Reptile community responses to an avian ecosystem engineer

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Birds; Community interactions; Ecosystem engineers; Reptile abundance; Reptile diversity; Sociable weaver



Abstract

In the Kalahari, sociable weavers (*Philetairus socius*) build huge, communal nests. Although Kalahari tree skinks (Trachylepis spilogaster) are known to preferentially use trees that host such colonies, the degree to which other reptile species use these trees is not well documented. Sociable weaver nests can provide benefits to different animals and can provide food and shelter for reptiles. I trapped reptiles at Tswalu Kalahari Reserve to assess the impact of sociable weaver colonies on selected reptile populations during weaver breeding and non-breeding seasons. I tested the hypothesis that the reptile community under trees with colonies would differ in diversity compared to those at nearby control trees without colonies, because the sociable weaver colonies provide more resources (food and shelter) to the reptiles than trees without colonies. I also tested whether the abundance of the Kalahari tree skink, Cape cobra (Naja nivea), and Cape thick-toed gecko (Pachydactylus capensis) under trees with colonies differed from those at nearby control trees without colonies, as these were the most abundant species found at the sociable weaver nests. Trapping for 11 days at 24 sites (12 colony trees, 12 control trees), on two occasions, once in March when weavers were breeding, and once in September before they were breeding, resulted in 665 total detections of 13 reptile species, including 148 total recaptures. Mean species richness was significantly higher at colony trees than at control trees during both surveys (2.5 times higher when the birds were breeding; 1.6 times higher when the birds were not breeding). Poisson Nmixture modelling revealed that Kalahari tree skink was significantly more abundant on colony trees during the breeding (3.2 times) and non-breeding seasons (3.7 times). Similarly, Royle-Nichols modelling revealed that Cape thick-toed gecko was more abundant on colony trees during both the breeding (10.5 times) and non-breeding seasons (5.6 times). Conversely, Cape cobra was ~13 times more abundant on colony trees during the breeding season but showed no difference in abundance between colony and non-colony trees in the absence of breeding. I interpret these results to suggest that lizards use colony trees for both food and shelter whereas cobras preferentially use colonies for food only. My work reveals that sociable weaver colonies can influence reptile communities through non-exclusive mechanisms such as microhabitat engineering, but also through food resource allocation.



Declaration

I declare that "**Reptile community responses to an avian ecosystem engineer**" is my own work, that it has not been submitted for any degree or examination at any university, and that all sources I have used or quoted have been indicated, and acknowledged by complete reference.

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Chapter 1. Introduction

1.1 Ecosystem engineers

The availability of resources, which might be concentrated in specific locations (Parrish & Edelstein-Keshet, 1999), typically determines the distribution of species in an area (McIntyre & Wiens, 1999; Hunter et al. 2012). Some species can alter the availability and distribution of those resources in the environment, which can influence the distribution and abundance of other species (Lowney & Thomson, 2021). These organisms that change the availability and distribution of resources in the environment are called ecosystem engineers (Jones et al. 1994). Organisms can structurally change ecosystems, but organisms can also modify environments through ecological interactions, which Jones et al. (1994) suggested as the ecosystem engineering concept (Berke, 2010). Jones et al. (1994) defined ecosystem engineers as organisms that impact the accessibility of resources for other species through physical changes in living and non-living materials therefore, modify, maintain and create habitats, and identified two types of engineers: allogenic and autogenic engineers.

Autogenic engineers are organisms that alter the environment by their own physical structures (Jones et al. 1994). Examples of autogenic engineers include corals and trees (Jones et al., 1994; Berke, 2010; Balzan et al., 2020; Phillips et al., 2022). Allogenic engineers are organisms that modify the environment by changing living or non-living materials from one state to another, by mechanical or alternative methods (Jones et al. 1994). Examples include woodpeckers (Picidae) that create holes in trees and beavers (*Castor* spp.), which build dams and create wetlands by altering hydrology (Jones et al. 1994). Allogenic engineers, also known as structural engineers, design habitats that provide shelter and food for animals (Berke, 2010; Lowney & Thomson, 2021). As a result, ecosystem engineers may be able to increase species' realized niches, thereby

increasing the species richness in the community (Bertness & Callaway, 1994; Wright et al., 2002; Castilla et al., 2004; Badano & Cavieres, 2006; Lowney & Thomson, 2021).

