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Integrating systematic and targeted scat collection approaches to estimate the abundance of a culturally significant threatened species on Indigenous lands

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Abstract

Estimating the abundance of threatened species can be extremely difficult. This is particularly true in remote regions, where surveys are often expensive and subject to logistical challenges. Where threatened species occur on Indigenous lands, collaborative work between Indigenous people and ecologists who share an interest in the conservation and management of these species may resolve some of these challenges while also meeting additional local objectives. Here, we show the value of integrating two on-ground methods for non-invasive genetic sampling of scat to estimate the abundance of the greater bilby (*Macrotis lagotis*), a species highly significant to Indigenous people of central Australia that is threatened with extinction. We compared two on-ground methods: (1) systematic surveys, designed to be repeatable, stratified, and standardized, and (2) targeted surveys, which focused on areas where bilby sign was present and involved a more flexible and intuitive search technique undertaken collaboratively with local Indigenous people and informed by their knowledge and skills. We compared different combinations of the two methods and different sampling intensities to explore how they affected modeled estimates of bilby abundance, derived by combining information on individual bilby identities (from DNA extracted from scat) with spatially explicit capture–recapture modeling. We found that combining targeted methods for scat collection with systematic sampling provided the best modeled estimates of bilby abundance and improved modeled estimates for lower overall effort than

increasing systematic sampling. This approach also allowed for the inclusion of diverse knowledges and approaches to detecting species (scat) presence. By weaving multiple approaches to find and identify bilby scat, we show how collaborative knowledge-sharing practices can also deliver multiple benefits to Indigenous and science partners.

1 | INTRODUCTION

Detecting the presence of threatened species in remote regions is notoriously difficult, and estimating their abundance is even more challenging. These species are often elusive, especially if populations are small, mobile, or scattered across large regions (Black, 2020). Consequently, there are many logistical challenges associated with surveying such species, especially for professional ecologists who often live in urban centers remote from the study region. This includes the prolonged time required to travel to remote sites and then detect and effectively survey elusive species (e.g., see Moore et al., 2023). Furthermore, many current modes of detection vary in effectiveness depending on the target species (e.g., live trapping, motion-sensor camera trapping) and are costly to implement, meaning substantial funds are required for field campaigns. Yet, even when extensive resources are put towards monitoring, there are often insufficient data for a reliable assessment of the status and population trends of species of interest (Lindenmayer et al., 2020). Indirect survey methods that involve searching for evidence of animal presence (e.g., tracks, diggings, scat (or feces)) have become increasingly popular for monitoring wildlife populations and may offer an ethical, efficient, and cost-effective alternative to other survey approaches that are more invasive and resource intensive (Dziminski et al., 2021; Piggott & Taylor, 2003; Smith et al., 2022).

Indirect sampling reduces or eliminates the need to directly disturb animals and has long been used for deriving indices of species abundance or confirming the presence or absence of a species from a location (e.g., see Hema et al., 2017; Southgate et al., 2018; Stephens et al., 2006). However, more recently, there has been an increase in the use of non-invasive methods to collect genetic material (e.g., from hair, scat, or feathers; hereafter referred to as non-invasive genetic sampling), which has substantially expanded the utility of this type of sampling. Some examples include quantifying population sizes (Banks et al., 2003; Ruibal et al., 2009; Sollmann et al., 2012), studying demographics (Proença-Ferreira et al., 2019), investigating animal dispersal and movement (Lucchini et al., 2002), assessing population genetic parameters (i.e., structure and gene flow) (Hogg et al., 2024), and assessing mating systems and behavioral ecology (Beja-Pereira et al., 2009; Petit & Valiere, 2006). Scat is one of the most used materials in non-invasive genetic studies because, for many species, it is easy to find in the wild, and it provides more information (e.g., about diet, stress-hormone status, reproductive hormones, parasite infection, parasite DNA) than other sample types (Proença-Ferreira et al., 2019). DNA extracted from scat also allows the identification of individuals, which can be combined with other methods to estimate population parameters that would otherwise be difficult to obtain over large spatial scales (Cheng et al., 2017; Hedges et al., 2013; Petit & Valiere, 2006).

In Australia, many threatened species occur on lands in remote areas that are owned and managed by Indigenous people, and these species often have great cultural significance (Garnett et al., 2018; Lilleyman et al., 2024). Indigenous governance and knowledge systems often recognize threatened species as important components of the ecosystem, but also as cultural entities, sometimes considered kin within a broader framework of relational connections with the natural world. This presents an additional, and arguably even more compelling reason to protect these species than the threatened-species classifications bestowed upon them by current bureaucratic and non-Indigenous classification systems and monitoring methods. In any case, the desire from multiple cultural perspectives to protect such species brings both opportunities and imperatives for ecologists and Indigenous people to work together to meet shared objectives.

Any surveys on lands owned or managed by Indigenous people, and particularly those targeting culturally important species, should be carefully considered (Goolmeer et al., 2022). For example, survey methods may need to be designed or adapted to adhere to cultural protocols, including avoidance of sacred sites, receiving consent from Elders, and respecting and acknowledging

local and cultural knowledge (Barbour & Schlesinger, 2012; Macdonald et al., 2021; Robinson et al., 2022). Local Indigenous people are often eager to search for species to which they are connected or otherwise knowledgeable about, and they can have unique insights and knowledge about where these species can be found (Service et al., 2014) and how to track and interpret their signs in the landscape (Popp et al., 2020). A diverse array of approaches that involve local Indigenous people co-designing or participating in data collection or knowledge-sharing activities to find and monitor species now exists across the world (Danielsen et al., 2021; Mamun & Natcher, 2023), with the aim of co-producing useful knowledge for the stewardship of bio-cultural ecosystems (Robinson et al., 2022).

The greater bilby (*Macrotis lagotis*, hereafter referred to as the bilby) is an iconic burrowing marsupial that is threatened with extinction and persists only in widely dispersed populations in remote areas of arid and semi-arid Australia (Cramer et al., 2017; DCCEEW, 2023). The bilby has disappeared from approximately three-quarters of its historical range as a direct result of colonization processes; namely, the introduction of exotic species and changes to traditional burning practices (DCCEEW, 2023). Most of the bilby's extant range is on Indigenous freehold land, and the species is of great cultural significance to local Indigenous people. There are at least 60 different local language names for the species across Australia (Paltridge, 2016), and bilbies are included in many '*Jukurrpa*' creation stories and song lines. Local Elders and rangers have exceptional knowledge about bilbies, their threats, their foods, their behaviors, and the stewardship strategies needed to restore or sustain the health of bilby habitats into the future (Bradley et al., 2015). There is also a strong local desire to pass on this knowledge to younger generations (CLC, 2012, 2015). Efforts such as those by Skroblin et al. (2022) have shown the potential for monitoring programs based on Indigenous knowledge to enhance conservation outcomes. Any current or future management of bilbies should thus be a shared responsibility and draw on a range of tools and knowledge available to aid in bilby conservation.

From a western ecological perspective, surveys targeting bilbies have been used to estimate their broad geographic range but have yielded remarkably limited understanding of their abundance (DCCEEW, 2023; Dziminski et al., 2021). This is due, in part, to low capture success using conventional trap methods (e.g., live trapping using cage traps). Wild bilbies are usually trap-shy and uninterested in baits (McGregor & Moseby, 2014). They also use multiple burrows at a time, making it difficult to determine which burrows are occupied. Non-invasive surveys that rely on counts of burrows and other types of field sign (e.g., diggings, tracks) are consequently not good indicators of bilby abundance (Southgate et al., 2018). This hinders accurate monitoring of bilby population status and trends, including population responses to threatening processes or management interventions. For example, the control of introduced predators or appropriate fire management may facilitate bilby population growth and increase local abundance without detectable changes in bilby population distribution or occupancy, making the effectiveness of management actions difficult to assess without baseline data or post-intervention measures of population abundance. Lack of knowledge of bilby abundance also precludes making informed decisions about relocating wild bilbies to predator-free or fenced areas and monitoring the impacts that such translocations might have on wild source populations.

Local Indigenous people use scat and signs of diggings and burrows to determine the presence of bilbies (Hogg et al., 2024; Indigo et al., 2021). Importantly, scats also provide a valuable source of DNA that can be used for non-invasive genetic studies. Bilby scats have unique characteristics that make them readily distinguishable from the fecal deposits of other desert animals (Southgate et al., 2018). They are also rarely found far from bilby diggings and burrows (Southgate et al., 2018) and can be readily collected from sites where bilbies are known to occur. Smith et al. (2009) were the first to demonstrate that bilby scats provide a viable source of DNA for extraction and analysis. Subsequent studies have quantified DNA degradation and amplification rates (Carpenter & Dziminski, 2017) and combined systematic survey (i.e., standardized, repeatable sampling methods designed to reduce bias and improve population estimates) and the collection of scat with other techniques (e.g., spatially explicit capture–recapture (SECR)) to estimate the size of local bilby populations (Dziminski et al., 2021). It has been suggested that systematic scat collection can offer a cost-effective method for estimating bilby population sizes across larger spatial scales (Dziminski et al., 2021). While many Indigenous scientists and environmental managers are familiar and comfortable with systematic sampling, exclusively using such approaches may introduce barriers to the engagement of important Indigenous collaborators in on-ground data collection. This is because systematic sampling (1) is counterintuitive to local knowledge and the practice of tracking animals, (2) does not recognize or value local knowledge, and (3) does not offer opportunities for intergenerational transfer of local knowledge.

