics, one would expect low heterozygosity of WYP in comparison to larger and better-connected emu-wren populations in the Murray-Sunset and Hattah-Kulkyne regions. Comparable heterozygosity and allelic richness between WYP and all other sampled locations may suggest a larger mallee emu-wren population in Wyperfeld than currently thought. Such a population would be more likely to maintain the level of heterozygosity demonstrated in this study.

We found significant but weak genetic differentiation between mallee emu-wren populations according to both F_{ST} and MK. Of extant populations, and in contrast to *STRUCTURE* and PCoA, WYP had greatest differentiation from all other populations according to F_{ST} and MK, suggesting that this population will be a valuable source of novel genetic material for gene-pool mixing across mallee emu-wren populations.

Conclusions and management Implications

Our results support the conclusion of Brown *et al.* (2013) that the global mallee emu-wren population may be considered a single genetic unit for management purposes. We found little evidence of genetic structure between populations of mallee emu-wrens across the three remaining tracts of remnant vegetation that comprise the contemporary range of the species. Translocation has been highlighted as a potential strategy to broaden the global distribution of the species while providing insurance populations against wildfire in currently occupied habitat (Brown *et al.* 2009; Mitchell *et al.* 2021a; Chapter 4). To maximise genetic diversity in future translocated populations, founders should be drawn from all three regions inhabited by mallee emu-wrens. All populations had similar levels of heterozygosity and allelic richness, so to increase genetic diversity, managers should consider gene-pool mixing between populations with the highest level of differentiation. In this regard, WYP should be considered as the greatest potential source of novel genetic material given its clear distinction from all other sampling locations. MSC and MSE have similar levels of differentiation from WYP and also have the greatest genetic difference from HK of all sampling locations in Murray-Sunset. Sourcing

founders for translocation from WYP, HK and either MSC or MSE would result in the highest genetic diversity at the destination population.

Conservation managers must ensure that removing individuals from wild populations for translocation is sustainable (Mitchell *et al.* 2021b; Chapter 2). Little is known about mallee emu-wren population demographics in Wyperfeld. Prior to translocating mallee emu-wrens from this population, managers must assess the potential impact that harvesting may cause to it. Few emu-wrens have been detected in this region and the population is generally considered to be very small. If this is the case, it is unlikely that sourcing mallee emu-wrens from this population will be feasible. However, relatively high heterozygosity for WYP detected in this study may indicate a larger population than previously thought. A comprehensive assessment of the demographics of the mallee emu-wren population in Wyperfeld, including its capacity to sustain removals for translocation, is thus critically important, both in terms of protecting this isolated population and assessing its potential as a source of novel genetic material for newly established populations.

Observed heterozygosity at all sampling locations was lower than expected heterozygosity. This may suggest reciprocal translocations between populations as a beneficial management strategy to broaden genetic diversity (Frankham 2015). However, it is more likely that reduced heterozygosity was a result of subpopulation structure associated with sampling of family groups (i.e. Wahlund effect, Wahlund 1928). Gene-pool mixing in this scenario would result in a short term increase in heterozygosity before introduced individuals settled into typical mallee emu-wren mating structures, precipitating a decline in heterozygosity in line with that detected here. Differentiation between mallee emu-wren populations in this study was significant but weak. Individuals undergoing translocation experience elevated risk of mortality, either through stress associated with capture and transport or the difficulty of surviving in a novel environment (Dickens *et al.* 2010; Berger-Tal *et al.* 2019). Given genetic similarity between sampling locations and the inherent risk to translocated individuals, conservation managers must carefully weigh the potential benefit of reciprocal translocations against the potential risk of exacerbating population decline through increased probability of mortality to translocated birds. At present, the risk of mortality outweighs any small gain in genetic diversity that may be achieved through reciprocal translocation of mallee emu-wrens, though this may not be the case in future. Other potential sources of genetic material are also worthy of consideration. The rufous-crowned emu-wren *S. ruficeps* is the most closely related species to the mallee emu-wren (Donnellan *et al.* 2009). These two species diverged between 1.5 and 3.3 million years ago (Donnellan *et al.* 2009). The rufous-crowned emu-wren is not considered threatened and has a distribution that spans from the western Australian coastline to the Simpson Desert, across much of Australia's arid interior (Higgins *et al.* 2001). The rufous-crowned emu-wren may be a source for genetic rescue of the mallee emu-wren that poses little risk to extant populations

of either species. In addition, rufous-crowned emu-wren are found in habitat that is typically hotter and drier than that of the Victorian mallee (Higgins *et al.* 2001). Introducing rufous-crowned emu-wren genetic material to mallee emu-wren populations may provide adaptive potential in the face of increased drought associated with climate change. Gene pool mixing between genetically and morphologically distinct populations poses some risk of outbreeding depression, however, comprehensive reviews of case studies suggest that the benefits of genetic rescue are common while the risk of outbreeding depression is rarely realised (Frankham *et al.* 2011; Thavornkanlapachai *et al.* 2019; Liddell *et al.* 2021). Assessing the feasibility of interbreeding between these two emu-wren species would be a conservative first step to assess whether genetic rescue using rufous-crowned emu-wrens is worth pursuing as an avenue of research, especially in the event of future population declines or major genetic bottlenecks resulting from wildfire in currently occupied habitat.

References

- Allendorf, FW (1986) Genetic drift and the loss of alleles versus heterozygosity. *Zoo Biology* **5**, 181-190.
- Andersen, A, Simcox, DJ, Thomas, JA, Nash, DR (2014) Assessing reintroduction schemes by comparing genetic diversity of reintroduced and source populations: A case study of the globally threatened large blue butterfly (*Maculinea anion*). *Biological Conservation* **175**, 34-41.
- Anderson, EC, Dunham, KK (2008) The influence of family groups on inferences made with the program Structure. *Molecular Ecology Resources* **8**, 1219-29.
- Berger-Tal, O, Blumstein, DT, Swaisgood, RR (2019) Conservation translocations: a review of common difficulties and promising directions. *Animal Conservation* **23**, 121-131.
- Binks, RM, Kennington, WJ, Johnson, MS (2007) Rapid evolutionary responses in a translocated population of intertidal snail (*Bembicium vittatum*) utilise variation from different source populations. *Conservation Genetics* **8**, 1421-1429.
- Boulton, RL, Lau, J, 2015. Threatened Mallee Birds Conservation Action Plan, Report June 2015. Report to the Threatened Mallee Birds Implementation Team, Birdlife Australia.
- Bouzat, JL (2010) Conservation genetics of population bottlenecks: the role of chance, selection, and history. *Conservation Genetics* **11**, 463-478.

- Brown, S, Clarke, M, Clarke, R (2009) Fire is a key element in the landscape-scale habitat requirements and global population status of a threatened bird: The Mallee Emu-wren (*Stipiturus mallee*). *Biological Conservation* **142**, 432-445.
- Brown, SM, Harrison, KA, Clarke, RH, Bennett, AF, Sunnucks, P (2013) Limited population structure, genetic drift and bottlenecks characterise an endangered bird species in a dynamic, fire-prone ecosystem. *PLoS One* **8**, e59732.
- Ceballos, G, Ehrlich, PR, Barnosky, AD, García, A, Pringle, RM, Palmer, TM (2015) Accelerated modern human-induced species losses: Entering the sixth mass extinction. *Science advances* **1**, e1400253.
- Chapin, FS, Zavaleta, ES, Eviner, VT, Naylor, RL, Vitousek, PM, Reynolds, HL, Hooper, DU, Lavorel, S, Sala, OE, Hobbie, SE (2000) Consequences of changing biodiversity. *Nature* **405**, 234-242.
- Clarke, RH, Gordon, IR, Clarke, MF (2001) Intraspecific phenotypic variability in the black-eared miner (*Manorina melanotis*); human-facilitated introgression and the consequences for an endangered taxon. *Biological Conservation* **99**, 145-155.
- Connell, J, Hall, MA, Nimmo, DG, Watson, SJ, Clarke, MF, Parr, C (2021) Fire, drought and flooding rains: The effect of climatic extremes on bird species' responses to time since fire. *Diversity and Distributions* **00**, 1-22.
- Connell, J, Watson, SJ, Taylor, RS, Avitabile, SC, Clarke, RH, Bennett, AF, Clarke, MF, Elith, J (2017) Testing the effects of a century of fires: Requirements for post-fire succession predict the distribution of threatened bird species. *Diversity and Distributions* **23**, 1078-1089.
- Cook, CN, Sgro, CM (2017) Aligning science and policy to achieve evolutionarily enlightened conservation. *Conservation Biology* **31**, 501-512.
- Courchamp, F, Berec, L, Gascoigne, J (2008) 'Allee effects in ecology and conservation.' (Oxford University Press: New York).
- Crnokrak, P, Roff, DA (1999) Inbreeding depression in the wild. *Heredity* **83**, 260-270.
- Department of Environment Land Water and Planning (2021) 'Bioregions and EVC benchmarks.' Available at <https://www.environment.vic.gov.au/biodiversity/bioregions-and-evc-benchmarks> [Accessed 26/12/2021].
- Department of the Environment (2014) 'Estimated Pre-1750 Major Vegetation Subgroups. Bioregional Assessment Source Dataset.' Available at <http://data.bioregionalassessments.gov.au/dataset/2208babe-8e88-4423-91e6-b9a3fa6f31b6> [Accessed 29 December 2021].

- DeWoody, JA, Harder, AM, Mathur, S, Willoughby, JR (2021) The long-standing significance of genetic diversity in conservation. *Molecular Ecology* **30**, 4147-4154.
- Dickens, MJ, Delehanty, DJ, Michael Romero, L (2010) Stress: An inevitable component of animal translocation. *Biological Conservation* **143**, 1329-1341.
- Donnellan, SC, Armstrong, J, Pickett, M, Milne, T, Baulderstone, J, Hollfelder, T, Bertozzi, T (2009) Systematic and conservation implications of mitochondrial DNA diversity in emu-wrens, *Stipiturus* (Aves: Maluridae). *Emu - Austral Ornithology* **109**, 143-152.
- Evanno, G, Regnaut, S, Goudet, J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology* **14**, 2611-2620.
- Fernandez-Fournier, P, Lewthwaite, JMM, Mooers, AØ (2021) Do We Need to Identify Adaptive Genetic Variation When Prioritizing Populations for Conservation? *Conservation Genetics* **22**, 205-216.
- Fischer, J, Lindenmayer, DB (2000) An assessment of the published results of animal relocations. *Biological Conservation* **96**, 1-11.
- Frankham, R (2015) Genetic rescue of small inbred populations: meta-analysis reveals large and consistent benefits of gene flow. *Molecular Ecology* **24**, 2610-8.
- Frankham, R, Ballou, JD, Eldridge, MD, Lacy, RC, Ralls, K, Dudash, MR, Fenster, CB (2011) Predicting the probability of outbreeding depression. *Conservation Biology* **25**, 465-75.
- Frankham, R, Ballou, JD, Ralls, K, Eldridge, MDB, Dudash, MR, Fenster, CB, Lacy, RC, Sunnucks, P (2017) 'Genetic management of fragmented animal and plant populations.' (Oxford University Press: Oxford).
- Furlan, E, Stoklosa, J, Griffiths, J, Gust, N, Ellis, R, Huggins, RM, Weeks, AR (2012) Small population size and extremely low levels of genetic diversity in island populations of the platypus, *Ornithorhynchus anatinus*. *Ecology and Evolution* **2**, 844-57.
- Goudet, J (2005) Hierfstat, a package for R to compute and test hierarchical F-statistics. *Molecular Ecology Notes* **5**, 184-186.
- Gruber, B, Unmack, PJ, Berry, OF, Georges, A (2018) dartr: An r package to facilitate analysis of SNP data generated from reduced representation genome sequencing. *Molecular Ecology Resources* **18**, 691-699.
- Grueber, CE, Sutton, JT, Heber, S, Briskie, JV, Jamieson, IG, Robertson, BC (2017) Reciprocal translocation of small numbers of inbred individuals rescues immunogenetic diversity. *Molecular Ecology* **26**, 2660-2673.

- He, X, Johansson, ML, Heath, DD (2016) Role of genomics and transcriptomics in selection of reintroduction source populations. *Conservation Biology* **30**, 1010-1018.
- Heber, S, Varsani, A, Kuhn, S, Girg, A, Kempenaers, B, Briskie, J (2013) The genetic rescue of two bottlenecked South Island robin populations using translocations of inbred donors. *Proceedings of the Royal Society B: Biological Sciences* **280**, 20122228.
- Higgins, PJ, Peter, JM, Steele, WK (2001) 'Handbook of Australian, New Zealand and Antarctic Birds.' (Oxford University Press: Melbourne).
- Hundertmark, KJ, Van Daele, LJ (2010) Founder effect and bottleneck signatures in an introduced, insular population of elk. *Conservation Genetics* **11**, 139-147.
- IUCN/SSC (2013) 'Guidelines for Reintroductions and Other Translocations. Version 1.0.' (IUCN Species Survival Commission: Gland, Switzerland).
- Keller, LF, Waller, DM (2002) Inbreeding effects in wild populations. *Trends in Ecology & Evolution* **17**, 230-241.
- Kilian, A, Wenzl, P, Huttner, E, Carling, J, Xia, L, Blois, H, Caig, V, Heller-Uszynska, K, Jaccoud, D, Hopper, C (2012) Diversity arrays technology: a generic genome profiling technology on open platforms. In 'Data production and analysis in population genomics.' pp. 67-89. (Springer: New York, NY).
- Kopelman, NM, Mayzel, J, Jakobsson, M, Rosenberg, NA, Mayrose, I (2015) Clumpak: a program for identifying clustering modes and packaging population structure inferences across K. *Molecular Ecology Resources* **15**, 1179-1191.
- Laikre, L, Allendorf, FW, Aroner, LC, Baker, CS, Gregovich, DP, Hansen, MM, Jackson, JA, Kendall, KC, McKELVEY, K, Neel, MC (2010) Neglect of genetic diversity in implementation of the convention on biological diversity. *Conservation Biology* **24**, 86-88.
- Lande, R (1995) Mutation and conservation. *Conservation Biology* **9**, 782-791.
- Langridge, J, Sordello, R, Reyjol, Y (2021) Existing evidence on the outcomes of wildlife translocations in protected areas: a systematic map. *Environmental Evidence* **10**, 29.
- Liddell, E, Sunnucks, P, Cook, CN (2021) To mix or not to mix gene pools for threatened species management? Few studies use genetic data to examine the risks of both actions, but failing to do so leads disproportionately to recommendations for separate management. *Biological Conservation* **256**, 109072.

- Maguire, GS, Mulder, RA (2004) Breeding biology and demography of the southern emu-wren (*Stipiturus malachurus*). *Australian Journal of Zoology* **52**, 583-604.
- Malone, EW, Perkin, JS, Leckie, BM, Kulp, MA, Hurt, CR, Walker, DM (2018) Which species, how many, and from where: Integrating habitat suitability, population genomics, and abundance estimates into species reintroduction planning. *Global Change Biology* **24**, 3729-3748.
- Mitchell, WF, Boulton, RL, Ireland, L, Hunt, TJ, Verdon, SJ, Olds, LGM, Hedger, C, Clarke, RH (2021a) Using experimental trials to improve translocation protocols for a cryptic, endangered passerine. *Pacific conservation biology* - online early
- Mitchell, WF, Boulton, RL, Sunnucks, P, Clarke, RH (2021b) Are we adequately assessing the demographic impacts of harvesting for wild-sourced conservation translocations? *Conservation Science and Practice* **4**, e569
- Morris, SD, Brook, BW, Moseby, KE, Johnson, CN (2021) Factors affecting success of conservation translocations of terrestrial vertebrates: A global systematic review. *Global Ecology and Conservation* **28**, e01630.
- Nei, M, Maruyama, T, Chakraborty, R (1975) The bottleneck effect and genetic variability in populations. *Evolution* **29**, 1-10.
- Newbold, T, Hudson, LN, Hill, SL, Contu, S, Lysenko, I, Senior, RA, Borger, L, Bennett, DJ, Choimes, A, Collen, B, Day, J, De Palma, A, Diaz, S, Echeverria-Londono, S, Edgar, MJ, Feldman, A, Garon, M, Harrison, ML, Alhusseini, T, Ingram, DJ, Itescu, Y, Kattge, J, Kemp, V, Kirkpatrick, L, Kleyer, M, Correia, DL, Martin, CD, Meiri, S, Novosolov, M, Pan, Y, Phillips, HR, Purves, DW, Robinson, A, Simpson, J, Tuck, SL, Weiher, E, White, HJ, Ewers, RM, Mace, GM, Scharlemann, JP, Purvis, A (2015) Global effects of land use on local terrestrial biodiversity. *Nature* **520**, 45-50.
- Pembleton, LW, Cogan, NOI, Forster, JW (2013) StAMPP: an R package for calculation of genetic differentiation and structure of mixed-ploidy level populations. *Molecular Ecology Resources* **13**, 946-952.
- Pierson, JC, Coates, DJ, Oostermeijer, JGB, Beissinger, SR, Bragg, JG, Sunnucks, P, Schumaker, NH, Young, AG (2016) Genetic factors in threatened species recovery plans on three continents. *Frontiers in Ecology and the Environment* **14**, 433-440.
- Pritchard, JK, Stephens, M, Donnelly, P (2000) Inference of population structure using multilocus genotype data. *Genetics* **155**, 945-959.