1.2 Birds as ecosystem engineers and ecosystem service providers

Animals can change the environment through a number of processes, which include physically disturbing the soil and vegetation by burrowing, trampling, and removing vegetation (Sobey & Kenworthy, 1979; Vidal et al., 1998; Mulder & Keall, 2001; Havik et al., 2014). Ecosystem engineering by means of faunal urine and faeces deposition can have effects on vegetation form and composition, as well as soil properties (García et al., 2002; Ellis, 2005). Birds that aggregate for an extended period can change the habitat, which include the vegetation and soil properties around the nests (García et al., 2002; Ellis, 2005). Faecal matter and guano deposit around nest sites can change the soil properties (Wait et al., 2004; Ellis, 2005; García et al., 2011; Otero et al., 2015) surrounding their sites, impacting on other ecosystem components (Natusch et al., 2017).

Bird nests come in a variety of shapes and sizes (Mainwaring et al., 2015) and they provide a variety of resources for the different species that use these nests (Bancroft et al., 2008; Mainwaring et al., 2015; Natusch et al., 2016; Delhey, 2018). The habitats created by birds benefit animal communities, for instance providing a safe escape for small vertebrates from their predators (Pringle, 2008). They can also improve small mammals foraging success (Valeix et al., 2011) and provide shelter from extreme temperatures to other animals (Lowney et al., 2020a). Bird nests vary across taxa, from simple scrapes on the ground and nests in vegetation to burrow nests below ground, and enormous communal structures (Maclean, 1973; Mainwaring et al., 2015). Where large communal nests remain in trees for long periods of time, they can have important effects on

the vegetation and soil properties below the trees by the continuous falling of carcasses, nest material, and faeces (Dean et al., 1999; Prayag et al., 2020; Aikins et al., 2023).

The ecosystem engineering concept relates to birds not only because they shape ecosystems, but also because they provide ecosystem services, which are important for the health of ecosystems and other species in the environment (Whelan et al., 2015). For example, birds play significant roles in pest control, seed dispersal, nutrient cycling, pollination, and scavenging, all of which modify the environment around them and benefit other species (Sekercioglu, 2006; Whelan et al., 2008). These are four different ecosystem services provided by birds: provisioning services (Moss & Bowers, 2007; Green & Elmberg, 2014), supporting services, cultural services (Sekercioglu, 2002; Greenwood, 2007; Ma et al., 2013; Kronenberg, 2014; White et al., 2014), and regulating services (Sekercioglu, 2006; Whelan et al., 2015). Provisioning services by birds include being a crucial role in our diets, serving as significant elements for subsistence, consumption, and recreational activities (Moss and Bowers 2007). Birds contribute to cultural services through activities such as birdwatching (Kronenberg 2014a; Ma et al. 2013; Sekercioglu 2002; White et al. 2014), which adds to recreation and tourism. Birds contribute to regulating and supporting services by participating in nutrient cycling, seed dispersal, pollination, and controlling pests (Sekercioglu 2006a; Whelan et al. 2008). Understanding the significance of these services and their ecosystem functions is crucial for quantifying their impact on ecosystems and other species benefitting from them. This knowledge is essential for public support for conserving bird populations and their contributions to the surrounding ecosystem (Whelan et al., 2015).