Here, we build on the work of Dziminski et al. (2021) to evaluate the efficiency and performance of alternative on-ground methods for collecting bilby scat for DNA extraction: (1) systematic surveys designed according to common ecological sampling protocols and premised on concepts of repeatable, stratified, and standardized survey effort, (2) targeted methods focused on areas where bilby sign is present and involving a more flexible and intuitive search technique, undertaken collaboratively with local Indigenous people (in our region, Warlpiri) and informed by their knowledge and skills, and (3) a combination of systematic and targeted sampling. Broadly, our aim was to find a cost-effective and engaging way of improving our understanding of a highly mobile and widely dispersed threatened species that is also of significant importance to the Indigenous people of central Australia. We predicted that using a mix of approaches would provide more comprehensive data and better estimates of local bilby abundance. To test this and, more generally, to determine the most efficient on-ground sampling regime, we investigated how different combinations of effort and approach to sampling influenced modeled estimates of bilby abundance.

2 | METHODS

2.1 | Local context

This study was undertaken in the Northern Tanami Indigenous Protected Area (IPA), located in the northern portion of the Tanami Desert, Northern Territory, Australia. Declared in 2007, the IPA incorporates an area of approximately 4,005,000 ha of Indigenous freehold land (CLC, 2015). The IPA is on the far northern limit of Australia's semi-arid rangelands and experiences a subtropical climate with distinct wet and dry seasons (CLC, 2015). Rainfall is generally limited to the summer months (November to March) with moderate to high temperatures prevailing throughout the year (CLC, 2015). 'Yapa' (local Warlpiri people) recognize four main seasons: (1) 'Kawalya' and 'Yulyurrpu' (cold weather), (2) 'Kara-purda' (windy weather), (3) 'Wanta' (hot weather), and (4) 'Ngapa-yiri-yiri' and 'Wajirrkinyi' (rainy weather) (CLC, 2015). The majority of the IPA is on the traditional lands of the northern Warlpiri people. However, the land on which the single permanent settlement of Lajamanu is located and the region to the north-west are the traditional lands of the Gurindji people. The western portion of the IPA borders on Jaru and Nyininy land, and the eastern portion of the IPA adjoins Warlmanpa land (CLC, 2015).

2.2 | Preliminary surveys

The study took place at Mirridi, approximately 40 km southeast of Lajamanu in the northern Tanami Desert. This area was chosen as a potential study site for several reasons: (1) preliminary surveys conducted in 2021 revealed fresh bilby activity in the area, (2) much of this fresh bilby activity was concentrated along the main access road, making the site readily accessible via vehicle, and (3) the site had been earmarked as a priority location for future field trips (unrelated to this project) by the Warlpiri and Gurindji Indigenous Traditional Owners and rangers during early consultations undertaken to negotiate the project's scope. In April 2022, we conducted seven helicopter surveys on and adjacent to the main road, with transects spaced 500 m apart. These surveys allowed us to confirm the extent to which bilbies were active in the area and create a broad-scale map of the distribution of fresh bilby sign. The final location for on-ground surveys was then chosen to overlay areas containing the majority of the observed bilby activity, covering an area of ~3,375 ha. The size of the survey area was determined based on bilby home-range sizes (i.e., to ensure that multiple bilby home ranges were likely to overlap with the study area; Moseby & O'Donnell, 2003), resource availability (i.e., the total number of motion-sensor camera traps available for use in a concurrent study investigating bilby–predator interactions in response to fire; Geyle et al., 2024) and feasibility of on-ground logistics (i.e., the time required and distance that would need to be covered for comprehensive surveys of the area).

2.3 | On-ground sampling approaches

2.3.1 | Systematic sampling

We established 20 parallel transects within the study area for systematic sampling, with each transect running perpendicular to the main access road (Figure 1). Transects were ~ 2.25 km long and ~750 m apart. Each transect was sampled three times between May 2022 and July 2022. Sampling involved walking along transect lines while scanning the ground for bilby sign and, where detected, sifting through soil spoil near diggings and burrows for scat. On each sampling occasion, all scat detected within ~20 m on either side of the transect was collected, resulting in a total search area of ~9 ha per transect. Systematic surveys were undertaken by 2–4 observers, with at least one experienced observer (the lead author) present during all surveys.
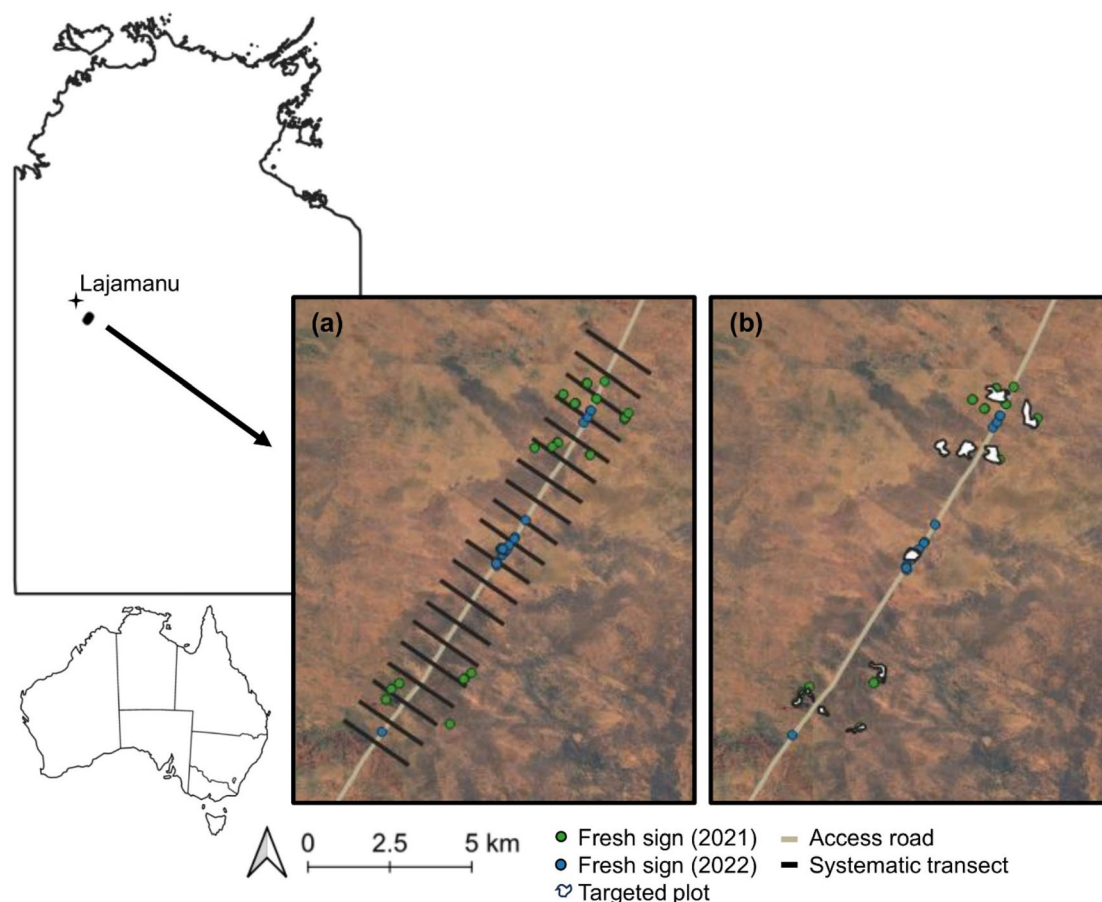
FIGURE 1 Map showing study area in the Northern Territory, including locations of (a) systematic transects and (b) targeted plots. Locations of fresh bilby *(Macrotis lagotis)* sign from surveys in 2021 (green) and 2022 (blue) are also shown. The inset map of Australia highlights the study region, while the regional map (top left) provides a closer view of the area surrounding Lajamanu, the nearest permanent settlement to the study area (marked with a black-filled rectangle).

2.3.2 | Targeted sampling guided by Indigenous ecological knowledge

We selected 10 locations within the study area for targeted sampling based on the locations of active burrows detected on preliminary helicopter surveys or with help from 'kuyu-pungu' (which in Warlpiri language means 'master tracker') (Figure 1). This approach to scat collection was designed with local Indigenous Traditional Owners and land managers to align priorities with a regional 'Yitaki Maninjaku Ngurungka' (Reading the Country) project. The surveys provided opportunities for on-the-job training, enabling the preservation of ancient tracking knowledge for future Warlpiri rangers (e.g., see CLC, 2024). Targeted surveys were particularly valued by Traditional Owners because they allowed for the sharing of cultural knowledge between Elders and younger generations, and were flexible enough to fit within existing ranger work programs and physical limitations. Sampling involved navigating from the road to an active

(pre-identified) burrow and undertaking time-standardized searches around the burrow (with the burrow as the starting point). A minimum of three observers were involved in each search. Surveys ranged from 4.5 to 9 h of search effort, and a survey would cease if 0.5 h passed without any observers detecting a new scat pile. Observer experience varied among surveys; observers were often volunteers but were accompanied by kuyu-pungu or a ranger with experience in tracking and identifying bilby sign. The same experienced observer was present on all surveys, ensuring consistency among surveys in scat detectability.