- Ralls, K, Ballou, JD, Dudash, MR, Eldridge, MDB, Fenster, CB, Lacy, RC, Sunnucks, P, Frankham, R (2018) Call for a Paradigm Shift in the Genetic Management of Fragmented Populations. *Conservation Letters* **11**, e12412.
- Ralls, K, Sunnucks, P, Lacy, RC, Frankham, R (2020) Genetic rescue: A critique of the evidence supports maximizing genetic diversity rather than minimizing the introduction of putatively harmful genetic variation. *Biological Conservation* **251**, 108784.
- Reuter, JA, Spacek, DV, Snyder, MP (2015) High-throughput sequencing technologies. *Molecular Cell* **58**, 586-97.
- Robledo-Ruiz, DA, Pavlova, A, Clarke, RH, Magrath, MJL, Quin, B, Harrison, KA, Gan, HM, Low, GW, Sunnucks, P (2022) A novel framework for evaluating in situ breeding management strategies in endangered populations. *Molecular Ecology Resources* **22**, 239-253.
- Saccheri, I, Kuussaari, M, Kankare, M, Vikman, P, Fortelius, W, Hanski, I (1998) Inbreeding and extinction in a butterfly metapopulation. *Nature* **392**, 491-494.
- Schlaepfer, DR, Braschler, B, Rusterholz, HP, Baur, B (2018) Genetic effects of anthropogenic habitat fragmentation on remnant animal and plant populations: a meta-analysis. *Ecosphere* **9**, e02488.
- Tanentzap, AJ, Lloyd, KM (2017) Fencing in nature? Predator exclusion restores habitat for native fauna and leads biodiversity to spill over into the wider landscape. *Biological Conservation* **214**, 119-126.
- Thavornkanlapachai, R, Mills, HR, Ottewell, K, Dunlop, J, Sims, C, Morris, K, Donaldson, F, Kennington, WJ (2019) Mixing Genetically and Morphologically Distinct Populations in Translocations: Asymmetrical Introgression in A Newly Established Population of the Boodie (*Bettongia lesueur*). *Genes* **10**, 729.
- Verdon, SJ, Mitchell, WF, Clarke, MF (2021) Can flexible timing of harvest for translocation reduce the impact on fluctuating source populations? *Wildlife Research* **48**, 458-469.
- Verdon, SJ, Watson, SJ, Clarke, MF (2019) Modeling variability in the fire response of an endangered bird to improve fire-management. *Ecological Applications* **29**, e01980.
- Verdon, SJ, Watson, SJ, Nimmo, DG, Clarke, MF (2020) Are all fauna associated with the same structural features of the foundation species *Triodia scariosa*? *Austral Ecology* **45**, 773-787.
- Weeks, AR, Sgro, CM, Young, AG, Frankham, R, Mitchell, NJ, Miller, KA, Byrne, M, Coates, DJ, Eldridge, MD, Sunnucks, P, Breed, MF, James, EA, Hoffmann, AA (2011) Assessing the benefits and risks of translocations in changing environments: a genetic perspective. *Evolutionary Applications* **4**, 709-725.

Weeks, AR, Stoklosa, J, Hoffmann, AA (2016) Conservation of genetic uniqueness of populations may increase extinction likelihood of endangered species: the case of Australian mammals. *Frontiers in Zoology* **13**, 1-9.

Wahlund, S (1928) Composition of populations and correlation appearances viewed in relation to the studies of inheritance. *Hereditas* **11**, 65-106.

Weir, BS, Cockerham, CC (1984) Estimating F-statistics for the analysis of population structure. *Evolution* **38**, 1358-1370.

Yi, X, Latch, EK (2021) Nonrandom missing data can bias Principal Component Analysis inference of population genetic structure. *Molecular Ecology Resources* **00**, 1-10.

6. Discussion

Translocation is increasingly employed as a conservation measure (Resende *et al.* 2020; Langridge *et al.* 2021). The potential benefits of this strategy are numerous. Translocations can broaden the distributions of threatened taxa, restore important ecological functions to damaged natural systems, alleviate declines in genetic diversity and fitness by restoring gene flow and can allow the establishment of havens for species decimated by novel predators or anthropogenic threats (Moseby *et al.* 2011; Ripple and Beschta 2012; Frankham 2015). The list of potential conservation benefits goes on. Overall, translocation has had a considerable and positive impact on threatened species management globally. Such benefits, however, are not always realised (Berger-Tal *et al.* 2019). Success is far from guaranteed despite the knowledge gained during decades of translocation management (Morris *et al.* 2021). To maximise conservation outcomes, research should provide decision-making support for translocation programs through their planning and execution (Taylor *et al.* 2017).

In this thesis, I have used a structured literature review to demonstrate empirically that the potential impact of removing individuals from wild populations for translocation is rarely addressed in the recent literature. I have proposed a framework for ensuring that harvesting for translocation is sustainable and I have advocated for standardised reporting on the rationale underlying management decisions regarding translocation source populations. I used the proposed translocation of five island-endemic passerines as a case study to demonstrate the implementation of this framework. Throughout this thesis, I have used real-world examples to investigate many of the knowledge gaps highlighted in recent reviews of conservation translocation practice. I have placed particular focus on implementing translocations adaptively, allowing explicit comparisons of competing management strategies and, in doing so, have directly informed conservation decision-making. I focused at the meta-population level, and considered the net outcome for focal taxa across source and release populations when evaluating the effectiveness of conservation translocations. I incorporated population genomics as a core feature of conservation planning for focal species and investigated avenues for broadening genetic diversity. By addressing these aspects of translocation practice, highlighted as areas in which the field needs to improve (Laikre *et al.* 2010; Pierson *et al.* 2016; Taylor *et al.* 2017), I have provided examples of best-practice translocation management with wide-ranging relevance.

My focus has been on broadly applicable strategies for evidence-based management of threatened species translocation programs. However, I have also contributed key ecological insight for those species used as case studies in this thesis. I have estimated population size for the five remaining passerines endemic to Norfolk Island. Given the twentieth century extinctions of seven endemic avian taxa from this Island, contemporary demographic knowledge is critical for the ongoing conservation of these threatened taxa. My research has also led to an improved understanding of the ecology of the endangered mallee emu-wren. I show that this charismatic mallee specialist is able to survive capture and transport, maintains group fidelity through translocation, and will attempt breeding soon after release if conditions are appropriate. I show that releasing mallee emu-wrens in spring, rather than autumn, leads to more favourable translocation outcomes. My research program also provided the first published evidence that the mallee emu-wren is a facultative cooperative breeder (Hunt *et al.* 2019). Whilst a new population of mallee emu-wrens could not be successfully established, by trialling a mallee emu-wren reintroduction within an experimental framework I was able to gain important insight that will improve and inform future mallee emu-wren conservation, including additional translocations.

Summary of core findings

In chapter two of this thesis, I sought to summarise common methods for assessing the capacity of translocation source populations to sustain removals of wild individuals for translocation programs. The catalyst for my PhD program was the (at the time) planned trial reintroduction of the mallee emu-wren to Ngarkat Conservation Park. During the planning of this program, I struggled with the problem of statistical power. The mallee emu-wren translocation team wanted to track the time it took source populations to recover from harvest, as recommended by best practice guidelines. We were planning to remove up to twenty-four birds from any one specific area. The removal of twenty-four birds had potential to have a considerable impact on the dynamics of a sparsely distributed local population but I was struggling to come up with a method that would have a reasonable statistical power to detect such an effect. To address this problem, I turned to the literature, and here I was surprised to find few studies that explicitly assessed the impact of harvesting in the context of translocation, despite a small number of studies that provided strong arguments in favour of such an approach (Dimond and Armstrong 2007; Pérez *et al.* 2012; Ferrer *et al.* 2014). From the outset, the mallee emu-wren reintroduction program was framed as a small-scale trial (phase one) that would inform larger-scale (phase two) reintroductions into other parts of the species' historic range. Relatively few birds would be removed in phase one but in the absence of a captive-breeding program, phase two would likely have a larger impact on extant mallee emu-wren populations. Especially as it became apparent that fewer mallee emu-wrens remained in wild populations than previous research had indicated (Verdon *et al.*

2021). This problem led me to pursue a deeper investigation of current literature to identify trends in current management of translocation source populations.

I carried out a structured review of 292 primary research articles with a focus on conservation translocation of wild-sourced terrestrial vertebrates and found that only 11% provided a justification for the removal of individuals from wild source populations. In 63% of studies, no reference was made to potential impact on, or indeed population demographics of, translocation source populations. Salafsky *et al.* (2002) argue that effective conservation is dependent on the pursuit of three questions: what are the goals of a conservation program and how can progress be measured in attaining those goals? How can conservation action be most effective? Finally, how can we learn to do conservation better? With so few references to draw on, it is difficult to answer any of these questions objectively regarding sustainable management of translocation source populations. To rectify this, I proposed a standardised framework for assessing and reporting on likely demographic impacts of harvesting for translocation. I suggested that demographic impacts on translocation source populations are routinely and quantitatively estimated *a priori* and that such estimates are reported. Critically, population recovery following harvesting must also be monitored to verify the accuracy of *a priori* assessments. I presented a detailed list of information that should be included in published summaries of translocation programs. General uptake of this framework will increase transparency in the field and provide a broad body of literature as a resource for current translocation practitioners seeking to minimise impacts on translocation source populations. Innovation in science relies on a firm foundation of knowledge, created by previous research, from which to build on—for this to occur, that research must be published.

In chapter three, I applied the framework presented in Mitchell *et al* (2021; Chapter 2) to estimate sustainable harvesting rates for five threatened passerines on Norfolk Island that are under consideration for translocation. This chapter acts as a widely applicable exemplar for best-practice management of translocation source populations. To make this example as broadly applicable as possible, I projected population trends for my focal species using the long-established population viability (PVA) modelling tool *Vortex* (Lacy and Pollak 2021). My aim was to provide an approach that would be easily applied by translocation managers that do not necessarily have a strong modelling background. *Vortex* incorporates an easy to use graphical user interface, includes extensive documentation to guide users and allows a wide variety of situations to be simulated (Lacy 2019). This approach is fully transparent, as the models that underlie population simulations have been extensively documented. The five passerines chosen as study species in this chapter are all considered threatened or near threatened (Garnett and Baker 2021), and stand to benefit from translocation. However, focal populations of these taxa also display a wide range of demographic traits. Population sizes ranged from ~1500 to ~7000, while reproductive output per nest attempt ranged from 0.56 to 1.52 between taxa. By

including this variation, I have provided a useful comparison of how demographic traits influence a population's capacity to recover from harvesting.

In chapter four, my focus returned to the trial translocation of the Endangered mallee emu-wren. I summarised the knowledge gained during the translocation of this cryptic and challenging species. Despite failing to establish a self-sufficient population in Ngarkat Conservation Park, this chapter provides a comprehensive summary of a translocation implemented in line with contemporary best-practice advice. By structuring releases as experimental treatments, I was able to show that translocating intact social groups can increase post-release group fidelity but, in this case, had little influence on survival or dispersal. Releasing birds in spring led to greater short-term survival, reduced dispersal and a higher proportion of individuals contributing to raising offspring. Temporal variation in animal behaviour is a near universal trait (Sutherland 1998). By timing releases to coincide with favourable seasonal behaviour of focal species, translocation managers can increase probability of success. Unfortunately, this translocation immediately preceded a two-year period of below average rainfall, highlighting the importance of climatic conditions when translocating species in dynamic environments. For maximum conservation benefit, future mallee emu-wren translocations should be timed to align with favourable climatic conditions (such as the *La Niña* phase of the *El Niño* Southern Oscillation). In addition, spring releases of familiar social groups should be prioritised while translocating larger numbers of emu-wrens than that trialled in the phase one translocation will likely increase the probability of successfully establishing a new population.

In my final data chapter, I described genetic characteristics of mallee emu-wren populations across their contemporary range. Genetic structure across sampling locations was weak despite considerable geographic barriers between populations. Mallee emu-wrens exhibited consistently low genetic diversity despite variation in size and connectivity. Genetics is infrequently incorporated into conservation management despite the role that genetic diversity plays in persistence of populations (Laikre *et al.* 2010; Cook and Sgro 2017). I used the results of this study to identify optimum locations to source mallee emu-wrens that will maximise genetic diversity in any new population established through translocation. I found that the poorly documented population of mallee emu-wren in Wyperfeld National Park is likely an important source of genetic material. To best utilise this population, it is critical that we invest in better understanding its demographics.

Future directions

In chapters two and three of this thesis I first presented, and then implemented, a framework for the sustainable management of translocation source populations. Ultimately, the effectiveness of this framework will be measured by its uptake in the field of translocation research. My results provide a point of reference,

against which future translocation practice might be compared as a means to measure improvement in the field.

Efforts to conserve the mallee emu-wren and endemic passerines of Norfolk Island are ongoing. For the endemic passerines of Norfolk Island, a key factor that will determine persistence of extant populations, as well the capacity of these populations to recover from harvesting, is the presence of invasive rodents (Nance *et al.* 2021). It is likely that important passerine vital rates, such as mortality and reproductive output are intricately linked to the dynamics of invasive rodent populations (Nance *et al.* 2021). Incorporating dynamic predation pressure associated with Norfolk Island's rodent population would lead to an improved ability to project population trends of passerine species on Norfolk Island.

I found that an important factor predicting a population's capacity to rapidly recover following harvesting was the strength of effect of population density on reproductive rate. Density-dependent reproductive rate refers to a reduction in offspring production as a population approaches carrying capacity (Sæther *et al.* 2002; Armstrong *et al.* 2005). This process may be driven by competition for resources or territories and frequently acts as the theoretical basis for sustainable harvest modelling (Pöysä *et al.* 2004; Brook and Bradshaw 2006; Bakker and Doak 2009; Hartmann *et al.* 2017). As individuals are harvested from a population, resources or territories become available, intra-species competition is reduced and reproductive output increases. Consequently, the impact of harvest is offset. It is difficult to quantify density dependent processes in wild populations, as to do so one requires data encompassing reproductive output and mortality across multiple seasons or years (Abadi *et al.* 2012). In my study, not all of the necessary data was available and so density dependence was estimated using the best available information. Density-dependent processes have been demonstrated as a common feature in several populations across a wide range of taxa (Brook and Bradshaw 2006), and it is reasonable to assume that this is also the case for the endemic passerines of Norfolk Island. The implementation of translocations on Norfolk Island will provide an important opportunity to improve our understanding of density dependent processes for these taxa. Monitoring of reproductive rate, mortality and territory size within passerine populations before and after individuals are removed for translocation, will allow assumptions pertaining to density dependence to be tested in a controlled experiment. Release populations will also provide an important opportunity to investigate density dependent processes for these taxa. Once a population has been established through translocation, it is typical to expect a period of rapid population increase followed by a gradual deceleration in reproductive output as that population approaches carrying capacity (Armstrong *et al.* 2005; Grueber *et al.* 2012). Assessing density dependence in these circumstances may be more feasible than at source populations as translocation provides an opportunity to mark all individuals released (aiding monitoring) and there is little capacity for immigration of neighbouring individuals

to introduce bias. Any new information gained from such studies should then be incorporated into updated harvest models if additional translocations are to occur.