1.3 Sociable weavers (Philetairus socius)

Sociable weavers (*Philetairus socius*) are small passerine birds that live in the arid and semi-arid parts of southwestern Africa, including the Kalahari (Maclean, 1973; Mendelsohn & Anderson, 1997). Sociable weavers are known to produce huge communal nests in trees (Fig. 1), built using grass and twigs (Maclean, 1973; Mendelsohn & Anderson, 1997). Sociable weavers maintain their nests for many years and house many generations of sociable weavers (Collias & Collias, 1964). Each sociable weaver colony can have up to 250 chambers, and house hundreds of weaver individuals (Maclean, 1973).



Figure 1: A sociable weaver colony in a camel thorn tree (*Vachellia erioloba*) at Tswalu Kalahari Reserve.

Colonies provide many benefits to different organisms that seek refuge from thermal extremes (Lowney et al., 2020a), which is important in arid environments. Other benefits include providing

shelter and food for certain mammals. Birds other than weavers use these colonies for breeding or roosting or thermal benefits (Lowney & Thomson, 2021). Some examples include the African pygmy falcon, acacia pied barbet (*Tricholaema leucomelas*), ashy tit (*Melaniparus cinerascens*), scaly-feathered finch (Sporopipes squamifrons), red-headed finch (Amadina erythrocephala) and cape sparrow (Passer melanurus) (Lowney & Thomson, 2022). Food and nutritional resources may also concentrate around these colonies, substantially enriching the soils beneath colonies with nutrients (Prayag et al., 2020). This enriched soil can have an impact on local vegetation and animals in this environment. Some examples include the continuous depositing of sociable weaver faeces, which can change the microbial communities below the trees and the low water infiltration rate preventing other vegetation from establishing below the canopy (Prayag et al., 2020). The animal community uses the sociable weaver nests for shade, territorial behaviours, foraging, and roosting sites (Lowney & Thomson, 2021). Therefore, sociable weaver nests increase biodiversity around them (Dean et al., 1999; Seymour, 2006; Lowney & Thomson, 2021). The colonies also offer a refuge from severe temperatures or provide food to animals during periods of poor plant productivity by altering the plant biomass in the areas surrounding the colony (Lowney & Thomson, 2021). Animals that live in arid environments frequently experience severe conditions and excessively harsh temperatures that can affect many species (Lowney & Thomson, 2021). Summer temperatures can cause animals to experience hyperthermia, while winter temperatures can cause animals to experience hypothermia (Cunningham et al., 2013; Andreasson et al., 2019). Precipitation is variable in arid ecosystems and can cause vegetation cover to vary (Hillel & Tadmor, 1962; Rosenzweig, 1968). Certain species rely on precipitation to start breeding (Dean et al., 1999). In such extremes, the influence of an ecosystem engineer that alleviates these environmental pressures may vary, depending on the context of the environment (Loreau et al.,

2001; Leung et al., 2012; Mellard et al., 2019). Lowney & Thomson (2021) found that sociable weaver colonies can mitigate environmental harshness. Sociable weaver nests house many different bird and non-avian species (Maclean, 1973), and evidence shows that these colonies are home to a diverse spectrum of non-obligate species (Maclean, 1973). Brain (1969) and Rymer et al. (2014) found that Kalahari tree skinks thrive in trees that house weaver colonies, while African pygmy falcons (*Polihierax semitorquatus*), and some arthropods are reliant on these structures (Rehn, 1965; Harvey et al., 2015).

Lowney & Thomson (2021) showed that sociable weavers can influence faunal communities. They found that sociable weaver colonies in trees created local biodiversity hotspots and the faunal community used the nests for shade, territorial behaviours, foraging, and roosting sites (Lowney & Thomson, 2021). They demonstrated that sociable weavers met the criteria for being an ecosystem engineer, as defined by Coggan et al. (2018). The colonies acted as important spots of activity in the landscape, creating habitat, increasing habitat heterogeneity, and potentially influencing the organization of animal communities (Lowney et al., 2020b).