2.3.3 | Opportunistic sampling with local Indigenous rangers

In addition to the two survey approaches described above, opportunistic sampling was undertaken between April and July 2022 at Mirridi. Samples were classified as

opportunistic when they were collected during other activities (e.g., ranger training activities) or when moving between transects or sites. Opportunistic sampling is easy to implement as part of other Indigenous stewardship or ranger monitoring work. While we did not expect this approach to yield reliable estimates of true abundance, we anticipated that it could help with filling in some knowledge gaps that may contribute to population indices (e.g., by providing better estimates of the minimum number of animals known to be alive).

2.4 | Scat collection, DNA extraction, and genotyping

All scat encountered on surveys was collected (see Supplementary Material S1 for further details) and sent to the Australian Genome Research Facility for extraction and genotyping. Genomic DNA extraction was performed using the Macherey-Nagel Nucleospin Tissue Kit with two modifications: (1) 25 mg of scat was homogenized in lysis buffer with a TissueLyser II and (2) following incubation at 56 °C, the lysate was precipitated with an acetate buffer solution. Custom genotyping was undertaken using the Agena MassArray platform to genotype individuals at a single-nucleotide polymorphism (SNP) panel developed by Hogg et al. (2024), which was made up of 35 autosomal and four sex-linked markers. This panel was designed using samples obtained from a population of bilbies in Western Australia (see supplementary note 2.5 of Hogg et al., 2024 for further details); however, early trials suggested that it was likely to work well for Northern Territory bilby populations. This approach has been shown to provide highly accurate identification of individual bilbies from scats (Hogg et al., 2024).

2.5 | Estimating bilby abundance

We used DNA extracted from bilby scat to identify unique individuals in the population (details are provided in Supplementary Material S2) and combined this with SECR modeling (Efford, 2004) to estimate bilby densities. Models were implemented via the 'secr' package in R (Efford, 2023a). In cases where animals leave multiple, individually identifiable 'cues' (i.e., scats), SECR accepts within-occasion 'recaptures' (Efford, 2011), so we could construct models from data obtained from targeted plots without the need for repeated searches. We created conceptual 'traps' by separating systematic transects into 100 m segments and assigning bilby scat to the nearest segment. For targeted surveys, we created conceptual traps by overlaying a 100 m × 100 m grid over plot

polygons, calculating the centroid for each grid cell, and assigning bilby scat to the nearest centroid. Centroids were clipped to the plot polygons with a 50 m buffer to ensure that all centroids inside a grid cell overlapping the polygons were retained. We used the 'count' detector for all models, meaning that individuals could be detected more than once at a trap on each occasion, and the 'Nelder–Mead' maximization method, as this has been shown to be more robust than the default (Efford, 2023b). Repeat searches of transects were each classified as a separate occasion (i.e., three total), while targeted sampling of plots was classified as a fourth occasion. We used a 4 km buffer around transects and plots to ensure that the area was large enough to encompass the home range of all bilbies detected during surveys, based on published estimates of bilby home-range size (e.g., Moseby & O'Donnell, 2003). Density estimates obtained from models fitted using the data from both the systematic and targeted surveys were used as the baseline for comparison. We estimated abundance by multiplying density by the size of our study area, which was ~21,989 ha (i.e., the area sampled plus the 4 km buffer).

2.6 | Subsampling of data

The full dataset used in the density estimates described above was generated by intensive sampling using two different methodological approaches (systematic and targeted), which involved the collection of all scats encountered on transects (over three separate sampling occasions) or within plots (within a pre-determined time limit), respectively. We compared estimates of density obtained using reduced systematic and targeted methodologies and combinations of both (a total of 88 model comparisons; Table 1) to the baseline estimates obtained using all the data collected. To explore how reduced sampling intensity would influence density estimates, bias (measured as the absolute difference in density between the subsampled model and the complete model) and precision (measured as the absolute difference in the standard error (SE) between the subsampled model and the complete model) were fitted using SECR models with subsets of the data collected. This process involved (1) reducing the number of systematic sampling occasions, (2) reducing the amount of time spent searching on targeted plots, (3) reducing the number of samples collected (i.e., one every 50 m), (4) sampling half the number of transects (i.e., 10 transects spaced 1500 m apart), and (5) searching half the number of plots (i.e., five plots spaced >1500 m apart). We considered subset models to provide reasonable density estimates if bias and precision scores were <0.001, if there was no

TABLE 1 Spatially explicit capture–recapture model comparisons, including the number of systematic occasions and transects, the number of targeted plots, time spent searching on targeted plots, whether samples were reduced (i.e., replicating collection of one sample every 50 m), relative costs (as a proportion of the total cost of the complete, baseline model), modeled density estimates (bilbies/ha), standard error (SE), and lower and upper confidence intervals (LCI and UCI, respectively).

Model	Systematic			Targeted			Relative cost	Density/ha	SE	LCI	UCI
	Occasions	Transects	Reduced	Time (hrs)	Plots	Reduced					
Complete	3	20	No	9	10	No	1.00	0.0037	0.0007	0.0026	0.0053
Systematic	3	20	No	NA	NA	NA	0.41	0.0044	0.0010	0.0028	0.0068
Targeted	NA	NA	NA	9	10	No	0.59	0.0097	0.0021	0.0064	0.0146
Reduced01	2	20	No	9	10	No	0.86	0.0035	0.0007	0.0024	0.0051
Reduced02	1	20	No	9	10	No	0.72	0.0052	0.0010	0.0035	0.0077
Reduced03	2	20	No	NA	NA	NA	0.28	0.0032	0.0009	0.0019	0.0054
Reduced04[a]	1	20	No	NA	NA	NA	0.14	NA	NA	NA	NA
Reduced05	2	20	No	6	10	No	0.68	0.0037	0.0007	0.0026	0.0055
Reduced06	2	20	No	3	10	No	0.50	0.0050	0.0011	0.0034	0.0076
Reduced07	1	20	No	6	10	No	0.54	0.0050	0.0010	0.0034	0.0075
Reduced08	1	20	No	3	10	No	0.36	0.0044	0.0010	0.0028	0.0069
Reduced09	NA	NA	NA	6	10	No	0.40	0.0079	0.0020	0.0049	0.0128
Reduced10	NA	NA	NA	3	10	No	0.22	0.0080	0.0021	0.0048	0.0133
Reduced11	2	20	Yes	9	10	Yes	0.59	0.0050	0.0010	0.0033	0.0075
Reduced12	1	20	Yes	9	10	Yes	0.49	0.0046	0.0010	0.0030	0.0070
Reduced13	2	20	Yes	NA	NA	NA	0.21	0.0033	0.0010	0.0018	0.0060
Reduced14[a]	1	20	Yes	NA	NA	NA	0.10	NA	NA	NA	NA
Reduced15	2	20	Yes	6	10	Yes	0.49	0.0051	0.0011	0.0033	0.0078
Reduced16	2	20	Yes	3	10	Yes	0.37	0.0055	0.0013	0.0035	0.0087
Reduced17	1	20	Yes	6	10	Yes	0.39	0.0047	0.0011	0.0030	0.0074
Reduced18	1	20	Yes	3	10	Yes	0.27	0.0047	0.0014	0.0027	0.0082
Reduced19	NA	NA	NA	6	10	Yes	0.29	0.0061	0.0017	0.0035	0.0104
Reduced20	NA	NA	NA	3	10	Yes	0.16	0.0058	0.0022	0.0028	0.0117
Reduced21	2	10	No	9	10	No	0.75	0.0036	0.0007	0.0025	0.0053
Reduced22	1	10	No	9	10	No	0.67	0.0060	0.0012	0.0041	0.0089
Reduced23	2	10	No	NA	NA	NA	0.17	0.0049	0.0017	0.0026	0.0094
Reduced24[a]	1	10	No	NA	NA	NA	0.08	NA	NA	NA	NA
Reduced25	2	10	No	6	10	No	0.57	0.0043	0.0008	0.0029	0.0063
Reduced26	2	10	No	3	10	No	0.39	0.0058	0.0013	0.0037	0.0089

(Continues)

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TABLE 1 (Continued)