Despite failure to establish a self-sufficient population of mallee emu-wrens in Ngarkat Conservation Park, translocation remains one of the best available strategies to address the decline of this species. The black summer bushfires that ravaged eastern Australia in the summer of 2019/2020 were a potent warning that we have little capacity to protect biodiversity assets from large-scale fire (Boer *et al.* 2020). Continued efforts to broaden the distribution of mallee emu-wrens will dilute, but never fully alleviate, the damage that could be caused to this species by a large wild fire in the Australian mallee. Mallee emu-wrens inhabiting '*triodia mallee*' vegetation have a time window of occurrence of 20–40 years since fire (though in optimum habitat they can persist indefinitely, Verdon *et al.* 2019; Department of Environment Land Water and Planning 2021). Large areas of historic mallee emu-wren habitat that were burnt by wildfire in 2003, 2006 and 2014 are approaching this time window and may be good candidates for future translocation release sites. Much of the research assessing the influence of time since fire on habitat suitability for mallee emu-wrens has focused on '*Triodia mallee*' as it is typical of Murray-Sunset and Hattah-Kulkyne National Parks where >95% of the contemporary mallee emu-wren population occurs (Brown *et al.* 2009; Connell *et al.* 2017; Verdon *et al.* 2019). Many of the areas that are currently in recovery are composed of semi-arid heathland (Department of Environment Land Water and Planning 2021). *Triodia* vegetation within heathland is structurally different to that found in *Tiodia mallee* and may respond differently following fire. Planning for future mallee emu-wren translocations would benefit from research investigating the factors affecting mallee emu-wren occurrence in heathy vegetation.

Mallee emu-wren occurrence may be influenced significantly by climatic conditions (Connell *et al.* 2021). Aligning future translocations with favourable climatic conditions may increase the probability of successfully establishing populations at release sites while minimising harm at translocation source sites. During my candidature, I contributed to a study that assessed the capacity of extant mallee emu-wren populations to sustain harvesting for translocation. We found that demographic impacts of harvesting for translocation were lowest during periods of population increase associated with favourable climatic conditions and recommended that future harvesting for translocation should occur during such climatic periods (Verdon *et al.* 2021). For this to be accomplished, translocation managers must be able to demonstrate that source populations are increasing prior to removing individuals. Autonomous acoustic recorders paired with automated call detection software may be a monitoring approach that will allow population trends at key source sites to be tracked. Such an approach would require relatively little financial investment or field labour and would ensure that source populations had the greatest possible capacity for recovery following harvesting. As an appendix to this thesis, I provide an emu-wren call recogniser capable of identifying mallee emu-wren

calls from field recordings with a high degree of accuracy and precision (see Appendix 5). Before this tool can be implemented, its effectiveness must be assessed using field trials. The establishment of a successful mallee emu-wren captive breeding program would further reduce the potential impact of removing birds for translocation from extant populations (Olds 2014; Harley *et al.* 2018). As well as a source for future translocations, thereby minimising impact on wild populations, such a program would provide a controlled environment to increase our understanding of mallee emu-wren behaviour and husbandry.

In this thesis, I have addressed several key gaps in our understanding of translocation practice but many areas require further research. Effective translocation management typically must incorporate population genetics, conservation ecology, botany, husbandry, behavioural ecology, veterinary medicine, logistics and community based social science (Cruz *et al.* 2016; Pierson *et al.* 2016; Ireland *et al.* 2018; Langridge *et al.* 2021). Translocation programs are complicated and interdisciplinary collaboration is essential for success. For the field of translocation science to progress, periodic critical review of current practice—such as that provided by Taylor *et al.* (2017), Berger-tal *et al.* (2019) or chapter two of this thesis—is necessary to assess performance and to provide a benchmark for future improvement. Conservation must also be dynamic. The current extinction crisis and ongoing global change (e.g. climate change) are likely to result in new challenges that we must be ready to adapt to (Seddon 2010). By implementing translocations collaboratively, experimentally and adaptively, translocation managers have the best chance of maximising conservation outcomes while improving our understanding of translocation science and the ecology of focal species.

Conclusion

In this thesis, I have used real-world case studies to investigate and improve translocation practice across its planning, implementation, post release monitoring and reporting. I have highlighted that sustainable management of translocation source populations is an important aspect of translocation practice that is rarely incorporated in published summaries of translocation research. To address this, I have proposed a framework for making an *a priori* assessment of the potential impact that may be caused by removing individuals from a wild population for translocation. I have provided a case study demonstrating the implementation of this framework using five island-endemic passerines currently under consideration for translocation. General uptake of this framework will improve transparency in the field of translocation science and reduce the chance that translocation practitioners may unwittingly cause significant demographic harm to translocation source populations. By implementing the translocation of an endangered semi-arid passerine within an experimental structure, I have shown that timing of release groups can influence post-release behaviour, survival and reproductive output. Similarly, familiarity of release groups can influence post-release group fidelity, though

in this case did not influence survival or reproductive output. I have characterised genetic diversity in the global population of the mallee emu-wren and used these data to inform future conservation priorities for this species, including identifying optimum founders for translocations.

These case studies have allowed me to investigate and inform translocation practice generally. However, in doing so I have contributed to our ecological understanding of these threatened species. Translocation is a viable conservation strategy for the mallee emu-wren. Capture, transport and release of mallee emu-wren was achieved efficiently and with few mortalities. Translocated birds survived in the short term and a relatively high proportion of groups successfully reproduced at the destination site. Ultimately, the population did not persist. However, the knowledge gained during this trial, and presented in this thesis, will greatly improve future translocations of mallee emu-wren. I have shown that translocation is also a feasible conservation strategy for the Norfolk robin, Norfolk grey fantail, Norfolk golden whistler, slender-billed white-eye and Norfolk gerygone. This is in the context that current populations are sufficiently robust to recover within ten years following removals of individuals for translocation. While this program is in the early stages of development, my research has shown that pursuing translocation, as a means to broaden the distribution of these threatened taxa, has potential.

References

- Abadi, F, Gimenez, O, Jakober, H, Stauber, W, Arlettaz, R, Schaub, M (2012) Estimating the strength of density dependence in the presence of observation errors using integrated population models. *Ecological Modelling* **242**, 1-9.
- Armstrong, DP, Davidson, RS, Perrott, JK, Roygard, JON, Buchanan, LEN (2005) Density-dependent population growth in a reintroduced population of North Island saddlebacks. *Journal of Animal Ecology* **74**, 160-170.
- Bakker, VJ, Doak, DF (2009) Population Viability Management: Ecological Standards to Guide Adaptive Management for Rare Species. *Frontiers in Ecology and the Environment* **7**, 158-165.
- Berger-Tal, O, Blumstein, DT, Swaisgood, RR (2019) Conservation translocations: a review of common difficulties and promising directions. *Animal Conservation* **23**, 121-131.
- Boer, MM, de Dios, VR, Bradstock, RA (2020) Unprecedented burn area of Australian mega forest fires. *Nature Climate Change* **10**, 171-172.

- Brook, BW, Bradshaw, CJA (2006) Strength of Evidence for density dependence in abundance time series of 1198 species. *Ecology* **87**, 1445–1451.
- Brown, S, Clarke, M, Clarke, R (2009) Fire is a key element in the landscape-scale habitat requirements and global population status of a threatened bird: The Mallee Emu-wren (*Stipiturus mallee*). *Biological Conservation* **142**, 432-445.
- Connell, J, Hall, MA, Nimmo, DG, Watson, SJ, Clarke, MF, Parr, C (2021) Fire, drought and flooding rains: The effect of climatic extremes on bird species' responses to time since fire. *Diversity and Distributions* **00**, 1-22.
- Connell, J, Watson, SJ, Taylor, RS, Avitabile, SC, Clarke, RH, Bennett, AF, Clarke, MF, Elith, J (2017) Testing the effects of a century of fires: Requirements for post-fire succession predict the distribution of threatened bird species. *Diversity and Distributions* **23**, 1078-1089.
- Cook, CN, Sgro, CM (2017) Aligning science and policy to achieve evolutionarily enlightened conservation. *Conservation Biology* **31**, 501-512.
- Cruz, CEF, Cerva, C, Andretta, I (2016) Financial Costs of Conserving Captive-bred Wild Birds. *Der Zoologische Garten* **85**, 354-362.
- Department of Environment Land Water and Planning (2021) 'Bioregions and EVC benchmarks.' Available at <https://www.environment.vic.gov.au/biodiversity/bioregions-and-evc-benchmarks> [Accessed 26/12/2021].
- Dimond, WJ, Armstrong, DP (2007) Adaptive Harvesting of Source Populations for Translocation: A Case Study with New Zealand Robins. *Conservation Biology* **21**, 114-124.
- Ferrer, M, Newton, I, Muriel, R, Báguena, G, Bustamante, J, Martini, M, Morandini, V, Pärt, T (2014) Using manipulation of density-dependent fecundity to recover an endangered species: the bearded vulture *Gypaetus barbatus* an example. *Journal of Applied Ecology* **51**, 1255-1263.
- Frankham, R (2015) Genetic rescue of small inbred populations: meta-analysis reveals large and consistent benefits of gene flow. *Molecular Ecology* **24**, 2610-8.
- Garnett, ST, Baker, GB (2021) 'The Action Plan for Australian Birds 2020.' (CSIRO publishing: Melbourne, Australia).
- Grueber, CE, Maxwell, JM, Jamieson, IG (2012) Are introduced takahe populations on offshore islands at carrying capacity? Implications for genetic management. *New Zealand Journal of Ecology* **36**, 223-227.

- Harley, D, Mawson, PR, Olds, L, McFadden, M, Hogg, C (2018) The contribution of captive breeding in zoos to the conservation of Australia's threatened fauna. In '*Recovering Australian Threatened Species: A Book of Hope.*' (Eds S Garnett, J Woinarski, D Lindenmayer, P Latch.) pp. 281-294. (CSIRO Publishing: Melbourne, Australia).
- Hartmann, SA, Oppel, S, Segelbacher, G, Juina, ME, Schaefer, HM (2017) Decline in territory size and fecundity as a response to carrying capacity in an endangered songbird. *Oecologia* **183**, 597-606.
- Hunt, T, Mitchell, W, Boulton, R, Hedger, C, Ireland, L (2019) Cooperative breeding recorded in the endangered Mallee Emu-wren *Stipiturus mallee*. *Australian Field Ornithology* **36**, 163-167.
- Ireland, L, Zabek, M, Galindez-Silva, C, Weir, S, West, R, Olds, L, Backhouse, B, Copley, P, Read, J (2018) More than just the animals: opportunities and costs of reintroducing threatened black-footed rock-wallabies to remote Indigenous land. *Pacific conservation biology* **24**, 388-396.
- Lacy, RC (2019) Lessons from 30 years of population viability analysis of wildlife populations. *Zoo Biology* **38**, 67-77.
- Lacy, RC, Pollak, JP (2021) 'Vortex: A stochastic simulation of the extinction process.' (Chicago Zoological Society: Brookfield, Illinois, USA).
- Laikre, L, Allendorf, FW, Aroner, LC, Baker, CS, Gregovich, DP, Hansen, MM, Jackson, JA, Kendall, KC, McKELVEY, K, Neel, MC (2010) Neglect of genetic diversity in implementation of the convention on biological diversity. *Conservation Biology* **24**, 86-88.
- Langridge, J, Sordello, R, Reyjol, Y (2021) Existing evidence on the outcomes of wildlife translocations in protected areas: a systematic map. *Environmental Evidence* **10**, 29.
- Morris, SD, Brook, BW, Moseby, KE, Johnson, CN (2021) Factors affecting success of conservation translocations of terrestrial vertebrates: A global systematic review. *Global Ecology and Conservation* **28**, e01630.
- Moseby, KE, Read, JL, Paton, DC, Copley, P, Hill, BM, Crisp, HA (2011) Predation determines the outcome of 10 reintroduction attempts in arid South Australia. *Biological Conservation* **144**, 2863-2872.
- Nance, AH, Mitchell, W, Clarke, RH, Wilson, M, Brown, SM, MacGregor, NA, Dutson, G, Garnett, ST (2021) Norfolk Island Robin *Petroica multicolor*. In '*The Action Plan for Australian Birds 2020.*' (Eds ST Garnett, GB Baker.) pp. 741-744. (CSIRO Publishing: Melbourne).

- Olds, L (2014) Preliminary feasibility study of establishing a captive bred Mallee Emu-wren *Stipiturus mallee* ex-situ insurance population. Report for Department of Environment, Water and Natural Resources, South Australia. Birdlife Australia.
- Pérez, I, Anadón, JD, Díaz, M, Nicola, GG, Tella, JL, Giménez, A (2012) What is wrong with current translocations? A review and a decision-making proposal. *Frontiers in Ecology and the Environment* **10**, 494-501.
- Pierson, JC, Coates, DJ, Oostermeijer, JGB, Beissinger, SR, Bragg, JG, Sunnucks, P, Schumaker, NH, Young, AG (2016) Genetic factors in threatened species recovery plans on three continents. *Frontiers in Ecology and the Environment* **14**, 433-440.
- Pöysä, H, Elmburg, J, Gunnarson, G, Nummi, P, Sjöberg, K (2004) Ecological basis of sustainable harvesting: is the prevailing paradigm of compensatory mortality still valid? *Oikos* **104**, 612-615.
- Resende, PS, Viana-Junior, AB, Young, RJ, de Azevedo, CS (2020) A global review of animal translocation programs. *Animal Biodiversity and Conservation* **43**, 221-232.
- Ripple, WJ, Beschta, RL (2012) Trophic cascades in Yellowstone: The first 15years after wolf reintroduction. *Biological Conservation* **145**, 205-213.
- Sæther, B-E, Engen, S, Matthysen, E (2002) Demographic Characteristics and Population Dynamical Patterns of Solitary Birds. *Science* **295**, 2070.
- Salafsky, N, Margoluis, R, Redford, KH, Robinson, JG (2002) Improving the practice of conservation: a conceptual framework and research agenda for conservation science. *Conservation Biology* **16**, 1469-1479.
- Seddon, PJ (2010) From Reintroduction to Assisted Colonization: Moving along the Conservation Translocation Spectrum. *Restoration Ecology* **18**, 796-802.
- Sutherland, WJ (1998) The importance of behavioural studies in conservation biology. *Animal Behaviour* **56**, 801-809.
- Taylor, G, Canessa, S, Clarke, RH, Ingwersen, D, Armstrong, DP, Seddon, PJ, Ewen, JG (2017) Is Reintroduction Biology an Effective Applied Science? *Trends in Ecology & Evolution* **32**, 873-880.
- Verdon, SJ, Mitchell, WF, Clarke, MF (2021) Can flexible timing of harvest for translocation reduce the impact on fluctuating source populations? *Wildlife Research* **48**, 458-469.

Verdon, SJ, Watson, SJ, Clarke, MF (2019) Modeling variability in the fire response of an endangered bird to improve fire-management. *Ecological Applications* **29**, e01980.

Appendices

Appendix 1 – Supplementary material to

Chapter 2

Table S2.1. Twenty articles that were used as references to assess the robustness of search terms used in a structured literature review investigating current management of source populations in translocation programs. Reference articles were chosen to be representative of the field of translocation ecology.