1.4 The Kalahari tree skink responses to sociable weaver colonies

The Kalahari tree skink forages on or near trees with sociable weaver nests (Brain, 1969; Cooper & Whiting, 2000; Rymer et al., 2014). These skinks are known to be more abundant on trees with colonies than trees without colonies (Brain, 1969; Rymer et al., 2014; Lowney et al., 2020b; Lowney & Thomson, 2022). The weaver colonies appear to help skinks in a variety of ways, including foraging benefits, a place to bask and providing shelter (Brain, 1969; Cooper & Whiting, 2000; Rymer et al., 2014; Lowney et al., 2020b). Lowney et al. (2020b) also found that Kalahari tree skinks react to the sociable weaver's alarm calls. This helped the skinks escape from possible

predators, broadening their realized niche, and allowing them to coexist with predators, which may normally drive them out (Lowney et al., 2020b). Lowney & Thompson (2022) found there to be an increase abundance of reptiles at trees with sociable weaver nests. The abundance of reptiles is primarily influenced by factors such as the availability of food and the ability to thermoregulate. Colonies play a crucial role by offering shelter and resources, leading to higher invertebrate abundance around colony trees. In arid environments, colonies become essential for reptiles as they provide the necessary resources, explaining the greater interactions between reptiles and colony trees compared to non-colony trees. Kalahari tree skinks occur at far greater population densities on trees with colonies (Brain, 1969; Rymer et al., 2014), however it is unknown if this is because more lizards colonize the trees with sociable weaver colonies, or if the skinks using those trees have increased fitness (Rymer et al., 2014).

1.5 Studying reptile diversity

Studying Kalahari tree skinks highlights the significance of investigating reptile diversity because they have adaptations and unique ecological roles within their ecosystems, which emphasize the value of protecting and understanding these species. Human activities in natural habitats produce changes in structure, biotic composition, and resource availability; these are among the most important anthropogenic influences on ecosystems (Cuarón, 2000; Hobbs et al., 2009). These disturbances have significant consequences for species diversity and microhabitats.

There are many ecological and biological significances of reptiles, including food source, raw materials and trade, medicinal use, traditional beliefs, disease control, dispersion and nutrient cycling (Valencia-Aguilar et al. 2013). Around the world certain species of reptiles played a significant role in historical and present-day sources of food for people living in rural areas

(Mittermeier et al. 1992; Thorbjarnarson et al. 2000). Many countries export reptiles which contribute to the trade activities around the world (Thorbjarnarson, 1991). Reptiles generate potent poisons that have various effects on humans, and these have had a role in advancing pharmaceuticals for treating human diseases (Mackessy, 2010). Traditional healing practices and cultural beliefs often incorporated by reptiles are vital components of folk medicine (Alves & Santana, 2008).

In the realm of disease control, the emergence of resistance to chemical insecticides among disease-carrying insects has posed challenges. The adoption of innovative approaches, such as biological controls, has proven effective in reducing both environmental and economic impacts (Jenkins, 1964). Reptiles play a role in seed dispersal as they consume the pulp of fruits contributing to ecological processes (Valido & Olesen, 2007). Reptiles can function as predators of invertebrates. They often act as generalists, they prey on eggs, tadpoles, juveniles, adults (Wells 2007), and decomposed bodies, (Sazima & Strüssmann, 1990; Mora 1999; DeVault & Krochmal, 2002), facilitating the transfer of nutrients within ecosystems through energy flow in food chains (Lavelle et al. 2005).

Snakes have different seasonal activity patterns within ecosystems over time (Beaupre & Douglas, 2009) and provide ecological functions. Lizards also provide ecological functions, which include distributing seeds, managing insect populations such as ants, and providing food for other animals (Valencia-Aguilar et al., 2013; Cortés-Gómez et al., 2015). Together, the combination of reptile diversity and the ecological roles of reptiles can offer valuable insights into the impacts of species on overall ecosystem dynamics.