Model	Systematic			Targeted			Relative cost	Density/ha	SE	LCI	UCI
	Occasions	Transects	Reduced	Time (hrs)	Plots	Reduced					
Reduced27	1	10	No	6	10	No	0.48	0.0058	0.0012	0.0039	0.0087
Reduced28	1	10	No	3	10	No	0.30	0.0054	0.0013	0.0034	0.0085
Reduced29	2	10	Yes	9	10	Yes	0.51	0.0052	0.0012	0.0034	0.0080
Reduced30	1	10	Yes	9	10	Yes	0.45	0.0050	0.0011	0.0032	0.0077
Reduced31	2	10	Yes	NA	NA	NA	0.13	0.0063	0.0033	0.0024	0.0164
Reduced32[a]	1	10	Yes	NA	NA	NA	0.06	NA	NA	NA	NA
Reduced33	2	10	Yes	6	10	Yes	0.41	0.0053	0.0012	0.0034	0.0084
Reduced34	2	10	Yes	3	10	Yes	0.29	0.0057	0.0015	0.0034	0.0095
Reduced35	1	10	Yes	6	10	Yes	0.35	0.0051	0.0012	0.0032	0.0081
Reduced36	1	10	Yes	3	10	Yes	0.23	0.0051	0.0015	0.0029	0.0091
Reduced37	2	10	No	9	5	No	0.31	0.0057	0.0012	0.0038	0.0087
Reduced38	1	10	No	9	5	No	0.22	0.0057	0.0013	0.0037	0.0087
Reduced39	2	10	No	6	5	No	0.41	0.0058	0.0013	0.0038	0.0089
Reduced40	2	10	No	3	5	No	0.30	0.0085	0.0022	0.0051	0.0142
Reduced41	1	10	No	6	5	No	0.33	0.0056	0.0013	0.0036	0.0089
Reduced42[a]	1	10	No	3	5	No	0.21	0.0156	0.0045	0.0090	0.0271
Reduced43	NA	NA	NA	6	5	No	0.24	0.0062	0.0019	0.0035	0.0111
Reduced44[a]	NA	NA	NA	3	5	No	0.13	0.0797	0.0223	0.0465	0.1365
Reduced45	NA	NA	NA	6	5	Yes	0.17	0.0047	0.0019	0.0021	0.0101
Reduced46[a]	NA	NA	NA	3	5	Yes	0.10	0.0923	0.0365	0.0437	0.1948
Reduced47	2	20	No	9	5	No	0.41	0.0052	0.0011	0.0035	0.0077
Reduced48	1	20	No	9	5	No	0.28	0.0046	0.0010	0.0030	0.0071
Reduced49	2	20	No	6	5	No	0.52	0.0052	0.0011	0.0035	0.0078
Reduced50	2	20	No	3	5	No	0.41	0.0052	0.0011	0.0034	0.0080
Reduced51	1	20	No	6	5	No	0.38	0.0048	0.0011	0.0031	0.0074
Reduced52	1	20	No	3	5	No	0.27	0.0053	0.0014	0.0032	0.0089
Reduced53	2	20	Yes	9	5	Yes	0.44	0.0048	0.0011	0.0031	0.0075
Reduced54	1	20	Yes	9	5	Yes	0.34	0.0044	0.0011	0.0027	0.0071
Reduced55	2	20	Yes	6	5	Yes	0.38	0.0049	0.0012	0.0031	0.0078
Reduced56	2	20	Yes	3	5	Yes	0.31	0.0063	0.0017	0.0038	0.0105
Reduced57	1	20	Yes	6	5	Yes	0.27	0.0047	0.0013	0.0027	0.0080

TABLE 1 (Continued)

| Model | Systematic | | | Targeted | | | Relative cost | Density/ha | SE | LCI | UCI |
	Occasions	Transects	Reduced	Time (hrs)	Plots	Reduced					
Reduced58[a]	1	20	Yes	3	5	Yes	0.20	0.0129	0.0054	0.0059	0.0284
Reduced59	3	20	Yes	9	10	Yes	0.69	0.0051	0.0010	0.0034	0.0076
Reduced60	3	20	Yes	NA	NA	NA	0.69	0.0039	0.0011	0.0023	0.0066
Reduced61	NA	NA	NA	9	10	Yes	0.38	0.0062	0.0016	0.0038	0.0102
Reduced62	3	10	No	9	10	No	0.84	0.004	0.001	0.003	0.005
Reduced63	3	10	Yes	9	10	Yes	0.57	0.005	0.001	0.003	0.008
Reduced64	3	10	No	9	5	No	0.39	0.006	0.001	0.004	0.009
Reduced65	3	10	Yes	9	5	Yes	0.42	0.005	0.001	0.003	0.008
Reduced66	3	10	No	6	5	No	0.50	0.006	0.001	0.004	0.009
Reduced67	3	10	No	3	5	No	0.38	0.008	0.002	0.005	0.013
Reduced68	3	10	Yes	6	5	Yes	0.36	0.005	0.001	0.003	0.008
Reduced69	3	10	Yes	3	5	Yes	0.29	0.009	0.003	0.005	0.018
Reduced70	3	20	No	9	5	No	0.55	0.004	0.001	0.003	0.007
Reduced71	3	20	No	6	5	No	0.65	0.005	0.001	0.003	0.007
Reduced72	3	20	No	3	5	No	0.54	0.017	0.005	0.010	0.030
Reduced73	3	20	Yes	9	5	Yes	0.54	0.004	0.001	0.002	0.006
Reduced74	3	20	Yes	6	5	Yes	0.48	0.004	0.001	0.002	0.007
Reduced75	3	20	Yes	3	5	Yes	0.41	0.025	0.011	0.011	0.056
Reduced76	3	10	No	NA	NA	NA	0.25	0.005	0.002	0.003	0.009
Reduced77	NA	NA	NA	9	10	No	0.59	0.006	0.002	0.003	0.011
Reduced78	NA	NA	NA	9	10	Yes	0.38	0.004	0.002	0.002	0.009
Reduced79	3	10	Yes	NA	NA	NA	0.19	0.005	0.002	0.002	0.012
Reduced80	2	10	Yes	9	5	Yes	0.32	0.005	0.001	0.003	0.008
Reduced81	1	10	Yes	9	5	Yes	0.24	0.005	0.001	0.003	0.008
Reduced82	2	10	Yes	6	5	Yes	0.28	0.005	0.001	0.003	0.008
Reduced83	2	10	Yes	3	5	Yes	0.25	0.010	0.004	0.005	0.020
Reduced84	1	10	Yes	6	5	Yes	0.20	0.005	0.001	0.003	0.009
Reduced85	1	10	Yes	3	5	Yes	0.17	0.019	0.008	0.008	0.043

Note: The 'complete' model (i.e., the one that used all the data to compute density estimates) was used as the baseline for comparison. Four models did not converge due to having too few observations. Abbreviation: NA, not applicable.

[a]Models that either did not compute or had very very imprecise estimates (evident by extremely wide lower and upper confidence limits). These models were excluded from figures used for interpretation. Shading indicates suitable models for density estimation.

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significant difference between the baseline density estimate and the subset model estimate (i.e., where there was considerable overlap in lower and upper confidence intervals), and where subset model density estimates were within the bounds of the estimated lower and upper baseline confidence intervals.

We tested for differences in models fitted with a reduced number of samples by conducting paired Wilcoxon signed-rank tests (i.e., where the only difference between paired models was the number of samples included in each analysis). We used the 'wilcox.exact' function from the 'exactRankTests' package (Hothorn & Hornik, 2022), as it is capable of handling tied observations. We considered the difference in density, bias, and/or precision to be significant if the *p* value was <0.01.

2.7 | Cost analysis

We calculated the major costs associated with conducting surveys to estimate bilby abundance under each of the different scenarios described above. These included costs associated with traveling to and from sites, field personnel, and extraction and genotyping expenses (details can be found in Supplementary Material S3). Our goal was not to quantify the total expenditure associated with estimating bilby abundance but rather to identify sampling intensities that were likely to be more cost-effective, relative to the complete sampling regime. Therefore, we did not consider minor expenses (e.g., camp and field consumables) or initial costs associated with mapping the distribution of bilby activity. Given the highly mobile nature of bilbies, we recommend this step be taken regardless of the planned sampling intensity to maximize the likelihood of successfully encountering bilby scat. Results are presented as relative costs (i.e., where the cost associated with each scenario represents the proportion of the total cost needed to estimate baseline density).

3 | RESULTS

3.1 | Minimum number of bilbies alive

We collected 124 scats on systematic surveys, 455 scats on targeted surveys, and 40 scats on opportunistic surveys, of which ~64%, ~54%, and ~55%, respectively, could be allocated to an individual bilby (Table 2). This equated to 20 individuals being detected on systematic surveys, 26 individuals being detected on targeted surveys, and 10 individuals being detected on opportunistic surveys. There was some overlap in individuals detected using the different methods. Four individuals were detected on all

three surveys, 12 individuals were detected on both systematic and targeted surveys, three individuals were detected on both targeted and opportunistic surveys, and one individual was detected on both systematic and opportunistic surveys (see Supplementary Material S4). All three methods detected individuals that were not detected on any other survey, although targeted surveys detected the greatest number of new individuals (seven), followed by systematic (three) and opportunistic (two). The minimum number of bilbies known to be alive at the study site, across all three methods, was 32 individuals.

3.2 | Bilby density estimates and spatially explicit capture–recapture model comparisons

Using SECR modeling and the complete dataset (including all data collected on systematic and targeted surveys), we estimated a baseline density of 0.0037 (confidence interval (CI) = 0.0026–0.0053) bilbies/ha (Table 1). This equates to a total abundance of 81 individuals (CI = 57–116) for our study area. Modeling of subsets of the data revealed that survey regimes using only targeted sampling approaches were likely to produce biased and imprecise density estimates when compared to the baseline (Figures 2a and 3c). By contrast, models built using only data collected systematically performed relatively well—of the 23 subset models considered to produce reasonable density estimates, five of these were models built using only data that were collected systematically (Figures 2b and 3b). The five top-performing models (i.e., those with the least bias and greatest precision), however, used a combination of data collected using both targeted and systematic approaches (Figure 2), and combination models generally produced density estimates comparable to those obtained from the baseline model (Figure 3a).