Reference	Inclusion justification
Armstrong D.P., Castro I. & Griffiths R. (2007) Using Adaptive Management to Determine Requirements of Re-Introduced Populations: The Case of the New Zealand Hihi. <i>Journal of Applied Ecology</i> , 44, 953-962.	This study describes a translocation within a comprehensive adaptive management framework. It was published prior to the focus window of our review but is an exemplar of conservation management informed by high quality quantitative evidence leading to improved outcomes for a focal species.
Bennett V.A., Doerr V.A.J., Doerr E.D., Manning A.D. & Lindenmayer D.B. (2012) The anatomy of a failed reintroduction: a case study with the Brown Treecreeper. <i>Emu</i> , 112, 298-312.	This study was chosen as a reference article because it encompasses many criteria that we were seeking to include in our study, i.e. it describes a wild-sourced translocation of a terrestrial vertebrate taxa where the motivation for translocation was conservation.
Bozzuto C., Hoeck P.E.A., Bagheri H.C. & Keller L.F. (2017) Modelling different reintroduction strategies for the critically endangered Floreana mockingbird. <i>Animal Conservation</i> , 20, 144-154.	A comprehensive case study demonstrating an approach for sustainable harvesting of wild source populations for the purpose of translocation. This study was included as a reference as it explicitly addresses the management actions we sought to investigate in our review.
Clarke R.H., Boulton R.L. & Clarke M.F. (2002) Translocation of the socially complex Black-eared Miner <i>Manorina melanotis</i> : a trial using hard and soft release techniques. <i>Pacific Conservation Biology</i> , 8, 223-234.	This study details a wild-sourced conservation translocation with particular focus on release protocols. It was chosen as a reference article because it encompasses many criteria that we were seeking to include in our study, i.e. it describes a wild-sourced translocation of a terrestrial vertebrate taxa where the motivation for translocation was conservation.
Davidson A.D., Hunter E.A., Erz J., Lightfoot D.C., McCarthy A.M., Mueller J.K. & Shoemaker K.T. (2018) Reintroducing a	This study was chosen as a reference article because it encompasses many criteria that we

keystone burrowing rodent to restore an arid North American grassland: challenges and successes. <i>Restoration Ecology</i> , 26, 909-920.	were seeking to include in our study, i.e. it describes a wild-sourced translocation of a terrestrial vertebrate taxa where the motivation for translocation was conservation.
Dimond W.J. & Armstrong D.P. (2007) Adaptive Harvesting of Source Populations for Translocation: A Case Study with New Zealand Robins. <i>Conservation Biology</i> , 21, 114-124.	A comprehensive case study demonstrating an approach for sustainable harvesting of wild source populations for the purpose of translocation. This study was included as a reference as it explicitly addresses the management actions we sought to investigate in our review.
Fischer J. & Lindenmayer D.B. (2000) An assessment of the published results of animal relocations. <i>Biological Conservation</i> , 96, 1-11.	This study was included as a reference article as it is a seminal and highly cited review of translocation research.
Griffiths A.D., Rankmore B., Brennan K. & Woinarski J.C.Z. (2017) Demographic evaluation of translocating the threatened northern quoll to two Australian islands. <i>Wildlife Research</i> , 44, 238-247.	This study was chosen as a reference article because it encompasses many criteria that we were seeking to include in our study, i.e. it describes a wild-sourced translocation of a terrestrial vertebrate taxa where the motivation for translocation was conservation. It also assesses population demography, though in this case, the focus is on destination, rather than source, populations.
He X., Johansson M.L. & Heath D.D. (2016) Role of genomics and transcriptomics in selection of reintroduction source populations. <i>Conservation Biology</i> , 30, 1010-1018.	This study was selected as a reference articles as it explicitly assesses management of translocation source populations. The focus here is on using genomics as a tool to select source populations which will maximise reintroduction success at destination populations.
Jamieson I.G. (2011) Founder Effects, Inbreeding, and Loss of Genetic Diversity in Four Avian Reintroduction Programs. <i>Conservation Biology</i> , 25, 115-123.	This study uses several case studies to illustrate the challenges associated with small population size following reintroduction. It was chosen as a reference article because it encompasses many criteria that we were seeking to include in our study, i.e. it describes a wild-sourced translocation of a terrestrial vertebrate taxa where the motivation for translocation was conservation.
Manlick P.J., Woodford J.E., Gilbert J.H., Eklund D. & Pauli J.N. (2017) Augmentation Provides Nominal Genetic and	This study assesses the effectiveness of translocations which were carried out as attempts to bolster genetic diversity of

Demographic Rescue for an Endangered Carnivore. *Conservation Letters*, 10, 178-185.

Margalida A., Colomer M.A., Oro D., Arlettaz R. & Donazar J.A. (2015) Assessing the impact of removal scenarios on population viability of a threatened, long-lived avian scavenger. *Scientific Reports*, 5, 16962.

Milligan M.C., Wells S.L. & McNew L.B. (2018) A Population Viability Analysis for Sharp-Tailed Grouse to Inform Reintroductions. *Journal of Fish and Wildlife Management*, 9, 565-581.

Ottewell K., Dunlop J., Thomas N., Morris K., Coates D. & Byrne M. (2014) Evaluating success of translocations in maintaining genetic diversity in a threatened mammal. *Biological Conservation*, 171, 209-219.

Parlato E.H. & Armstrong D.P. (2018) Predicting reintroduction outcomes for highly vulnerable species that do not currently coexist with their key threats. *Conservation Biology*, 32, 1346-1355.

Taylor G., Canessa S., Clarke R.H., Ingwersen D., Armstrong D.P., Seddon P.J. & Ewen J.G. (2017) Is Reintroduction Biology an Effective Applied Science? *Trends in Ecology & Evolution*, 32, 873-880.

destination populations. It was chosen as a reference article because it encompasses many of the criteria that we were seeking to include in our study, i.e. it describes a wild-sourced translocation of a terrestrial vertebrate taxa where the motivation for translocation was conservation.

A comprehensive case study demonstrating an approach for sustainable harvesting of wild source populations for the purpose of translocation. This study was included as a reference as it explicitly addresses the management actions we sought to investigate in our review.

We included this study as a reference article as it assess competing translocation scenarios within a population viability framework. We were interested to identify how frequently this approach is applied to translocation source populations.

This study evaluates levels of genetic diversity between a source and multiple translocated populations. It was chosen as a reference article because it encompasses many of the criteria that we were seeking to include in our study, i.e. it describes a wild-sourced translocation of a terrestrial vertebrate taxa where the motivation for translocation was conservation.

This study assesses competing translocation scenarios within a population modelling framework. Although the focus of this study is on persistence of release populations in the face of novel predators, we included it as a reference as it encompasses many criteria that we were seeking to include in our study, i.e. it describes a wild-sourced translocation of a terrestrial vertebrate taxa where the motivation for translocation was conservation.

This study was included as a reference article as it is a highly cited evaluation of current translocation practice.

<p>Troy R.J., Coates P.S., Connelly J.W., Gillette G. & Delehanty D.J. (2013) Survival of mountain quail translocated from two distinct source populations. <i>The Journal of Wildlife Management</i>, 77, 1031-1037.</p>	<p>Although the focus of this study is on improving persistence at the destination population, this study was included as a reference article as it explicitly investigates wild translocation source populations, though it does not assess their demographics.</p>
<p>Valderrama S.V., Molles L.E., Waas J.R., Slabbekoorn H. & Stephens P. (2013) Conservation implications of song divergence between source and translocated populations of the North Island Kōkako. <i>Journal of Applied Ecology</i>, 50, 950-960.</p>	<p>This study assesses the influence of translocation on transmission of behaviour. This study was included as a reference article as it explicitly investigates wild translocation source populations, though it does not assess their demographics.</p>
<p>Watson D.M. & Watson M.J. (2015) Wildlife restoration: Mainstreaming translocations to keep common species common. <i>Biological Conservation</i>, 191, 830-838.</p>	<p>This article argues that translocation should become more frequently implemented in management of common taxa. It was included as a reference article as provides a comprehensive summary of current translocation practice.</p>
<p>Weeks A.R., Sgro C.M., Young A.G., Frankham R., Mitchell N.J., Miller K.A., Byrne M., Coates D.J., Eldridge M.D., Sunnucks P., Breed M.F., James E.A. & Hoffmann A.A. (2011) Assessing the benefits and risks of translocations in changing environments: a genetic perspective. <i>Evolutionary Applications</i>, 4, 709-725.</p>	<p>This study proposes a framework for genetic management in translocation programs. It was included as a reference articles as we wanted to ensure our literature search encompassed conservation translocations with a focus on genetic management.</p>

Appendix 2 – Supplementary material to Chapter 3

Table S3.1. The influence of elevation on presence of five passerines endemic to Norfolk Island, determined with binomial regression.

Taxa	Estimate	Z value	p value
Norfolk gerygone	0.006	2.863	0.004
Norfolk golden whistler	0.002	0.990	0.322
Norfolk grey fantail	0.005	2.324	0.020
Norfolk robin	0.002	0.863	0.388
Slender-billed white-eye	< 0.001	0.188	0.851

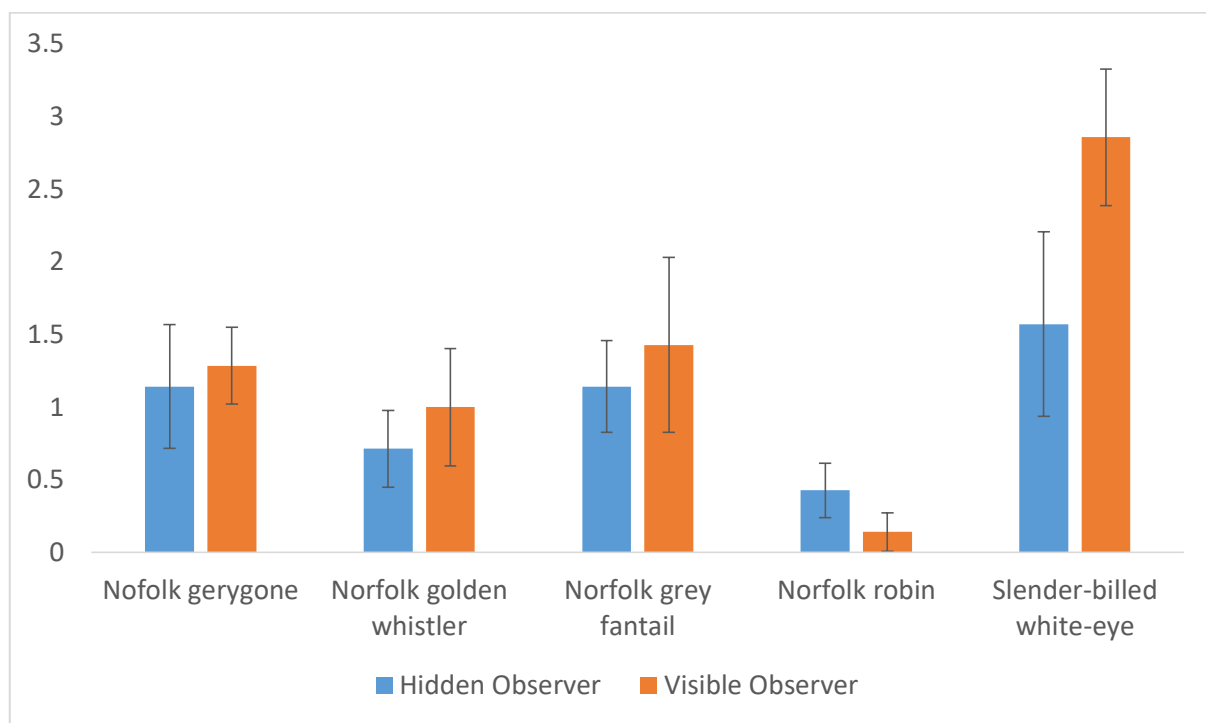


Figure S3.1. We compared mean detection rates of five Norfolk Island bird taxa between a hidden and visible observer. A hidden observer concealed themselves in a small portable hide constructed from camouflage material supported by a bamboo frame with a mesh viewing panel and waited for 15 minutes to allow surrounding bird life to return to normal behaviour following any disturbance. At the end of this settling in period, the observer began a five minute bird count, recording all aural detections and visual detections in front of the hide. Immediately following this, a second observer approached the point on foot and conducted an additional survey following the same protocol with no settling period after arrival (i.e. all aural detections were recorded but visual detections were only recorded in front of the hide. This process was repeated seven times. We performed paired two-sample t tests and found no significant difference in detection rate between observers for any taxa ($p > 0.05$). We conclude that observer attraction or avoidance behaviour of focal bird species is not a significant contributor of survey bias in this system. We also conclude that a settling period prior to beginning surveys is unlikely to influence detection rate.

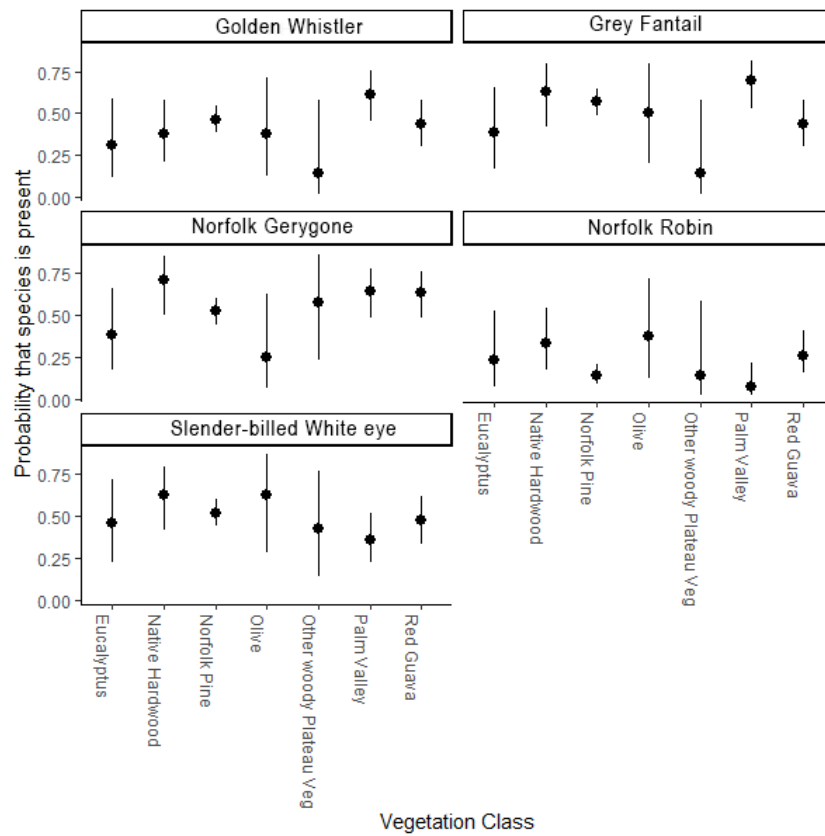


Figure S3.2. The probability that five passerines endemic to Norfolk Island would be present across a range of vegetation classes. Illustrated using a binomial generalised linear model. Vegetation classes were removed if sample size for that class had fewer than three observations. A post-hoc Tukey test revealed no significant differences between groups ($\alpha = 0.05$).

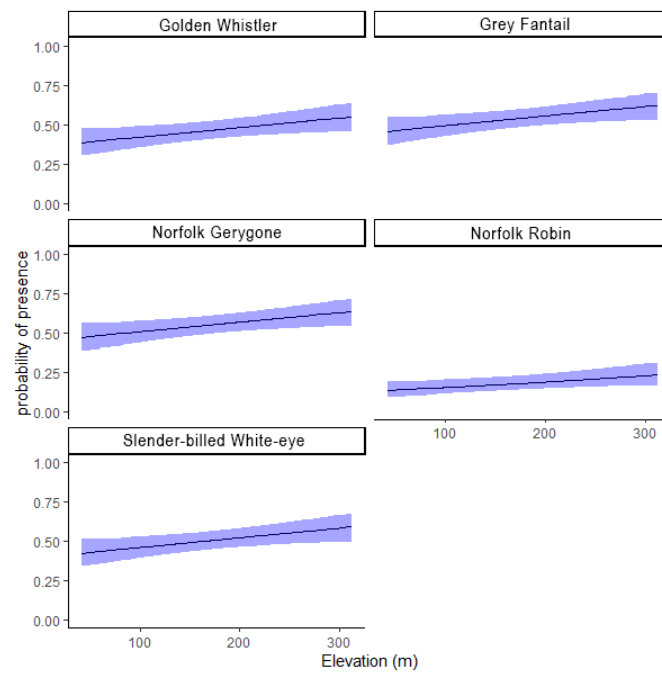


Figure S3.3. The influence of elevation on presence of five passerines endemic to Norfolk Island A shown by binomial regression. Significance values are presented in Table S3.1.