1.6 Problem statement

Systems where ecosystem engineers have an influence on animals around them, including reptiles, are poorly studied. The importance of bird nests to reptiles and how nests influence the abundance of reptiles is not well understood. In the Kalahari, sociable weavers build large colonial nests that are used by a host of commensal species, including reptiles such as Kalahari tree skinks. These nests offer food and refuge that may be of huge importance in harsh environments like the Kalahari. However, the degree to which other reptiles use these nests remains untested, and so the impact of sociable weaver colonies on reptile diversity and populations remains unclear.

1.7 Aims and objectives

I aimed to assess the impact of sociable weaver colonies on reptile diversity and populations in the Kalahari. Kalahari tree skinks are known to preferentially use trees that host such colonies, the degree to which other reptile species use these trees is not well documented. Sociable weaver nests can provide benefits to different animals and can provide food and shelter for reptiles.

The study included three objectives. These were (1) to assess the impact of sociable weaver colony presence on the diversity (both species richness and Shannon diversity) of reptiles, (2) to assess the impact of sociable weaver colony presence on the overall abundance of reptiles, and (3) to assess the impact of sociable weaver colony presence on the abundance of selected species of reptiles, as certain reptiles are more abundant at trees with sociable weaver nests. Because the impact of sociable weaver colonies might vary depending on whether or not the colony is breeding, I assessed each of the above relative to the breeding cycle of the birds.

Chapter 2. Methods

2.1 Study site

The Kalahari is a semi-arid area in southern Africa and is an ideal system to study the effects of birds and their nests on the ecosystem (Lowney et al., 2020a). The study took place at Tswalu Kalahari Reserve (TKR) in the Northern Cape Province, South Africa (27°27'35"S; 22°45'06"E). TKR has an area of 1020 km² (Davis et al., 2010; Tokura, 2016) and is home to approximately 264 bird, 84 mammal, 75 butterfly, 22 snake, 27 lizard, and seven amphibian species (Tswalu Kalahari Reserve, 2022). There are over 250 sociable weaver colonies on the reserve, which are mostly constructed in shepherd's trees (Boscia albitrunca) and camelthorn trees (Vachellia erioloba) (Rymer et al., 2014; Lowney & Thomson, 2021). TKR is comprised of rocky mountains, sandy plains, and dune fields (Davis et al., 2010). The area is part of the savanna biome and within the reserve there are five different vegetation types: Koranna-Langeberg Mountain Bushveld, Gordonia Duneveld, Gordonia Plains Shrubveld, Olifantshoek Plains Thornveld, and Kathu Bushveld (Mucina & Rutherford, 2006). The reserve includes the Korannaberg Mountains, which run north-south through the reserve. Van Rooyen et al. (2005) identified twelve vegetation communities in the reserve. Air temperatures can exceed 40 °C in summer and in winter the temperature can drop below freezing (Lowney & Thomson, 2021). Annual rainfall is variable (mean 361.4 mm \pm SD 169.2 mm) (Prayag et al., 2020; Lowney & Thomson, 2021) and falls in summer.

2.2 Sampling methods

I chose to study the response of reptile communities and populations at the patch scale, defined loosely as the area surrounding individual trees. To do this, I identified twenty-four trees, 12 of

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which contained sociable weaver nests (colony trees) and 12 of which did not (non-colony trees). I adopted a paired design, with each pair of trees including one colony and one non-colony tree of the same species in close proximity to each other (mean distance: 90.58 m; distance range: 53 – 231 m). I tried to select similarly sized trees within each pair. Under each tree, I trapped reptiles once in February/March, when the sociable weavers were breeding, and once in September/October, when temperatures were warm, but before the birds had commenced breeding.