Four models did not converge, while four more models produced highly imprecise estimates, evident by CIs that were magnitudes wider (Table 1). All models that did not converge corresponded to the single-occasion systematic-only sampling scenario (Table 1), while those with imprecise estimates corresponded to either reduced targeted-only sampling (3 h, five plots) or a combination of single-occasion systematic sampling and reduced targeted sampling (Table 1). This is likely because these approaches produced too few samples for reliable density estimation.

3.3 | Cost analysis

Of the five subset sampling regimes producing density estimates with the least bias and most precision (reduced01, reduced05, reduced21, reduced62, and

TABLE 2 Summary of the total number of scats collected, scats allocated to individual bilbies, and the number of bilbies detected using systematic, targeted, and opportunistic survey methods.

	No. scats collected	No. scats allocated	No. bilbies detected
Systematic	124	79	20
Targeted	455	245	26
Opportunistic	40	22	10
Total	619	346	32

Note: The total number of unique bilbies detected across all methods is also provided.
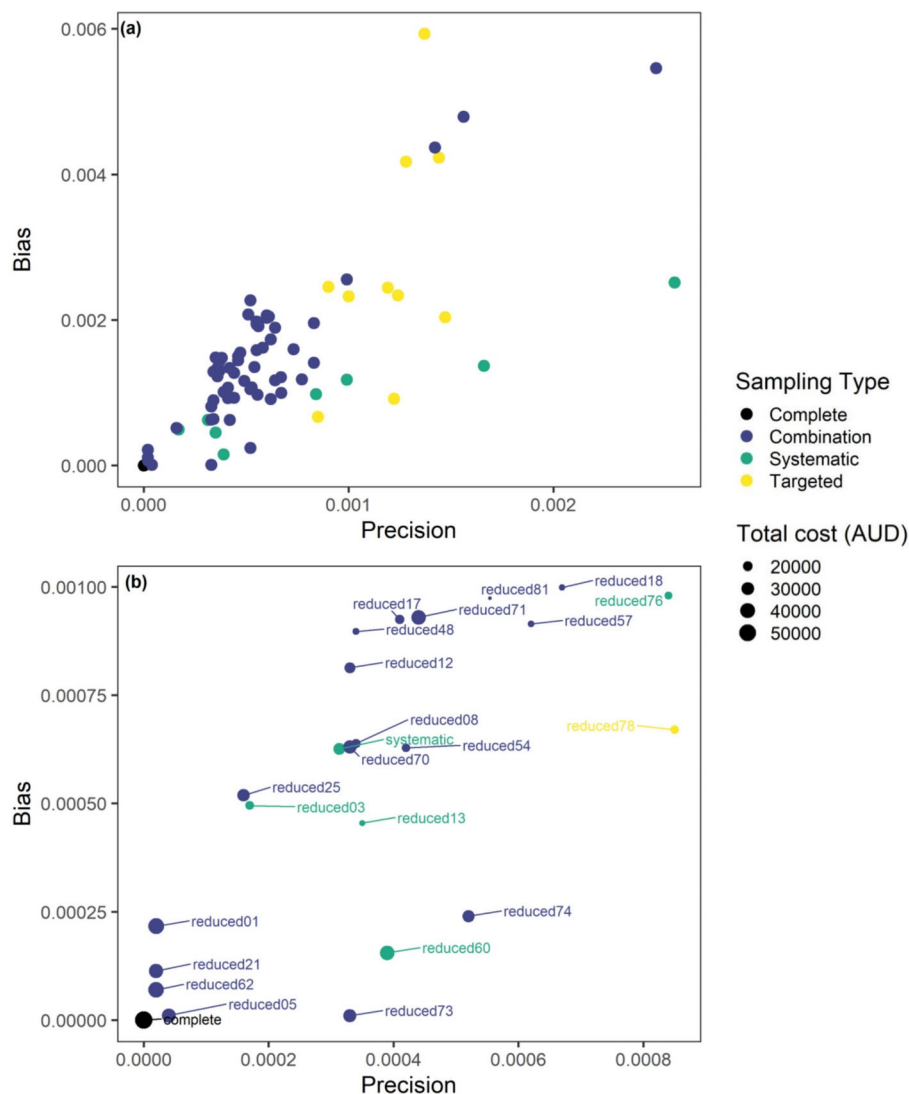
FIGURE 2 A comparison of (a) the subsampled spatially explicit capture–recapture models (excluding four models that did not compute and four models with highly imprecise estimates; see Table 1) and (b) the best models (i.e., those with bias and precision scores <0.001) and relative costs associated with undertaking sampling (as a proportion of the total costs associated with the complete model). The y-axes show the bias (the absolute difference in density between the subsampled models and the complete model), and the x-axes show the precision (the absolute difference in the standard error between the subsampled models and the complete model).

reduced73), reduced73 was cheapest (~46% cheaper when compared to the baseline regime; Table 1). Savings were made by reducing the number of targeted plots to five and reducing the number of samples collected to one every 50 m, although this likely came at a cost to precision. We found a significant difference in precision ($p < 0.01$), with models fitted from data obtained from a larger number of samples having greater precision than those fitted with data from only one sample collected every 50 m. Reduced73 was also
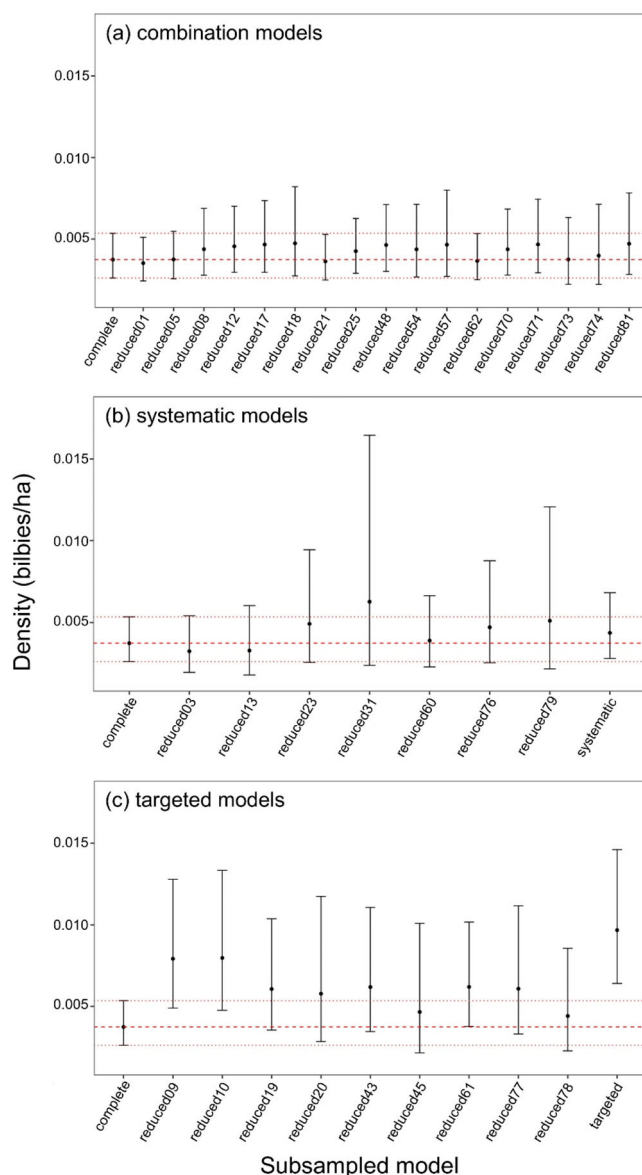
FIGURE 3 Comparison of bilby density estimates obtained from models fit with subsets of data: (a) a subset of combination models (using systematic and targeted approaches) where precision and bias <0.001, (b) systematic-only models, excluding those that did not compute, and (c) targeted-only models excluding two models with highly imprecise estimates (see Table 1 for details). Dashed red lines indicate baseline density estimates, and dotted red lines indicate lower and upper baseline confidence limits.

the least precise of the five best regimes considered (Figure 2b and Figure 3). By contrast, we found no significant difference in density ($p = 0.593$) or bias ($p = 0.7735$) between models fitted with and without a reduced number of samples.

The second cheapest regime, and the regime most comparable to the baseline, was reduced05, which was ~32% cheaper (Table 1). Savings were made by reducing

both the number of systematic occasions (to two) and the time spent searching for samples on targeted plots (to 6 h). In general, systematic-only regimes were cheaper to implement than combination regimes. The most intensive systematic-only sampling scenario was ~24% cheaper than the cheapest combination model (reduced73; Table 1); however, density estimates obtained from systematic-only models were more biased than the best combination models (Figures 2b and 3).