Appendix 3 – Supplementary material to

Chapter 4

Table S4.1. A breakdown of the cost of translocating 78 mallee emu-wren to Ngarkat Conservation Park from Victorian reserves

Description	Unit cost	Unit	Quantity (people days/vehicle days or straight unit)	TOTAL
Personnel				
Project Officers and field officers				\$164,000
Project Officer (permits and ethics)				\$10,000
Project management and overhead costs (several NR SAMDB Staff members)				\$141,099
Total				\$315,099
Field Equipment				
Sat Phone	\$750 ea		2	\$1,500
Garmin Rhino - UHF GPS	\$829 ea		8	\$6,632
Spot Tracker	\$350 ea		10	\$3,500
Spot tracker subscription (2 years for 10 devices)	\$25 month		240	\$6,000
First Aid Kit	\$250 ea		8	\$2,000
Mist nets	\$70 ea		6	\$420
Hand nets	\$80 ea		6	\$480
Misc. capture equipment	\$3,000		1	\$3,000
Transfer boxes	\$300		10	\$3,000
Heating pads	\$10		10	\$100
Bird food (tiny crickets	\$100		1	\$100
Misc. tranfer equipment	\$1,000		1	\$1,000
Total				\$27,732
Translocation Team in April and August: includes field staff, volunteers and vehicles				
April				
Staff	\$550 day		18	\$9,900
Zoos staff	\$550 day		13	\$7,150
volunteers	\$270 day		50	\$13,500
Vehicles	\$99 day		55	\$5,445
fuel	\$2 L		650	\$975
food /pers / day	\$20 day		113	\$2,260
catering and food storage	\$250 day		8	\$2,000
Accomodation at Lameroo	\$92 day		14	\$1,288
Food @ Lameroo, inlcuding meals at motel	\$25 day		24	\$600
Total				\$43,118
August				
DEW	\$550 day		21	\$11,550
Zoos staff	\$550 day		16	\$8,800
volunteers	\$270 day		106	\$28,620
Vehicles	per day \$99 day		62	\$6,138
fuel	\$2 L		800	\$1,200
food \$20 /pers / day	\$20 day		177	\$3,540
catering and food storage	\$2,000			\$2,000
Accomodation at Lameroo	\$92 day		28	\$2,576
Food @ Lameroo, inlcuding meals at motel	\$25 day		32	\$800
Total				\$65,224
Source Site Monitoring - 4 days at each capture site prior to each removal and then yearly follow up surveys at each				
Field Assistant (WFM)	\$350 day		32	\$11,200
DEW vehicle	per day \$99 day		64	\$6,336
fuel	\$1.50 L		600	\$900

Food / pers / day	\$20 day	96	\$1,920
Total			\$20,356
Release Site Monitoring: Includes intensive monitoring for up to 3 weeks following the commencement of each release			
April intensive monitoring			
Volunteer-person days	\$270 day	28	\$7,560
Field Assistant (WFM)	\$350 day	18	\$6,300
Vehicle DEW	per day	36	\$3,564
	fuel	440	\$660
staff + volunteer food / pers / day	\$20 day	73	\$1,460
Total			\$19,544
August intensive monitoring			
Volunteers	\$270 day	75	\$20,250
Field Officer (WFM)	\$350	19	\$6,650
Vehicle DEW	per day	49	\$4,851
	fuel	460	\$690
staff + volunteer food / pers / day	\$20 day	121	\$2,420
Total			\$34,861
Follow Up Occupancy monitoring - includes four trips, each at least 4 days, surveying for Mallee Emu-wren in Ngar			
Paid contractors	\$350.00 day	64	\$22,400
DEW staff	\$550.00 day	3	\$1,650
Field Assistant (WFM)	\$350.00 day	19	\$6,650
Volunteers	\$270.00 day	44	\$11,880
DEW vehicle	\$99.00 day	41	\$4,059
Fuel	\$1.50 L	780	\$1,170
Food	\$20.00 day	156	\$3,120
Total			\$47,809
Total			\$538,882
funded			\$287,958
in-kind			\$250,924

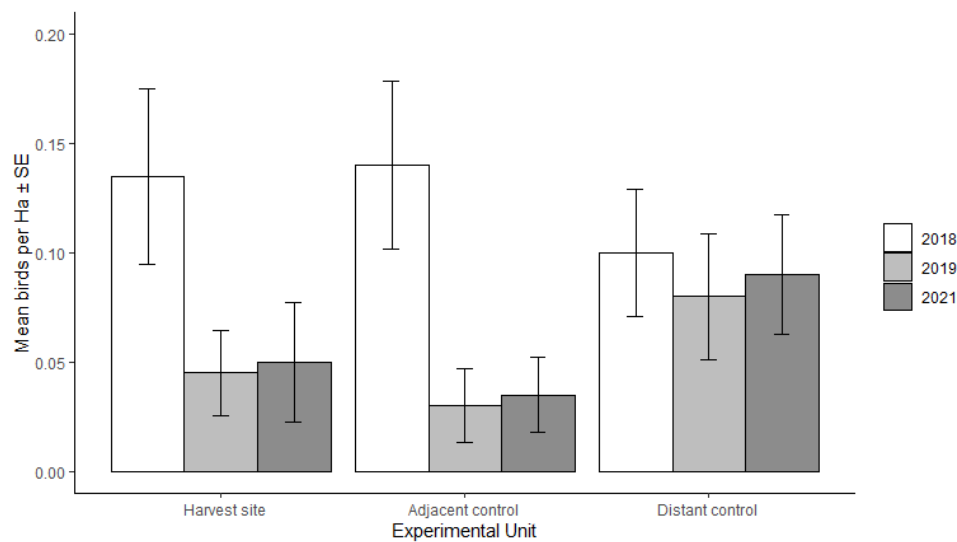


Figure S4.1. Maximum abundance of mallee emu-wrens at translocation harvest and control sites immediately prior to, 12 months after, and 36 months after removals occurred in Nowingi State Forest. Surveys took place in the Austral spring of 2018, 2019 and 2021. Distant control surveys took place at least 2 km from harvest sites in similar habitat. An adjacent control survey took place in similar habitat that abutted the harvest site.

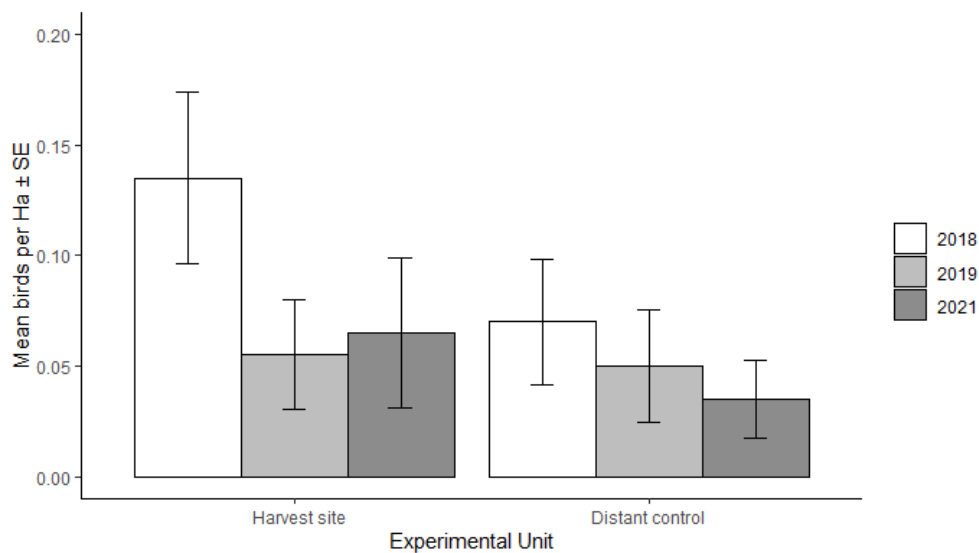


Figure S4.2. Maximum abundance of mallee emu-wrens detected at translocation harvest and control sites before, 12 months after and 36 months after removals occurred in Murray-Sunset National Park. Surveys took place in the Austral spring of 2018, 2019 and 2021. Distant control surveys took place at least 2 km from harvest sites in similar habitat.

Appendix 4 – Supplementary material to

Chapter 5

DArTseq uses complexity-reduction methods with combinations of restriction enzymes targeted at low-copy genomic regions to detect large numbers of informative SNPs within 69 base pair sequences (Kilian et al., 2012). A combination of *Pst*I and *Sph*I restriction enzymes were used in digestion/ligation reactions. Fragments were amplified in 30 rounds of PCR with an initial 94°C denaturation step for 1 min, 30 denaturation steps at 94°C lasting 20 s, 30 s annealing at 58°C, 45 s extension at 72°C, and a final extension step at 72°C. After PCR, equimolar amounts of PCR products were pooled and applied to an Illumina c-bot for bridge PCR for sequencing on an Illumina HiSeq 2500. Single-read sequences were generated with 77 cycles.

The resulting sequences were filtered using the DArT proprietary primary pipeline to remove poor quality sequences and apply more stringent filtering criteria to the barcode region compared to the rest of the sequence (minimum barcode Phred score 30, pass percentage 75; minimum whole-read Phred score 10, pass percentage 50). This higher stringency allowed for reliable assignment of sequences to the same sample. Identical sequences were collapsed into tags, which served as templates against which low quality bases in singleton tags were corrected. SNP calling was performed using the DArT proprietary pipeline, which clusters sequences then parses clusters into separate SNP loci using a range of technical parameters, balancing read counts per allelic pair. Scoring consistency of alleles (repeatability) was determined using technical replicates for 25% of samples.

Table S5.1. Proportion of polymorphic loci and allelic richness in six extant and one extinct mallee emu-wren population. When initial analyses revealed allelic richness values nearly identical for each population we attempted rarefying to a higher value and comparing values of AR with the proportion of polymorphic loci in each population. The results are below.

Pop	Sample size	Monomorphic-polymorphic loci	Proportion of loci polymorphic	AR when rarefaction = 3	AR when rarefaction = 8	AR using package PopGenReport*
Hattah-Kulkyne	31	3,230-10,658	0.77	1.259	1.453	1.396
Central MSNP	8	5,720-8,168	0.59	1.266	1.467	1.394
Eastern MSNP	8	6,357-7,531	0.54	1.257	1.444	1.382
Western MSNP	11	5,654-8,234	0.59	1.242	1.426	1.368
Ngarkat	4	7,893-5,983	0.43	1.262		1.362
MSS	5	7,177-6,710	0.48	1.260		1.375
Wyperfeld	3	8,483-5,389	0.39	1.269		1.354

*This package does not allow NAs in the dataset so I filtered out all missing data for this analysis. Resultant genind object had 70 individuals and 7,769 loci. This function sets the sample size for each combination of population and locus as equal to the smallest number of alleles seen in a sample across all combinations of population and locus.

Table S5.2. Heterozygosity and kinship between individuals that were highlighted as outliers in structure analysis. All HKNP structure outliers were sampled within 500 m of each other. 4 of the seven were confirmed as a family group (female provisioning three nestlings), while high kinship was detected between many individuals. Sampling of family groups may bias structure by inflating inferred k.

Population	Individual	Ho	Known relatedness
HK	MEW_BIOBANK_07	0.1411916	High kinship (0.2–0.24) with siblings 87, 88, 89. Low kinship with mother (<0).
HK	MEW_BIOBANK_30	0.1434363	Mother of 87,88,89
HK	MEW_BIOBANK_89	0.1548157	Sibling of 87 and 88 (kinship 0.24 to 0.25)
HK	MEW_BIOBANK_08	0.1339505	High kinship with 07
HK	MEW_BIOBANK_88	0.1379204	Sibling of 87 and 89
HK	MEW_BIOBANK_87	0.1570340	Sibling of 88 and 89
MSW	MEW_BIOBANK_42	0.1425396	Three individuals (39, 40, 42) with similar structure profiles all sampled within 500 m of each other in a relatively isolated patch of veg. kinship between these individuals ranged between 0.17 and 0.32 (scaled such that 0 = global mean kinship.)
MSW	MEW_BIOBANK_39	0.1343446	
MSW	MEW_BIOBANK_40	0.1351156	
NGA	MEW_BIOBANK_76	0.1546629	76 and 74 share low kinship despite similar profile on structure
NGA	MEW_BIOBANK_74	0.1575474	

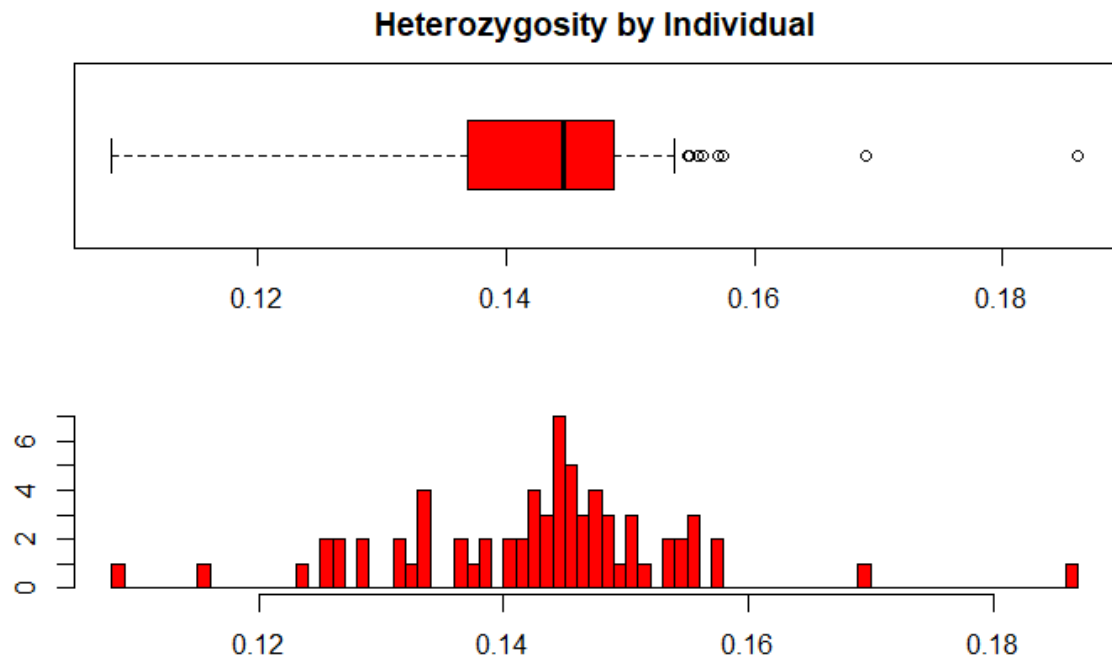


Figure S5.1. Summary (boxplot and histogram) of individual heterozygosity of 70 mallee emu-wrens across six sampling locations within their contemporary range and one location from which they have become extinct.