Together with volunteers, I installed a six-meter drift fence under each tree (Fig. 2). The drift fence was constructed by combining five plastic boards, each 5 mm thick, cut into 1200 mm x 500 mm sections, tied together with cable ties. The bottom edge of each fence was buried in a shallow trench and supported in an upright position by six metal poles. Funnel traps were placed on each side of the drift fence, as well as at each end of the drift fence. Each funnel trap was made of a mesh cylinder with two inverted funnels at each end (Fitch, 1987; Simmons, 2002; Maritz et al., 2007). The funnel traps followed the design of Mohamed (2023). The material that I used for the funnel traps was 3 mm high-density polyethylene mesh. This material is pliable, retains long-term structural integrity and resists deformation. The cylinder was created by cutting a 680 mm by 510 mm rectangle, bending it into a tube, and using cable ties to secure the joining edges. The funnels were created out of the same polyethylene mesh material. A metal wire was used to hold the funnel in place. I covered every funnel trap with vegetation, which provided shelter for any animals caught in the traps. This trapping method was ethically approved by the Animal Research Ethics Committee of the University of the Western Cape under the permit number AR 20/10/2.

The drift fences and funnel traps were found to be very effective in this study. Trapping surveys that include drift fences (Gibbons & Semlitsch, 1981) and funnel traps are advantageous in many reptile and amphibian studies (Enge, 2001). An Advantage of funnel trapping is that it can improve

capture efficiency, giving an accurate measure of species richness. It allows one to sample multiple species at different sites with an efficient sampling effort. If the trapping is done properly, it provides a good comparison between different sites that are being tested (Maritz et al., 2007).



Figure 2: A sociable weaver colony showing the trap design, drift fence and funnel traps with vegetation cover.

I conducted two trapping surveys of eleven days each. The first survey ran from 28 February 2022 to 10 March 2022. The second survey ran from 15 September 2022 to 25 September 2022. I went out twice a day, every morning (7am-9am) and afternoon (2pm-6pm), to check the funnel traps, and record every individual animal that was caught in the traps. At every site, when a reptile was

captured in the trap, the individual was removed from the trap and placed safely into a bucket. I recorded the tree site ID, the time of arrival at each site, the reptile species name, the snout-vent length (SVL), mass and tail length of the individual that was captured, and whether the lizards had an original or regrown tail. I noted whether the animals had any marks indicating recapture, and if it did not, I marked it temporarily with a marker pen. Once the individual was processed, it was released. When non-target taxa (Appendix 1; Table A1.1) were caught in the traps, the species name was recorded, and they were safely removed and released. After each survey the fences and funnels were removed from each site.

To ensure the capture rates were not affected, I needed to ensure that the funnel trap was tight against the drift fence. A gap between the funnel trap and drift fence would provide a way for animals to avoid the trap, thereby reducing the trapping efficiency (Maritz et al., 2007). Shortfalls of my methodology included releasing the animals into buckets, where some climbed out and escaped. Some animals in the traps were being eaten and killed by crickets and some of the captured animals were not specifically trying to access the colony or non-colony trees. Finally, I had to make sure all necessary measurements were recorded for the animals in the traps and record the animals that were not caught in the traps but were on or around the traps.

Two perpendicular photographs were taken at every site, with snake tongs as a reference, to calculate tree measurements. For every photograph, I used ImageJ software package (Schneider et al., 2012) to calculate the tree width, canopy height and height of the canopy from the ground. From these measurements, I calculated the total tree height and canopy volume for every photograph. Total tree height was calculated by adding the canopy height and height above the ground for the canopy. Canopy volume was calculated, using this equation: canopy volume = $(\pi r^2)/2$, where r = (canopy height + tree width)/2 (Witkowski et al., 1994). For each variable (tree

width, canopy height, height above the ground for the canopy, total tree height and canopy volume), I calculated the mean of the two values, so that there would be one value for each variable for every tree. Although pairs of trees were selected to be as similar in structure as possible, I recorded a number of tree covariates to either confirm similarity or to account for systematic differences should these exist. These tree covariates included tree species, whether pygmy falcons were present or absent (Krochuk et al., 2018), amount (high, medium or low) of vegetation under the colony and if the tree stem was single or multiple.