4 | DISCUSSION

Inclusive approaches to conservation, including data collection and analytical approaches that are respectfully negotiated between conservation scientists and Indigenous and local people, are gaining traction (Barbour & Schlesinger, 2012; Robinson et al., 2022). Here, ecologists and Indigenous Traditional Owners and rangers worked together to investigate how combinations of different on-ground sampling methods (both systematic and targeted) and intensities affected the reliability of modeled estimates of bilby abundance. We found that data from systematic surveys alone could be incorporated into SECR models to generate a reliable estimate of bilby abundance (when compared to baseline estimates), while data generated from targeted surveys generally led to higher estimates of bilby abundance. From a modeling perspective, it is not surprising that targeted on-ground sampling produced inflated estimates of bilby abundance when extrapolated to the entire study area. We only undertook targeted sampling in areas of high bilby activity or where bilby presence was known (i.e., by the presence of an active burrow), whereas the systematic approach better represented areas in the landscape where bilbies may have been absent, likely leading to a more realistic estimate of total abundance in the region. Additionally, using only targeted data in SECR models may violate a key assumption that individuals' activity centers are randomly distributed throughout the landscape (Efford, 2004). By focusing solely on areas of high activity, targeted surveys risk introducing spatial bias and overestimating density. However, our results show that systematic-only models with high-intensity sampling (i.e., three repeat visits) produced estimates comparable to the baseline, while incorporating data from targeted sampling allowed for reliable abundance estimates with fewer systematic repeat visits. This suggests that combining both methods improves model efficiency by reducing effort while maintaining robust abundance estimates. Future studies could further refine abundance estimates by incorporating habitat covariates or habitat masks within SECR models, particularly in heterogeneous landscapes. Nevertheless, our results show that

including targeted methods for scat collection (in combination with systematic approaches) can improve modeled estimates of bilby abundance for lower overall cost and effort (compared to increasing systematic sampling). Additionally, the inclusion of targeted methods to look for scat is likely to provide other benefits. Warlpiri land managers involved in the study reported that looking for bilby sign in locations that aligned with local knowledge of suitable areas (i.e., rather than at sites informed by a random sampling strategy required by a statistical model) was more satisfying, enjoyable, and logical (e.g., it made the most sense that we would follow the distinct tracks left by our target species in order to find its scat). Warlpiri were enthusiastic and highly engaged in targeted surveys, which aligned well with their day-to-day work and priorities, for example, by facilitating intergenerational knowledge transfer (a high priority of ranger programs in the central desert region of Australia; e.g., see CLC, 2012, 2015). In contrast, systematic surveys presented logistical and cultural challenges. These surveys required >60 km of walking through *Acacia* shrubland and hummock grasslands in hot, humid conditions, and their rigid design limited opportunities for Elders and rangers to select culturally significant sites or incorporate traditional knowledge in the process. Participation in systematic surveys required exceptional levels of motivation, driven by a clear understanding of their scientific value. By comparison, targeted surveys were more flexible and offered practical, on-the-job opportunities for Elders and rangers to work together, aligning better with community priorities and attracting greater participation.

Targeted methods are also likely to be useful for ecological applications in other settings, depending on the priorities of the research and the question of interest. However, because they focus on high-activity areas, they should not be used in isolation for estimating population density. Instead, targeted sampling may be used to measure relative change in abundance in response to management intervention (e.g., fire management; see Geyle et al., 2024) or for obtaining an estimate of the minimum number of bilbies present in a location to assess a site's suitability as a source population for translocations. Indeed, we detected more individual bilbies on targeted surveys than on any other kind of survey and with less overall effort than on systematic surveys. Opportunistic surveys are likely to be efficient to implement logistically and may be useful for sampling the genetic diversity in a population. They can also contribute to other surveys by improving estimates of the minimum number of bilbies known to be alive, particularly if collected from areas away from targeted plots or systematic transects. Additionally, if sampled over long periods in the same locations (e.g., wet–dry periods), this could reveal whether

and how bilbies are maintaining genetic diversity. This is likely an important question in a species that is undergoing widespread decline but also goes through temporal and spatial booms and busts (Stringer et al., 2024).

Here, we show that DNA obtained from non-invasive sources can be used to answer questions about bilby population parameters. Some other benefits of using this approach include the ease of finding samples, especially compared to more invasive methods (e.g., live trapping) (Cheng et al., 2017; Hedges et al., 2013). Live trapping is generally difficult to implement over large spatial and temporal scales, and it can be expensive (Cheng et al., 2017). Furthermore, because it involves the containment and handling of animals, as well as blood or tissue sampling, it can often cause physiological or behavioral changes as a result of heightened stress (De Bondi et al., 2010; Ferreira et al., 2018; Piggott & Taylor, 2003). Live trapping also requires an additional set of skills, such as inserting microchips or writing ethics applications, which do not always align with the skills or interests of Traditional Owner groups, particularly where literacy barriers exist. By contrast, non-invasive genetic sampling allows for similar questions to be answered without disturbing, or even seeing, the target animals (Beja-Pereira et al., 2009), and for species like the bilby that are not easily trapped, it is far more likely to yield larger sample sizes (Hedges et al., 2013).

However, there are some limitations. Non-invasive genetic sampling provides little information on individual traits like animal age, body mass, or reproductive condition (Cheng et al., 2017; Ferreira et al., 2018), and successfully genotyping DNA from scat comes with other challenges. For example, we used an existing SNP panel (Hogg et al., 2024), which may not be available for other target fauna. If this is the case, there would be an additional cost and sampling requirement associated with developing an informative genetic-marker panel. Similarly, in situations where obtaining a population estimate per unit area is the goal, an understanding of the likely home range of the species of interest is required (Romairone et al., 2018). While this can be obtained from non-invasive genetic sampling, the costs associated with doing so may be much greater than what is reported here.

Another challenge encountered in this study was the overall low genotyping success rates. This may be attributed to the time that elapsed between collection and eventual DNA extraction and genotyping, which, due to the need to troubleshoot lab protocols, took longer than expected. Early unpublished trials conducted on a small subset of the samples collected as part of this study suggest that this may be ameliorated by sending repeat samples (i.e., additional pellets collected from the same bilby

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scat pile) to the lab for extraction and genotyping. However, this will inevitably lead to increased costs. It may also be possible to obtain DNA from other non-invasive samples; for example, from hair collected from snares set at the entrance of bilby burrows. Hair sampling is a commonly used method for obtaining animal DNA (e.g., see Rounsville et al., 2022; Schultz et al., 2022; Stricker et al., 2012), and it may be worth investigating the applicability of this approach to bilbies.

Here, we provide the first estimate of bilby abundance in the Northern Territory's central deserts, although we acknowledge that there is still much uncertainty regarding the true population size. Future study may benefit from testing each of our approaches in areas where the true population size is known (e.g., within fenced reserves) to see if our assumptions hold and if these methodologies can be used in other scenarios where initial abundance and detectability may differ. This will assist in developing a best-practice standard for bilby scat collection, depending on the local conditions present.

5 | CONCLUSIONS

Obtaining an estimate of animal abundance or density per unit area (in this case the number of bilbies per hectare) is a common method used to quantify population sizes in western ecological studies (e.g., see Ash et al., 2020; Fonda et al., 2022; Owen-Ramos et al., 2022). While systematic surveys provide robust population estimates, the selection of sites and sampling methods used may not be very intuitive to Indigenous and local communities. In seeking to identify an efficient way to derive a measure of bilby abundance that was appropriate to the bio-cultural context in which we were working, we showed that multiple benefits can be achieved from inclusive monitoring practices and identified ways in which we might be able to adapt research to enable more meaningful local collaborations. Bilbies are just one of many culturally significant and threatened wildlife species that occur on lands owned or managed by Indigenous people. Indigenous Elders worry about if and where bilbies occur on their land, and scientists often struggle to establish baselines to address declines of these populations and the bio-cultural ecosystems that support them. Surveys generally involve travel to remote locations and, in some cases, may require walking long distances (e.g., in areas where vegetation precludes vehicle access), often in trying conditions (e.g., extreme heat). Observers must also learn to identify scat and other sources of bilby sign. Funding for wildlife conservation is often tight, and fieldwork, particularly in remote locations, is expensive. Therefore, it is imperative that cost-effective and efficient approaches are developed to enable assessment of population parameters and direct on-ground action to protect species of conservation concern. As we show here, weaving multiple approaches to find bilby scats not only offers a practical approach to improve estimates of bilby abundance but also shows why and how collaborative knowledge-sharing practices to find sign of these unique animals can deliver multiple benefits to both Indigenous and scientific partners.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

The data that support this study are owned by multiple parties, and cannot be made publicly available. Data may be shared upon reasonable request to the corresponding author if all parties agree, and pending the establishment of appropriate data sharing agreements.