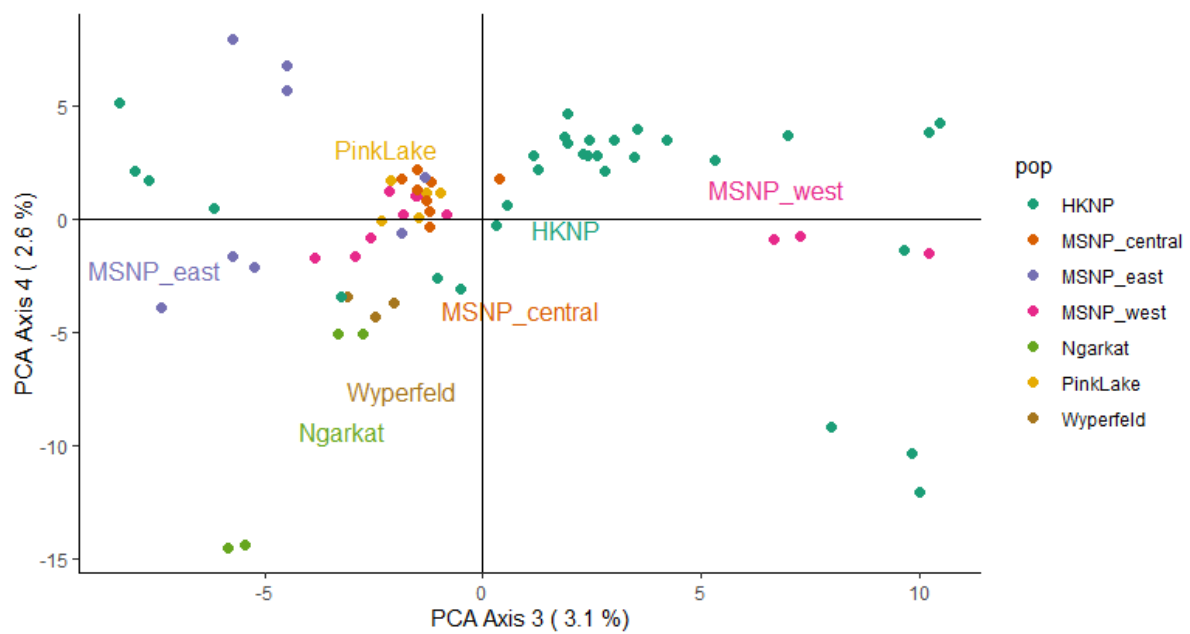


Figure S5.2. Ordinance plot displaying axes 3 and 4 of principal coordinate analysis results for 70 mallee emu-wrens sampled across the contemporary range of the species and one location from which they have become extinct (NGA). HK = Hattah Kulkyne, MSC = Murray-Sunset central, MSE = Murray-Sunset east, MSS = Murray-Sunset south, MSW = Murray-Sunset west, NGA = Ngarkat, WYP = Wyperfeld.

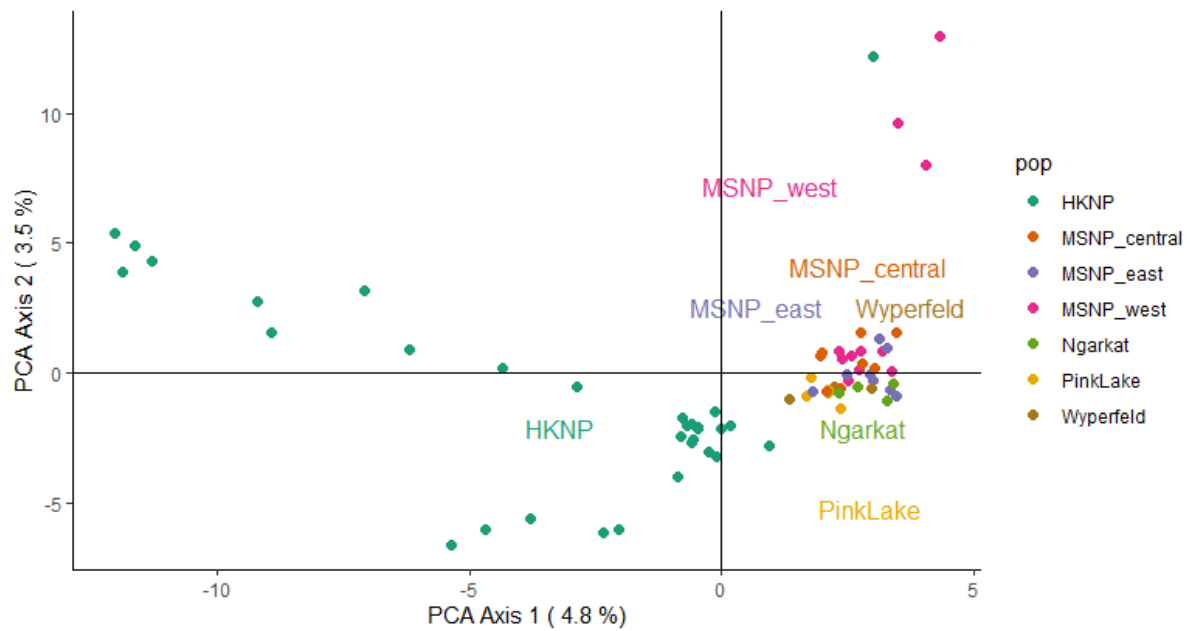


Figure S5.3. Ordinance plot displaying principal coordinate analysis results for 70 mallee emu-wrens sampled across the contemporary range of the species and one location from which they have become extinct (NGA). HK = Hattah Kulkyne, MSC = Murray-Sunset central, MSE = Murray-Sunset east, MSS = Murray-Sunset south, MSW = Murray-Sunset west, NGA = Ngarkat, WYP = Wyperfeld. This dataset contained no missing data (70 individuals 7,769 SNPs).

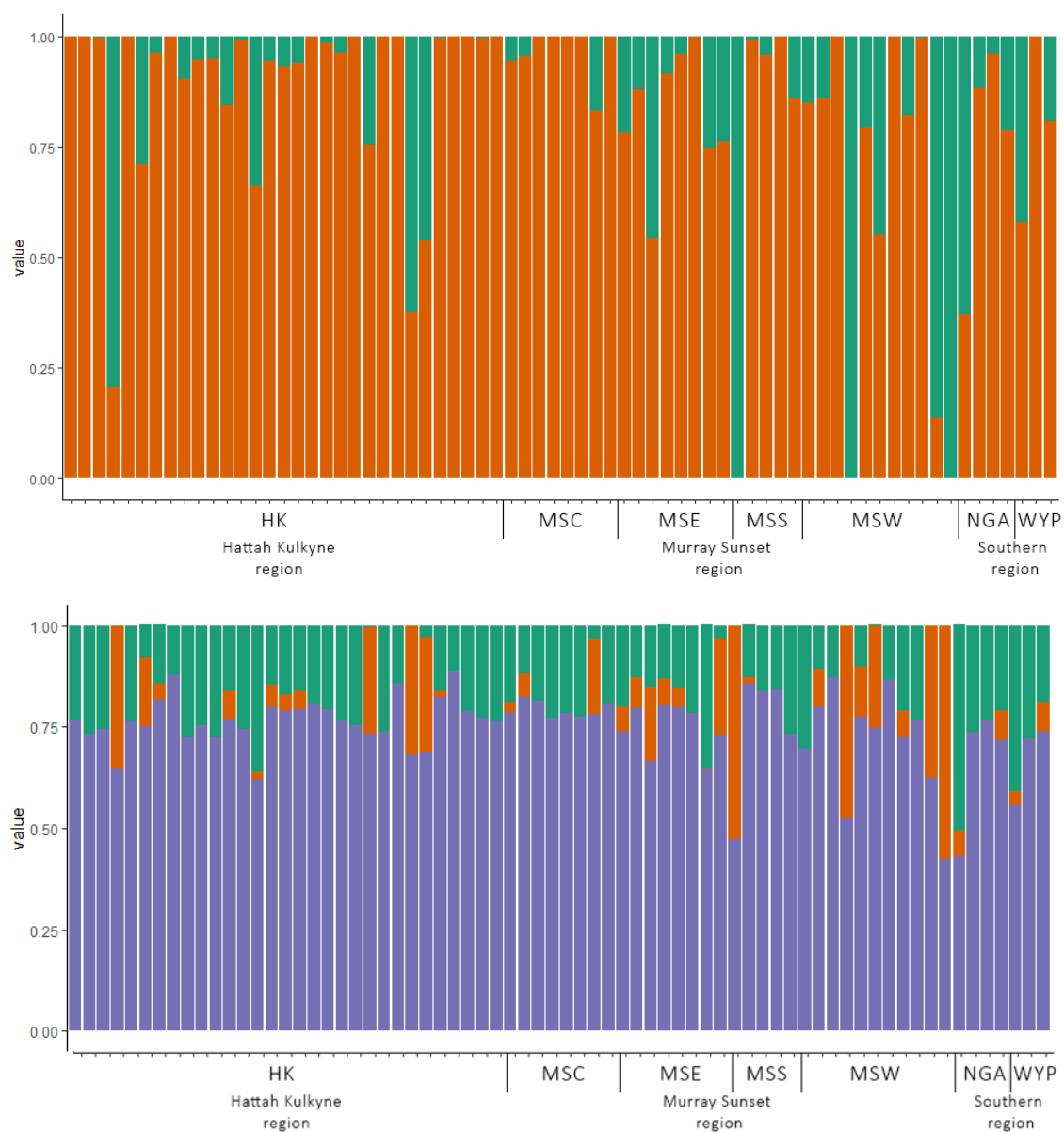


Figure S5.4. Barplot displaying structure in 70 mallee emu-wrens sampled across the contemporary range of the species. K = 2 (above) and 3 (below). HK = Hattah Kulkyne, MSC = Murray-Sunset central, MSE = Murray-Sunset east, MSS = Murray-Sunset south, MSW = Murray-Sunset west, NGA = Ngarkat, WYP = Wyperfeld.

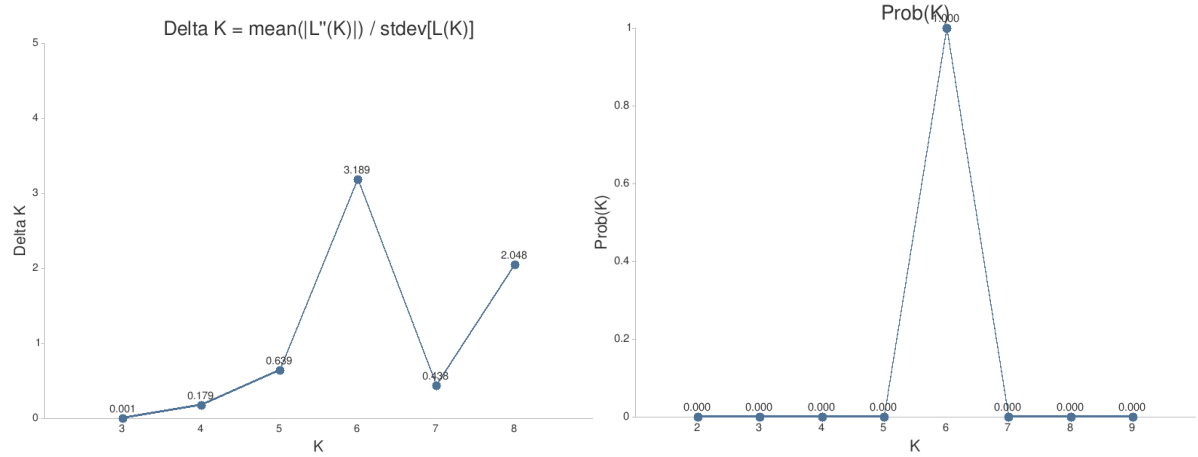


Figure S5.5. Best K calculated using CLUMPAK software. left = Evanno method, right = Pritchard method

Appendix 5 – An evaluation of acoustic field recorders paired with automated call recognition as a monitoring tool for Mallee Emu-wren *Stipiturus mallee*

*Mitchell, WF, Clarke, RH (2022) An evaluation of acoustic recorders paired with automated call recognition as a monitoring tool for Mallee Emu-wren *Stipiturus mallee*. *Australian Field Ornithology* – In review

Abstract

Advances in technology are changing the way that ecological monitoring is carried out, especially for those species with ecological characteristics that have traditionally made monitoring difficult. Autonomous acoustic recorders coupled with automated signal detection software is one such approach where technological advances are delivering rapid improvements in the passive monitoring of vocal fauna. Here we characterise the three common call types of the Endangered mallee emu-wren, *Stipiturus mallee* and present a signal detection template, or call recogniser, for the species. We evaluate the performance of this tool against an independent dataset of field recordings containing mallee emu-wren vocalisations. The recogniser performed well with mean precision and recall metrics ranging between 0.55–0.97 and 0.70–0.95 respectively, depending on user parameters. This tool is widely applicable in the ongoing conservation of mallee emu-wren, particularly as a low cost method for post-release monitoring following a future mallee emu-wren translocation.

Introduction

The mallee emu-wren, *Stipiturus mallee*, is a small, Endangered passerine (EPBC Act 1999, IUCN Red List of Threatened Species), specialised to live in hummock grass, *Triodia scariosa*, dominated habitat (Brown *et al.* 2009; Verdon *et al.* 2020). Because mallee emu-wrens are shy, secretive and often occur at low density at the landscape scale, detection in the field may be challenging and is best achieved by listening for vocalisations (Higgins *et al.* 2001). Clearance of native vegetation, primarily in the early 20th century, has restricted the mallee emu-wren to a fragmented network of large reserves, between 48,000 and 633,000 ha in size, located in the Murray mallee region of north-western Victoria, Australia (Brown *et al.* 2009). Fire and drought are a natural part of the Australian landscape. However, land-use change since European settlement and a changing climate have led to longer droughts, and larger and more intense wildfires (Connell *et al.* 2017). By 2018, whole reserve-scale wildfires had led to the local extinction of mallee emu-wrens from six of nine reserves previously occupied by the species, including all South Australian populations (Boulton & Lau 2015). In an attempt to mitigate these threats, a mallee emu-wren translocation from Murray Sunset National Park, Hattah-Kulkyne National Park and Nowingi State Forest in Victoria to Ngarkat Conservation Park in South Australia was implemented in 2018 (Mitchell *et al.* 2021a). This translocation provided an opportunity to assess autonomous acoustic recording units and automated acoustic detection software as a passive, long-term monitoring tool following translocation.

To demonstrate the long-term persistence of translocated populations, conservation managers require a detailed understanding of the dynamics of those populations. A failure to detect individuals when they are present (i.e. a false negative), can lead to considerable bias in population estimates (Tyre *et al.* 2003; Buckland *et al.* 2012). This problem is exacerbated when target species are cryptic and occur at low-densities, as might be expected for mallee emu-wren at a release site following translocation. Dynamic occupancy modelling is a method to estimate population size that explicitly accounts for bias associated with false negative survey error (MacKenzie *et al.* 2018). This method allows probability of detection, probability of occurrence, and other vital

rates to be estimated by recording the presence or absence of a target species during repeated visits to survey sites (MacKenzie *et al.* 2018). Increasing the number of visits to each sampling site, whilst resulting in a demonstrated increase in accuracy of population parameter estimates (MacKenzie *et al.* 2018), increases the time and resources necessary to carry out such (already expensive and labour intensive) surveys. Automating aspects of the data collection process may increase efficiency, without sacrificing precision.

One method showing promise for vocal fauna, including songbirds, is autonomous acoustic recording units (ARU, Knight *et al.* 2017; Shonfield & Bayne 2017). Recordings that either contain or do not contain vocalisations of target species can be used to populate dynamic occupancy models (Campos-Cerqueira *et al.* 2016; Metcalf *et al.* 2019). An added advantage of this technique is that it is passive and minimises bias associated with observer avoidance or observer skill (Shonfield & Bayne 2017). Whilst initial investment in equipment may be greater than that of a typical observer-based survey, the cost of continued surveys becomes cheaper per unit effort, the longer monitoring continues. Data-driven conservation management of threatened populations relies on monitoring that encompasses the natural variation populations exhibit over time. However, such monitoring is not always implemented. A review by Taylor *et al.* (2017) concluded that translocation studies rarely incorporate long-term persistence into success criteria. Several factors have likely contributed to this trend (e.g. the cost of monitoring, funding cycles, research position periods of employment, or difficulty in obtaining funding for monitoring in comparison to more active conservation initiatives). However, reducing the commitment to extended field seasons and the realisation of cost savings that can be achieved with automated data collection will enhance management capacity to maintain long-term monitoring post-translocation.