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REFERENCES

Ash, E., Hallam, C., Chanteap, P., Kaszta, Z., Macdonald, D. W., Rojanachinda, W., Redford, T., & Harihar, A. (2020). Estimating the density of a globally important tiger (*Panthera tigris*) population: Using simulations to evaluate survey design in eastern Thailand. *Biological Conservation*, *241*, 108349. https://doi.org/10.1016/j.biocon.2019.108349

Banks, S. C., Hoyle, S. D., Horsup, A., Sunnucks, P., & Taylor, A. C. (2003). Demographic monitoring of an entire species (the northern hairy-nosed wombat, *Lasiorhinus krefftii*) by genetic analysis of non-invasively collected material. *Animal Conservation*, *6*, 101–107. https://doi.org/10.1017/s1367943003003135

Barbour, W., & Schlesinger, C. (2012). Who's the boss? Post-colonialism, ecological research and conservation management on Australian indigenous lands. *Ecological Management & Restoration*, *13*(1), 36–41. https://doi.org/10.1111/j.1442-8903.2011.00632.x

Beja-Pereira, A., Oliveira, R., Alves, P. C., Schwartz, M. K., & Luikart, G. (2009). Advancing ecological understandings through technological transformations in noninvasive genetics. *Molecular Ecology Resources*, *9*(5), 1279–1301. https://doi.org/10.1111/j.1755-0998.2009.02699.x

Black, S. A. (2020). Assessing presence, decline, and extinction for the conservation of difficult-to-observe species. In F. M. Angelici & L. Rossi (Eds.), *Problematic wildlife II: New conservation and management challenges in the human-wildlife interactions* (pp. 359–392). Springer International Publishing. https://doi.org/10.1007/978-3-030-42335-3_11

Bradley, K., Lees, C., Lundie-Jenkins, G., Copley, P., Paltridge, R., Dziminski, M., Southgate, R., Nally, S., & Kemp, L. (2015). Greater bilby recovery summit 2015. Report and interim conservation plan: An initiative of the save the bilby fund. A. V. IUCN SSC Conservation Breeding Specialist Group, MN.

Carpenter, F. M., & Dziminski, M. A. (2017). Breaking down scats: Degradation of DNA from greater bilby (*Macrotis lagotis*) faecal pellets. *Australian Mammalogy*, *39*(2), 197–204. https://doi.org/10.1071/AM16030

Cheng, E., Hodges, K. E., Sollmann, R., & Mills, L. S. (2017). Genetic sampling for estimating density of common species. *Ecology and Evolution*, *7*(16), 6210–6219. https://doi.org/10.1002/ece3.3137

CLC. (2012). Ngurra walalja warra warra kanjaku: looking after our country: Southern Tanami indigenous protected area plan of management 2012. Central Land Council (CLC). https://walyaku.org.au/Southern-Tanami-IPA-Plan-of-Management.pdf

CLC. (2015). Mardarnilipa ngurra manu kuruwarri tarnngangku pirrjirdili: Keeping country alive and healthy: Northern Tanami indigenous protected area plan of management 2015. Central Land Council, National Library of Australia.

CLC. (2024). Yitaki maninjaku ngurungka: Reading the country: Animal tracking framework. Warlpiri Knowledge Holders, Central Land Council. Alice Springs, Australia.

Cramer, V. A., Dziminski, M. A., Southgate, R., Carpenter, F. M., Ellis, R. J., & van Leeuwen, S. (2017). A conceptual framework for habitat use and research priorities for the greater bilby (*Macrotis lagotis*) in the north of Western Australia. *Australian Mammalogy*, *39*(2), 137–151. https://doi.org/10.1071/AM16009

Danielsen, F., Enghoff, M., Poulsen, M. K., Funder, M., Jensen, P. M., & Burgess, N. D. (2021). The concept, practice, application, and results of locally based monitoring of the environment. *Bioscience*, *71*(5), 484–502. https://doi.org/10.1093/biosci/biab021

DCCEEW. (2023). Recovery plan for the greater bilby (*Macrotis lagotis*). Department of Climate Change, the Environment and Water (DCCEEW), Australian Government, Canberra.

de Bondi, N., White, J. G., Stevens, M., & Cooke, R. (2010). A comparison of the effectiveness of camera trapping and live trapping for sampling terrestrial small-mammal communities. *Wildlife Research*, *37*(6), 456–465. https://doi.org/10.1071/WR10046

Dziminski, M. A., Carpenter, F. M., & Morris, F. (2021). Monitoring the abundance of wild and reintroduced bilby populations. *The Journal of Wildlife Management*, *85*(2), 240–253. https://doi.org/10.1002/jwmg.21981

Efford, M. (2004). Density estimation in live-trapping studies. *Oikos*, *106*(3), 598–610. https://doi.org/10.1111/j.0030-1299.2004.13043.x

Efford, M. (2023b). What could possibly go wrong? Troubleshooting spatially explicit capture-recapture models in secr 4.6. University of Otago. https://www.otago.ac.nz/density/pdfs/secr-troubleshooting.pdf

Efford, M. G. (2011). Estimation of population density by spatially explicit capture-recapture analysis of data from area searches. *Ecology*, *92*(12), 2202–2207. https://doi.org/10.1890/11-0332.1

Efford, M. G. (2023a). secr: Spatially explicit capture-recapture models (Version 4.6.0) [R package]. CRAN. https://CRAN.R-project.org/package=secr

Ferreira, C. M., Sabino-Marques, H., Barbosa, S., Costa, P., Encarnação, C., Alpizar-Jara, R., Pita, R., Beja, P., Mira, A., Searle, J. B., Paupério, J., & Alves, P. C. (2018). Genetic non-invasive sampling (gNIS) as a cost-effective tool for monitoring elusive small mammals. *European Journal of Wildlife Research*, *64*(4), 46. https://doi.org/10.1007/s10344-018-1188-8

Fonda, F., Bacaro, G., Battistella, S., Chiatante, G., Pecorella, S., & Pavanello, M. (2022). Population density of European wildcats in a pre-alpine area (northeast Italy) and an assessment of estimate robustness. *Mammal Research*, *67*(1), 9–20. https://doi.org/10.1007/s13364-021-00609-z

Garnett, S. T., Burgess, N. D., Fa, J. E., Fernández-Llamazares, Á., Molnár, Z., Robinson, C. J., Watson, J. E. M., Zander, K. K., Austin, B., Brondizio, E. S., Collier, N. F., Duncan, T., Ellis, E., Geyle, H., Jackson, M. V., Jonas, H., Malmer, P., McGowan, B., Sivongxay, A., & Leiper, I. (2018). A spatial overview of the global importance of indigenous lands for conservation. *Nature Sustainability*, *1*(7), 369–374. https://doi.org/10.1038/s41893-018-0100-6

Geyle, H. M., Schlesinger, C., Banks, S., Dixon, K., Murphy, B. P., Paltridge, R., Doolan, L., Herbert, M., Rangers, N. T., & Dickman, C. R. (2024). Unravelling predator-prey interactions in response to planned fire: A case study from the Tanami Desert. *Wildlife Research*, *51*(8), WR24059. https://doi.org/10.1071/WR24059

Goolmeer, T., Skroblin, A., Grant, C., van Leeuwen, S., Archer, R., Gore-Birch, C., & Wintle, B. A. (2022). Recognizing culturally

significant species and indigenous-led management is key to meeting international biodiversity obligations. *Conservation Letters*, *15*(6), e12899. https://doi.org/10.1111/conl.12899

Hedges, S., Johnson, A., Ahlering, M., Tyson, M., & Eggert, L. S. (2013). Accuracy, precision, and cost-effectiveness of conventional dung density and fecal DNA based survey methods to estimate Asian elephant (Elephas maximus) population size and structure. *Biological Conservation*, *159*, 101–108. https://doi.org/10.1016/j.biocon.2012.12.010

Hema, E. M., Di Vittorio, M., Barnes, R. F. W., Guenda, W., & Luiselli, L. (2017). Detection of interannual population trends in seven herbivores from a west African savannah: A comparison between dung counts and direct counts of individuals. *African Journal of Ecology*, *55*(4), 609–617. https://doi.org/10.1111/aje.12397

Hogg, C. J., Edwards, R. J., Farquharson, K. A., Silver, L. W., Brandies, P., Peel, E., Escalona, M., Jaya, F. R., Thavornkanlapachai, R., Batley, K., Bradford, T. M., Chang, J. K., Chen, Z., Deshpande, N., Dziminski, M., Ewart, K., Griffith, O., Marin-Gual, L., Moon, K. L., ... Belov, K. (2024). Extant and extinct bilby genomes combined with indigenous knowledge improve conservation of a unique Australian marsupial. *Nature Ecology and Evolution*, *8*, 1311–1326. https://doi.org/10.1038/s41559-024-02519-0

Hothorn, T., & Hornik, K. (2022). exactRankTests: exact distributions for rank and permutation tests. R package version 0.8-35. https://CRAN.R-project.org/package=exactRankTests

Indigo, N., Skroblin, A., Southwell, D., Grimmett, L., Nou, T., Young, A., AZM Project Partners, & Legge, L. (2021). Arid zone monitoring project report (Project, Issue 3.2.5). NESP Threatened Species Recovery Hub.