The use of ARUs has been demonstrated to reduce field labour by up to 97% (Digby *et al.* 2013). However, field recordings require a substantial investment in time for data processing to identify calls of targeted species (Shonfield & Bayne 2017). This process may be streamlined with the use of automated signal recognition software, hereafter referred to as 'recognisers' (e.g. de Oliveira *et al.* 2015; Katz *et al.* 2016; Priyadarshani *et*

al. 2018; Marsland *et al.* 2019; Prince *et al.* 2019). Several methods exist but typically a user will ‘train’ the software to recognise the spectrogram signature of targeted species’ vocalisations. The software then analyses field recordings using a moving window approach and any potential matches are given a similarity score (for the software used in this study, that score will fall between 0 and 1, Knight *et al.* 2017). Any similarity score that exceeds a user-determined threshold is highlighted as a detection by the software. A detailed summary and comprehensive evaluation of popular recogniser software is presented in a review by Knight *et al.* (2017).

Here we characterise three common vocalisations of the mallee emu-wren and report on development and performance of an automated call recogniser for the species using spectrogram cross correlation with the R package *monitoR* (Katz *et al.* 2016).

Study Area and Methods

Recogniser development

Mallee emu-wren vocalisations are poorly described, though are generally considered to include three primary vocalisations: a short buzzing alarm call, a contact call comprising one to three high-pitched staccato notes, and a complex song (Higgins *et al.* 2001; Menkhorst *et al.* 2017). The first step in developing a mallee emu-wren call recogniser was to clearly define each of these vocalisations and assess their suitability as templates for a recogniser. We produced spectrograms of each call using the R package *seewave* (Sueur *et al.* 2008) and visually assessed calls for two characteristics that would be favourable in automated call recognition. Namely, intra-species consistency and inter-species uniqueness (Figs S6.1 and S6.2). Of the three common mallee emu-wren vocalisations, we identified the contact call as the best candidate for automated recognition. We chose 14 individual mallee emu-wren contact calls, each comprising two or three syllables as the basis for our recogniser (Table S6.1). We began with six three-syllable contact calls and then added an additional three two-syllable contact calls. We conducted unstructured tests of this preliminary recogniser and ultimately added an

additional five vocalisations that the preliminary recogniser failed to detect. These calls were representative of the subtle variation that is typically found in mallee emu-wren calls, including intensity, pitch, ambient noise and recording quality.

Table S6.1. Recordings used as templates for the development of a mallee emu-wren call recogniser

Call template		Location	Date	Author	Notes
Contact templates 1–7	call	¹ Ngarkat Conservation Park	03/05/2018	William Mitchell	Free-roaming translocated mallee emu-wrens in Ngarkat Conservation Park.
Contact templates 8–11,13 and 14	call	¹ Ngarkat Conservation Park	20/04/2018	Luke Ireland	mallee emu-wrens calling from within transport boxes prior to release
Contact template 12	call	Hattah-Kulkyne National Park	17/01/2016	Andrew Spencer	² Call sourced from Xeno-Canto (2020)

¹Translocated birds originally sourced from Hattah-Kulkyne and Murray-Sunset National Parks.

²Available at <https://www.xeno-canto.org/312210>, accessed on 1 October 2020.

To develop a recogniser for detection of mallee emu-wren calls in field recordings we used the package *monitoR* in the statistical environment R (Hafner & Katz 2018; R Core Team 2020). *MonitoR* includes two methods for signal detection: spectrogram cross-correlation and binary point matching (Katz *et al.* 2016). We used spectrogram cross-correlation using automatic point selection following Katz *et al.* (2016). We provide the resultant recogniser and additional code allowing batch-processing of field survey files as an annotated R script with associated .wav files as supplementary material (10.6084/m9.figshare.16915957). Our recogniser comprises fourteen individual call templates, each consisting of a complete, two or three syllable mallee emu-wren contact call. *MonitoR* searches field recordings for matches with each call template individually and then provides a list of every detection associated with each template. We used a sample rate of 44,100 Hz as more than half of the files used to create this recogniser were provided at this frequency. Those recorded at different (higher) frequencies were resampled to 44,100 Hz using the function ‘changeSampRate’ in the *monitoR* package. To ensure that audio information is not lost, it is recommended that recording frequency be set to twice the maximum frequency of the targeted signal (i.e. the Nyquist frequency, Knight *et al.* 2017). Mallee

emu-wren calls typically fall in the range between 5,000 and 12,000 Hz. To maximise recording time of ARUs per unit of memory without sacrificing quality, a sample rate of $\sim 24,000$ Hz may be used for future field recordings of mallee emu-wren calls.

Recogniser Performance

The effectiveness of acoustic recognisers must be manually evaluated against a test dataset that is independent of any recordings used to build the recogniser (Knight *et al.* 2017). As a performance benchmark, we used twenty-five 15 s audio recordings, each including one to 13 (mean = 6.7) known emu-wren vocalisations. This test dataset contained 169 individual mallee emu-wren vocalisations that ranged in intensity from soft to loud. Vocalisations were manually verified by visual inspection of spectrograms and human listening. Recordings also included environmental noise and the calls of non-target species. Test audio was recorded in Nowingi State Forest, Hattah-Kulkyne National Park and Murray Sunset National Park in 2020 and 2021 by WFM. Mallee emu-wren recordings were verified by direct observation of the calling bird at the time of recording.

We used the recogniser described above to search for emu-wren recordings within the test audio files. To investigate the effect of similarity threshold on recogniser performance we repeated this process with threshold values of 0.15, 0.2, 0.25 and 0.3. Similarity threshold is a user determined value which controls the sensitivity of the recogniser (Knight *et al.* 2017). Potential signal matches within an audio spectrogram are given a similarity score between 0 and 1. Any scores below the threshold value are dismissed, while signals with a similarity score above the threshold are retained as detections. For each test file at each threshold, we calculated three performance metrics advocated for by Knight *et al.* (2017); 1) recall, the proportion of existing mallee emu-wren vocalisations in each field recording of the test dataset (verified manually) that were detected by the recogniser; 2) precision, the proportion of all detections that were true positives, and; 3) F-score, a metric which combines precision and recall to aid users in identifying optimum threshold values based on the user's priorities (Knight *et al.* 2017). We calculated mean precision and mean recall across all field

recordings in the test dataset at each threshold value and present the results as a box and whisker plot (Fig. S6.3).

Recall is calculated as

$$\frac{\text{true positives}}{\text{true positives} + \text{false negatives}}$$

precision is calculated as

$$\frac{\text{true positives}}{\text{true positives} + \text{false positives}}$$

and F-score is calculated as

$$\frac{(\beta^2 + 1) * \text{precision} * \text{recall}}{\beta^2 * \text{precision} + \text{recall}}$$

where β is a metric, defined by the user, which allows prioritisation of either precision or recall (Knight *et al.* 2017). Values of $\beta > 1$ prioritise recall, $\beta < 1$ prioritise precision and when $\beta = 1$ neither precision or recall is favoured (Knight *et al.* 2017). We calculated F-scores with β set to 0.5 (precision twice as important as recall), 1 (precision and recall equally important) and 2 (precision half as important as recall) to compare optimum threshold choice under a range of priorities.

Results

The mallee emu-wren contact call is a good candidate for automated signal recognition for several reasons: few other species which share the same habitat have calls that overlap in frequency due to its high pitch (approximately 6.5–7.5 KHz); it is simple and consistent; and because it is frequently incorporated into mallee emu-wren song, it makes up a high proportion of all mallee emu-wren vocalisations (Fig. S6.1). Despite this call being described as thin, high-pitched and insect-like (Higgins *et al.* 2001), its spectrogram structure is

distinct from that of insects (longer pulses and distinct frequency, Montealegre-Z & Mason 2005). By contrast, the alarm call is a poor candidate for recogniser development as it has many similarities with the alarm calls of other *Maluridae* species that overlap in range and habitat use with that of the mallee emu-wren (in particular splendid fairy-wren *Malurus splendens* and striated grasswren *Amytornis striatus*; fairy-wren and emu-wren calls presented in Figs S6.1 and S6.2). Such similarities would increase the likelihood of false positive detections.

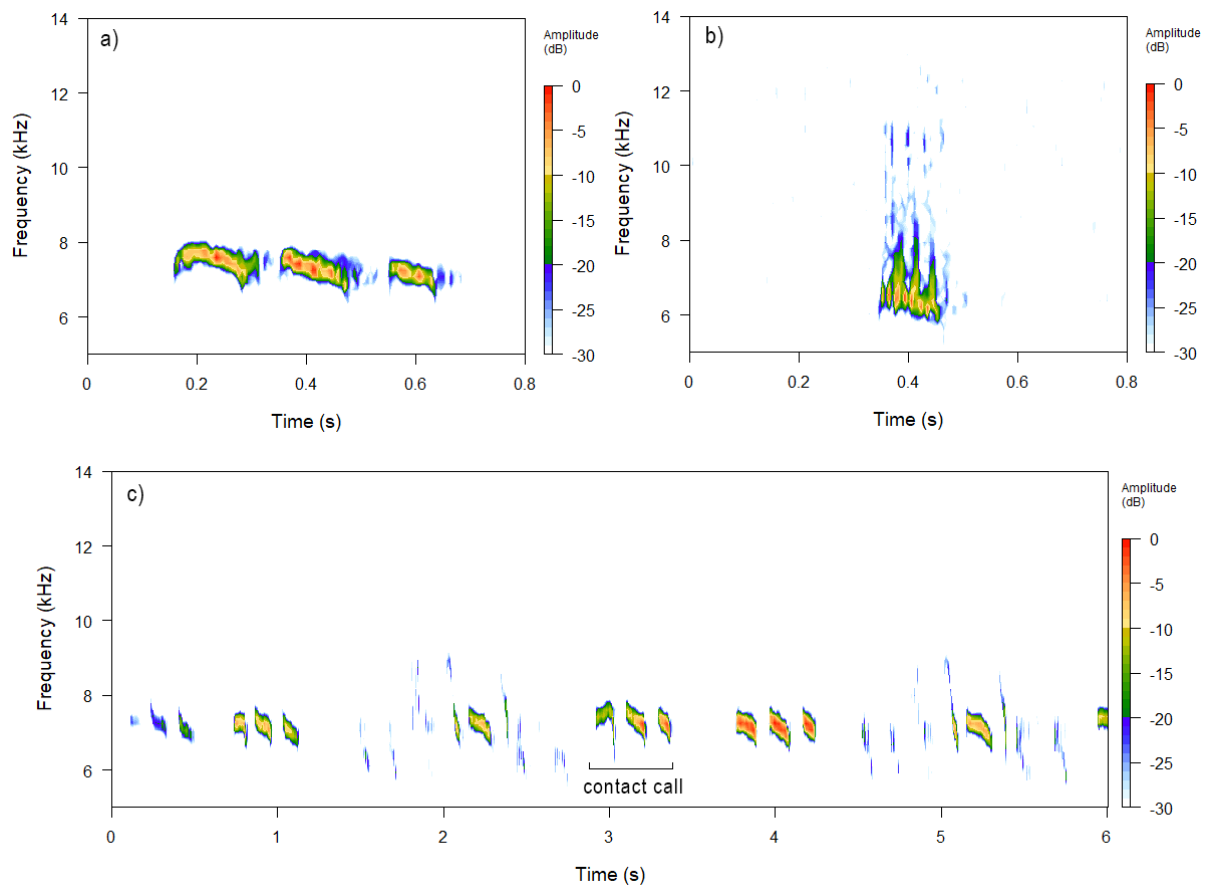


Figure S6.1. Primary vocalisations of the mallee emu-wren *S. mallee*: a) typical contact call, b) alarm call and c) song incorporating the typical contact call. All vocalisations recorded by WFM in Nowingi State Forest, Victoria in November 2020 using an AudioMoth autonomous acoustic recorder (Hill *et al.* 2019).

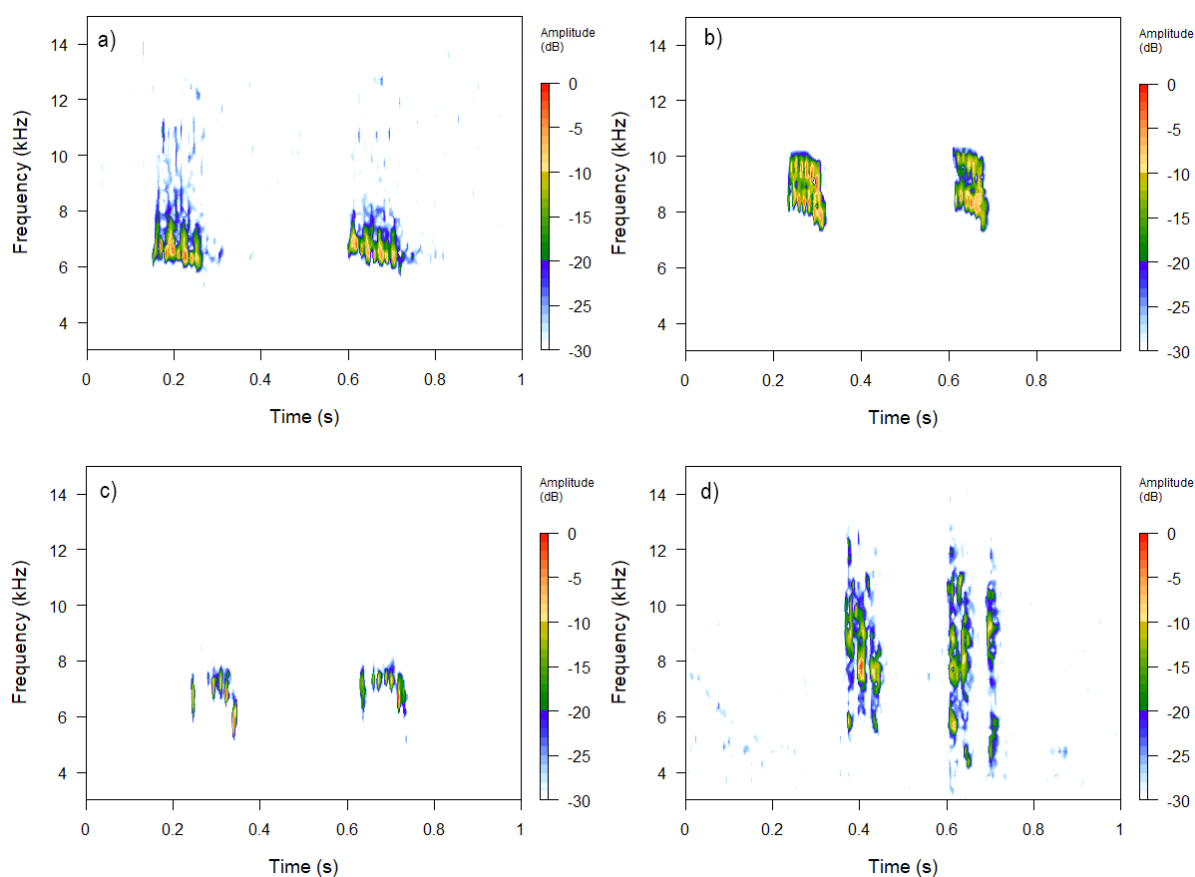


Figure S6.2. A series of spectrogram images displaying the alarm calls of a) mallee emu-wren *S. mallee*, b) splendid fairy-wren *Malarus splendens*, c) superb fairy-wren *M. cyaneus* and d) purple-backed fairy-wren *M. assimilis*. Mallee emu-wren calls were recorded by WFM in Nowingi State Forest, Victoria in November 2020. All fairy-wren calls were obtained from Xeno-Canto (2020). *M. splendens* available at <https://www.xeno-canto.org/372259>, accessed on 17 August 2021. *M. cyaneus* available at <https://www.xeno-canto.org/370623>, accessed on 17 August 2021. *M. assimilis* available at <https://www.xeno-canto.org/165132> assessed on 17 August 2021.

The recogniser we developed successfully identified mallee emu-wren vocalisations in the test dataset of field recordings. Similarity threshold influenced both precision and recall performance, with lower threshold values associated with higher recall and lower precision, while higher threshold values led to lower recall and higher

precision (Fig. S6.3). When recall was prioritised, the optimum recogniser similarity threshold was 0.15 (Table S6.2). When precision was prioritised, the optimum recogniser threshold was 0.3 (Table S6.2). When recall and precision were considered equal priority, the optimum recogniser threshold was 0.25 (Table S6.2).

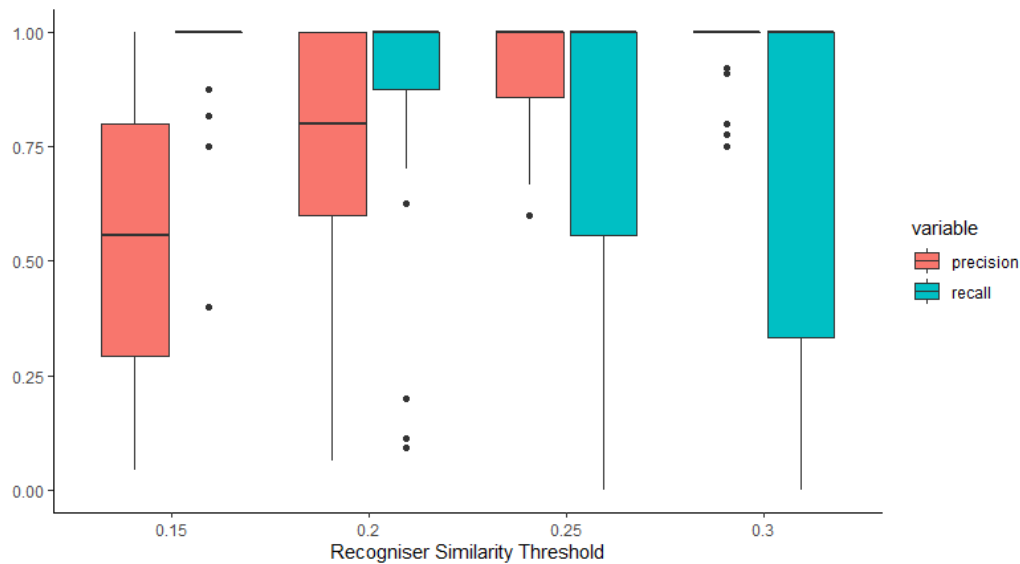


Figure S6.3. Performance metrics for an automated mallee emu-wren *S. mallee* call recogniser. The recogniser was tested against a dataset of 25 independent 15 s field recordings containing vocalisations of mallee emu-wrens. Each detection made by the recogniser was manually verified to assess whether it was a true or false positive detection. Precision refers to the proportion of detections that were true positives. Recall refers to the proportion of vocalisations that were present in the recording (verified manually from spectrogram images) which were detected by the recogniser.

Table S6.2. F-scores for different threshold values and β values. F-score is a performance metric for automated signal detection that allows the user to prioritise precision and/or recall. β is a metric, defined by the user, which allows prioritisation of either precision or recall. Values of $\beta > 1$ prioritise recall, $\beta < 1$ prioritise precision and when $\beta = 1$ neither precision nor recall is favoured (Knight *et al.* 2017).

Threshold	F-score, $\beta = 0.5$	F-score, $\beta = 1$	F-score, $\beta = 2$
0.15	0.601	0.696	0.829
0.2	0.756	0.790	0.827
0.25	0.876	0.831	0.790
0.3	0.897	0.811	0.739

Discussion

We characterised the three common call types of the mallee emu-wren and successfully developed a mallee emu-wren acoustic recogniser utilising the contact call of the species. Our recogniser performed well on the test dataset in terms of both precision (0.55–0.97) and recall (0.70–0.95), indicating that passive acoustic recording represents a feasible monitoring tool for this species. Acoustic monitoring has potential to reduce expense in any future mallee emu-wren translocation by considerably reducing field labour requirements, and may facilitate long-term passive monitoring of key populations within their current distribution (Mitchell *et al.* 2021a).

Context is important when evaluating recogniser performance (Knight *et al.* 2017; Leseberg *et al.* 2020). Performance metrics should only be considered reliable under the environmental conditions in which they were tested (Knight *et al.* 2017). Many bird species may exhibit regional variation in vocalisations (e.g. Valderrama *et al.* 2013; Goretskaia *et al.* 2018), potentially leading to reduced performance. Similarly, the potential for false positive detections may vary as a response to the soundscape in which ARUs are deployed (Knight *et al.* 2017). The contextual information associated with field recordings may also provide an opportunity for improved performance. A recent study by Leseberg *et al.* (2020) was able to increase

recogniser precision and recall by modelling the influence of contextual and intrinsic variables on the likelihood that each detection was either a true or false positive. While performance metrics described here are informative, potential users should consider them as a guide only and make context-specific evaluations of recogniser performance in line with their research goals.

Research goals must be carefully considered when choosing recogniser parameters (Shonfield & Bayne 2017). A high call similarity threshold will lead to high precision and low recall, while a low threshold will have the opposite effect. Precision is paramount when there is limited time available for manual verification of detections (Knight *et al.* 2017). False negatives as a result of emphasis on precision may be accounted for using statistical approaches such as dynamic occupancy modelling (Metcalf *et al.* 2019). When trying to detect sparsely distributed species of conservation concern, where a single detection has high value, low threshold values should be considered.

Many of the locations highlighted as potential release sites for future mallee emu-wren translocations have environmental characteristics that favour passive acoustic monitoring. Mallee emu-wren have a strong association with hummock grass (Verdon *et al.* 2020). Most extent mallee emu-wren populations in north-western Victoria inhabit '*Triodia mallee*' vegetation characterised by relatively large areas of mallee Eucalypt trees with partial groundcover of hummock grass. Mallee emu-wren home range size in this vegetation type has been estimated at ~5 ha (Brown 2011). To adequately cover such an area, multiple ARUs would be required. By comparison, potential translocation release sites, including parts of Ngarkat Conservation Park, South Australia, are composed of 'mallee heath' vegetation: mostly treeless shrub-land with dense pockets of hummock grass forming at drainage points, such as at the base of dunes (Mitchell *et al.* 2021a). Mallee emu-wren move throughout this matrix of vegetation, but home ranges are typically anchored to those pockets of dense hummock grass. In this system, ARUs would have the greatest likelihood of capturing mallee emu-wren vocalisations if placed within these hummock grass pockets. For this reason, a single ARU may effectively cover a single home range. With this ARU placement, researchers may expect a territorial group of mallee emu-wren

to spend a high proportion of their time in the audible vicinity of an ARU. As such, recogniser parameters that prioritise precision over recall would allow efficient monitoring of changing occupancy at release sites following translocation.

Autonomous acoustic recorders provide a low-cost and efficient tool for the long-term monitoring of any translocated mallee emu-wren population. Acoustic monitoring may also be applied to conservation management of translocation source populations. The 2018 mallee emu-wren translocation program was not successful in establishing a viable population in Ngarkat Conservation Park (for a detailed discussion of the factors contributing to this outcome, see Mitchell *et al.* 2021a). Nevertheless, this program, framed primarily around trialling and optimising translocation methods, generated considerable new knowledge that will inform a future larger-scale mallee emu-wren translocation (Mitchell *et al.* 2021a). Mallee emu-wren populations experience fluctuations in size in response to prevailing climatic conditions (Connell 2019). In the context of harvesting of mallee emu-wrens for the purpose of future translocations, impact on source populations has been predicted to be lowest during periods of population growth associated with favourable climatic conditions (Verdon *et al.* 2021). It is critical that conservation benefits from translocating birds are not outweighed by the negative impacts of harvesting for translocation (Mitchell *et al.* 2021b). ARUs may be deployed to monitor mallee emu-wren occupancy at proposed translocation source sites, providing quantitative evidence that occupancy is increasing prior to any harvesting event. For such an approach to be efficient, recogniser parameters must prioritise precision over recall.

The acoustic recogniser presented here (10.6084/m9.figshare.16915957) has potential to be applied widely in conservation management of the Endangered mallee emu-wren. ARUs in tandem with automated signal detection have surged in popularity over the last decade (Towsey *et al.* 2012; Shonfield & Bayne 2017; Priyadarshani *et al.* 2018) and as this field develops, it is likely that cost and efficiency will further improve.

References

Boulton, RL, Lau, J (2015) Threatened Mallee Birds Conservation Action Plan, Report June 2015. Report to the Threatened Mallee Birds Implementation Team, Birdlife Australia.

Brown, S (2011) Mallee Emu-wren (*Stipiturus mallee*): Multi-scale habitat requirements and population structure. Deakin University.

Brown, S, Clarke, M, Clarke, R (2009) Fire is a key element in the landscape-scale habitat requirements and global population status of a threatened bird: The Mallee Emu-wren (*Stipiturus mallee*). *Biological Conservation* **142**, 432-445.

Buckland, ST, Anderson, DR, Burnham, KP, Laake, JL (2012) 'Distance sampling: estimating abundance of biological populations.' (Springer Science & Business Media: Berlin, Germany).

Campos-Cerqueira, M, Aide, TM, Jones, K (2016) Improving distribution data of threatened species by combining acoustic monitoring and occupancy modelling. *Methods in Ecology and Evolution* **7**, 1340-1348.

Connell, J (2019) Fire and Rain: Investigating How Major Ecological Drivers Shape a Semi-Arid Bird Community over Space and Time. PhD thesis, La Trobe University.

Connell, J, Watson, SJ, Taylor, RS, Avitabile, SC, Clarke, RH, Bennett, AF, Clarke, MF, Elith, J (2017) Testing the effects of a century of fires: Requirements for post-fire succession predict the distribution of threatened bird species. *Diversity and Distributions* **23**, 1078-1089.

de Oliveira, AG, Ventura, TM, Ganchev, TD, de Figueiredo, JM, Jahn, O, Marques, MI, Schuchmann, KL (2015) Bird acoustic activity detection based on morphological filtering of the spectrogram. *Applied Acoustics* **98**, 34-42.

Digby, A, Towsey, M, Bell, BD, Teal, PD, Giuggioli, L (2013) A practical comparison of manual and autonomous methods for acoustic monitoring. *Methods in Ecology and Evolution* **4**, 675-683.

Goretskaia, MI, Beme, IR, Popova, DV, Amos, N, Buchanan, KL, Sunnucks, P, Pavlova, A (2018) Song parameters of the fuscous honeyeater *Lichenostomus fuscus* correlate with habitat characteristics in fragmented landscapes. *Journal of Avian Biology* **49**, e01493.

Hafner, SD, Katz, J (2018) 'monitoR: Acoustic template detection in R.'

Higgins, PJ, Peter, JM, Steele, WK (2001) 'Handbook of Australian, New Zealand and Antarctic Birds.' (Oxford University Press: Melbourne).

- Hill, AP, Prince, P, Snaddon, JL, Doncaster, CP, Rogers, A (2019) AudioMoth: A low-cost acoustic device for monitoring biodiversity and the environment. *HardwareX* **6**, e00073.
- Katz, J, Hafner, SD, Donovan, T (2016) Tools for automated acoustic monitoring within the R package monitor. *Bioacoustics* **25**, 197-210.
- Knight, EC, Hannah, KC, Foley, GJ, Scott, CD, Brigham, RM, Bayne, E (2017) Recommendations for acoustic recognizer performance assessment with application to five common automated signal recognition programs. *Avian Conservation and Ecology* **12**, 14.
- Leseberg, NP, Venables, WN, Murphy, SA, Watson, JEM (2020) Using intrinsic and contextual information associated with automated signal detections to improve call recognizer performance: A case study using the cryptic and critically endangered Night Parrot *Pezoporus occidentalis*. *Methods in Ecology and Evolution* **11**, 1520-1530.
- MacKenzie, DI, Nichols, JD, Royle, JA, Pollock, KH, Bailey, LL, Hines, JE (2018) Chapter 11 - Design of Single-Season Occupancy Studies. In '*Occupancy Estimation and Modeling (Second edition)*.' pp. 439-476. (Academic Press: Boston).
- Marsland, S, Priyadarshani, N, Juodakis, J, Castro, I, Poisot, T (2019) AviaNZ: A future-proofed program for annotation and recognition of animal sounds in long-time field recordings. *Methods in Ecology and Evolution* **10**, 1189-1195.
- Menkhorst, P, Rogers, DI, Clarke, R (2017) 'The Australian bird guide.' (Csiro Publishing: Melbourne, Victoria).
- Metcalf, OC, Ewen, JG, McCready, M, Williams, EM, Rowcliffe, JM, Kurle, C (2019) A novel method for using ecoacoustics to monitor post - translocation behaviour in an endangered passerine. *Methods in Ecology and Evolution* **10**, 626-636.
- Mitchell, WF, Boulton, RL, Ireland, L, Hunt, TJ, Verdon, SJ, Olds, LGM, Hedger, C, Clarke, RH (2021a) Using experimental trials to improve translocation protocols for a cryptic, endangered passerine. *Pacific conservation biology*, online early.
- Mitchell, WF, Boulton, RL, Sunnucks, P, Clarke, RH (2021b) Are we adequately assessing the demographic impacts of harvesting for wild - sourced conservation translocations? *Conservation Science and Practice* **4**, e569

- Montealegre-Z, F, Mason, AC (2005) The mechanics of sound production in *Panacanthus pallicornis* (Orthoptera: Tettigoniidae: Conocephalinae): the stridulatory motor patterns. *Journal of Experimental Biology* **208**, 1219-1237.
- Prince, P, Hill, A, Piña Covarrubias, E, Doncaster, P, Snaddon, J, Rogers, A (2019) Deploying Acoustic Detection Algorithms on Low-Cost, Open-Source Acoustic Sensors for Environmental Monitoring. *Sensors* **19**, 553.
- Priyadarshani, N, Marsland, S, Castro, I (2018) Automated birdsong recognition in complex acoustic environments: a review. *Journal of Avian Biology* **49**, e01447.
- R Core Team (2020) 'R: A language and environment for statistical computing.' (R Foundation for Statistical Computing: Viena, Austria).
- Shonfield, J, Bayne, EM (2017) Autonomous recording units in avian ecological research: current use and future applications. *Avian Conservation and Ecology* **12**, 14.
- Sueur, J, Aubin, T, Simonis, C (2008) Seewave, a free modular tool for sound analysis and synthesis. *Bioacoustics* **18**, 213-226.
- Taylor, G, Canessa, S, Clarke, RH, Ingwersen, D, Armstrong, DP, Seddon, PJ, Ewen, JG (2017) Is Reintroduction Biology an Effective Applied Science? *Trends in Ecology & Evolution* **32**, 873-880.
- Towsey, M, Planitz, B, Nantes, A, Wimmer, J, Roe, P (2012) A toolbox for animal call recognition. *Bioacoustics* **21**, 107-125.
- Tyre, AJ, Tenhumberg, B, Field, SA, Darren, N, Kirsten, P, Possingham, HP (2003) Improving Precision and Reducing Bias in Biological Surveys: Estimating False-Negative Error Rates. *Ecological Applications* **13**, 1790-1801.
- Valderrama, SV, Molles, LE, Waas, JR, Slabbekoorn, H, Stephens, P (2013) Conservation implications of song divergence between source and translocated populations of the North Island Kōkako. *Journal of Applied Ecology* **50**, 950-960.
- Verdon, SJ, Mitchell, WF, Clarke, MF (2021) Can flexible timing of harvest for translocation reduce the impact on fluctuating source populations? *Wildlife Research* **48**, 458-469.
- Verdon, SJ, Watson, SJ, Nimmo, DG, Clarke, MF (2020) Are all fauna associated with the same structural features of the foundation species *Triodia scariosa*? *Austral Ecology* **45**, 773-787.

Xeno-Canto (2020) 'Xeno-Canto. Sharing bird sounds from around the world.' Available at <https://www.xeno-canto.org/> [Accessed 1 December 2020].