Lilleyman, A., Pascoe, J., J. Robinson, C., Legge, S. M., Woinarski, J. C. Z., & Garnett, S. T. (2024). Imperilled birds and first peoples' land and sea country in Australia. *Emu*, *124*(1), 108–122. https://doi.org/10.1080/01584197.2023.2290008

Lindenmayer, D., Woinarski, J., Legge, S., Southwell, D., Lavery, T., Robinson, N., Scheele, B., & Wintle, B. (2020). A checklist of attributes for effective monitoring of threatened species and threatened ecosystems. *Journal of Environmental Management*, *262*, 110312. https://doi.org/10.1016/j.jenvman.2020.110312

Lucchini, V., Fabbri, E., Marucco, F., Ricci, S., Boitani, L., & Randi, E. (2002). Noninvasive molecular tracking of colonizing wolf (Canis lupus) packs in the western Italian Alps. *Molecular Ecology*, *11*(5), 857–868. https://doi.org/10.1046/j.1365-294X.2002.01489.x

Macdonald, J. M., Robinson, C. J., Perry, J., Lee, M., Barrowei, R., Coleman, B., Markham, J., Barrowei, A., Markham, B., Ford, H., Douglas, J., Hunter, J., Gayoso, E., Ahwon, T., Cooper, D., May, K., Setterfield, S., & Douglas, M. (2021). Indigenous-led responsible innovation: Lessons from co-developed protocols to guide the use of drones to monitor a biocultural landscape in Kakadu National Park, Australia. *Journal of Responsible Innovation*, *8*(2), 300–319. https://doi.org/10.1080/23299460.2021.1964321

Mamun, A. A., & Natcher, D. C. (2023). The promise and pitfalls of community-based monitoring with a focus on Canadian examples. *Environmental Monitoring and Assessment*, *195*(4), 445. https://doi.org/10.1007/s10661-022-10841-y

McGregor, H. M., & Moseby, K. E. (2014). Improved technique for capturing the greater bilby (Macrotis lagotis) using burrow cage traps. *Australian Mammalogy*, *36*(2), 259–260. https://doi.org/10.1071/AM14011

Moore, H. A., Dunlop, J. A., Geyle, H. M., Greenwood, L., & Nimmo, D. G. (2023). First you get the money, then you get the power: Comparing the cost and power of monitoring programs to detect changes in occupancy of a threatened marsupial predator. *Conservation Science and Practice*, *5*(2), e12881. https://doi.org/10.1111/csp2.12881

Moseby, K. E., & O'Donnell, E. (2003). Reintroduction of the greater bilby, *Macrotis lagotis* (Reid) (Marsupialia: Thylacomyidae), to northern South Australia: Survival, ecology and notes on reintroduction protocols. *Wildlife Research*, *30*(1), 15–27. https://doi.org/10.1071/WR02012

Owen-Ramos, J. D., Sanchez, C. J., Blair, S., Holm, S., Furnas, B. J., & Sacks, B. N. (2022). Use of fecal DNA to estimate black bear density in an urban-wildland interface. *Wildlife Society Bulletin*, *46*(4), e1347. https://doi.org/10.1002/wsb.1347

Paltridge, R. (2016). What did we learn from the 2016 Ninu festival? [unpublished report].

Petit, E., & Valiere, N. (2006). Estimating population size with noninvasive capture-mark-recapture data. *Conservation Biology*, *20*(4), 1062–1073. https://doi.org/10.1111/j.1523-1739.2006.00417.x

Piggott, M. P., & Taylor, A. C. (2003). Remote collection of animal DNA and its applications in conservation management and understanding the population biology of rare and cryptic species. *Wildlife Research*, *30*(1), 1–13. https://doi.org/10.1071/WR02077

Popp, J. N., Priadka, P., Young, M., Koch, K., & Morgan, J. (2020). Indigenous guardianship and moose monitoring: Weaving indigenous and Western ways of knowing. *Human–Wildlife Interactions*, *14*, 296–308. https://doi.org/10.26077/67f5-d36b

Proença-Ferreira, A., Ferreira, C., Leitão, I., Paupério, J., Sabino-Marques, H., Barbosa, S., Lambin, X., Alves, P. C., Beja, P., Moreira, F., Mira, A., & Pita, R. (2019). Drivers of survival in a small mammal of conservation concern: An assessment using extensive genetic non-invasive sampling in fragmented farmland. *Biological Conservation*, *230*, 131–140. https://doi.org/10.1016/j.biocon.2018.12.021

Robinson, C. J., Macdonald, J. M., Perry, J., Bangalang, N.-G., Nayinggul, A., Nadji, J., Nayinggul, A., Dempsey, S., Nadji, S., McCartney, S., Taylor, A., Hunter, F., May, K., Cooper, D., Moyle, F., Drummond, A., Borovac, C., van Bodegraven, S., Gilfedder, M., ... Douglas, M. M. (2022). Coproduction mechanisms to weave indigenous knowledge, artificial intelligence, and technical data to enable indigenous-led adaptive decision making: Lessons from Australia's joint managed Kakadu National Park. *Ecology and Society*, *27*(4), 36. https://doi.org/10.5751/ES-13747-270436

Romairone, J., Jiménez, J., Luque-Larena, J. J., & Mougeot, F. (2018). Spatial capture-recapture design and modelling for the study of small mammals. *PLoS One*, *13*(6), e0198766. https://doi.org/10.1371/journal.pone.0198766

Rounsville, T. F., Rogers, R. E., Welsh, A. B., Ryan, C. W., & Anderson, J. T. (2022). Novel hair snare and genetic methods for non-invasive bobcat detection. *Ecology and Evolution*, *12*(1), e8435. https://doi.org/10.1002/ece3.8435

Ruibal, M., Peakall, R., Claridge, A., & Firestone, K. (2009). Field-based evaluation of scat DNA methods to estimate population abundance of the spotted-tailed quoll (Dasyurus maculatus), a rare Australian marsupial. *Wildlife Research*, *36*(8), 721–736. https://doi.org/10.1071/WR09086

Schultz, A. J., Strickland, K., Cristescu, R. H., Hanger, J., de Villiers, D., & Frère, C. H. (2022). Testing the effectiveness of genetic monitoring using genetic non-invasive sampling. _Ecology and Evolution_, _12_(1), e8459. https://doi.org/10.1002/ece3.8459

Service, C. N., Adams, M. S., Artelle, K. A., Paquet, P., Grant, L. V., & Darimont, C. T. (2014). Indigenous knowledge and science unite to reveal spatial and temporal dimensions of distributional shift in wildlife of conservation concern. _PLoS One_, _9_(7), e101595. https://doi.org/10.1371/journal.pone.0101595

Skroblin, A., Carboon, T., Bidu, G., Taylor, M., Bidu, N., Taylor, W., Taylor, K., Miller, M., Robinson, L., Williams, C., Chapman, N., Marney, M., Marney, C., Biljabu, J., Biljabu, L., Jeffries, P., Samson, H., Charles, P., Game, E. T., & Wintle, B. (2022). Developing a two-way learning monitoring program for Mankarr (greater bilby) in the Western Desert, Western Australia. _Ecological Management & Restoration_, _23_, 129–138. https://doi.org/10.1111/emr.12543

Smith, B. P., Waudby, H. P., Dickman, C. R., Soennichsen, K., Mills, C., Howe, A., Woolley, L.-A., Griffiths, S. R., Cox, T. E., Clayton, J., Penton, C., Morrant, D. S., Letnic, M., Cullen, D., Stobo-Wilson, A., Taggart, D. A., Gleeson, D., Cripps, J. K., Gill, M. J., & MacDonald, A. J. (2022). Observing wildlife and its signs. In B. P. Smith, H. P. Waudby, C. Alberthsen, & J. O. Hampton (Eds.), _Wildlife research in Australia: Practical and applied methods_. CSIRO Publishing.

Smith, S., McRae, P., & Hughes, J. (2009). Faecal DNA analysis enables genetic monitoring of the species recovery program for an arid-dwelling marsupial. _Australian Journal of Zoology_, _57_(2), 139–148. https://doi.org/10.1071/ZO09035

Sollmann, R., Gardner, B., & Belant, J. L. (2012). How does spatial study design influence density estimates from spatial capture-recapture models? _PLoS One_, _7_(4), e34575. https://doi.org/10.1371/journal.pone.0034575

Southgate, R., Dziminski, M. A., Paltridge, R., Schubert, A., & Gaikhorst, G. (2018). Verifying bilby presence and the systematic sampling of wild populations using sign-based protocols: With notes on aerial and ground survey techniques and asserting absence. _Australian Mammalogy_, _41_(1), 27–38. https://doi.org/10.1071/AM17028

Stephens, P. A., Zaumyslova, O. Y., Miquelle, D. G., Myslenkov, A. I., & Hayward, G. D. (2006). Estimating population density from indirect sign: Track counts and the Formozov–Malyshev–Pereleshin formula. _Animal Conservation_, _9_(3), 339–348. https://doi.org/10.1111/j.1469-1795.2006.00044.x

Stricker, H. K., Belant, J. L., Beyer, D. E., Kanefsky, J., Scribner, K. T., Etter, D. R., & Fierke, J. (2012). Use of modified snares to estimate bobcat abundance. _Wildlife Society Bulletin_, _36_(2), 257–263. https://doi.org/10.1002/wsb.137

Stringer, E. J., Gruber, B., Sarre, S. D., Wardle, G. M., Edwards, S. V., Dickman, C. R., Greenville, A. C., & Duncan, R. P. (2024). Boom-bust population dynamics drive rapid genetic change. _Proceedings of the National Academy of Sciences_, _121_(18), e2320590121. https://doi.org/10.1073/pnas.2320590121

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