Since temporal differences in detection probability can impact comparison among seasons, I measured a number of time-dependent covariates thought to impact the detection of animals. I controlled the effect of temperature/humidity on detection probability, which may be different between seasons. I statistically tested for seasonal effects while controlling environmental conditions. During both seasons, Maxim iButton data loggers (Maxim Integrated, 2019) were installed at three of the trees to measure air temperature, relative humidity, sub-surface temperature, and surface temperature. These variables were measured at half-hour intervals. One hygrochron, which measures temperature and relative humidity, was installed in a tree, less than a meter above the ground to measure the air temperature and ambient relative humidity of that site. The hygrochron was placed inside an upside-down polystyrene cup for protection from direct light/heat and tied to a tree branch with a cable tie. Two thermochrons, which measure surface and subsurface temperatures were placed nearby, one on the surface and one 10 cm underground in the soil. The thermochrons were attached to a metal pole with cable ties.

After each survey was completed, the raw iButton data were downloaded and I created a spreadsheet with the data. I sorted and arranged the iButton data according to the dates I recorded reptiles in the field, two weeks in March and September. I calculated the minimum air temperature,

mean air temperature, maximum air temperature, relative humidity, substrate temperature, and surface temperature and I analyzed this iButton data in R Software V.4.1.1 (R Core Team, 2021). I grouped the data according to the day and hour and calculated the average temperature for each hour. The temperatures and relative humidity were sorted so that the minimum, mean, and maximum values were split into morning and afternoon captures. This was used to classify diurnal animals captured in the afternoon and nocturnal animals captured in the morning. For the morning data, I calculated the descriptive statistics for each day between 19:00-00:00, and for the afternoon data I calculated the descriptive statistics for each day between 11:00-19:00. The overall mean, mean minimum, and mean maximum from iButton data was calculated for two weeks in March and September. The mean, maximum, and minimum for air temperature, surface temperature, subsurface temperature, surface temperature, subsurface temperature, and humidity were used in the population analysis to control for the effect of air temperature, surface temperature, subsurface temperature, and humidity on detection probability, in order to measure the seasonal effects on detection probability.

2.3 Diversity response

2.3.1 Data Preparation

I tested whether experimental trees and control trees differed systematically in their attributes. I ran a paired t-test in excel for the continuous data (total tree height, canopy height, canopy volume, height above the ground for the canopy and tree width) to compare any systematic biases in the pairs of the trees (Table 1). I performed a Chi-squared test for the categorical data (tree species, pygmy falcons present or absent, vegetation under the colony, or if the tree stem was single or multiple: Table 1). Canopy height (paired t-test: $t_{df=11} = 3.91$, p < 0.01) and total tree height (paired t-test: $t_{df=11} = 3.35$, p < 0.01) were the only two significant tree covariates. There were systematic

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bias in the pairs of trees for the different structural variables, except for total tree height and canopy height. I ran a correlation test between canopy height and total tree height, and it showed that the two variables are strongly correlated ($r^2 = 0.90$, p < 0.001). Therefore, I incorporated only total tree height as a covariate in the population analysis and in the diversity analyses.

Table 1: Summary of statistical analysis results for categorical and continuous tree covariates.Statistically significant values (alpha = 0.05) highlighted with asterisk. See methods fordescription of covariates.

Measure	Statistical test	Test statistic	P value
Total tree height	Paired t-test	$t_{11} = 3.35$	0.0065*
Canopy height	Paired t-test	t ₁₁ =3.91	0.0024*
Canopy volume	Paired t-test	$t_{11} = 1.85$	0.0912
Height above the ground for the canopy	Paired t-test	t ₁₁ =0.43	0.858
Tree width	Paired t-test	$t_{11} = 1.20$	0.127
Tree species	Chi-squared test	$X_{2}^{2} = 0.00$	1.000
Presence/absence of pygmy falcons	Chi-squared test	$X_{2}^{2} = 2.70$	0.100
Amount of vegetation below the canopy	Chi-squared test	$X_{2}^{2} = 8.42$	0.0149*
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Tree trunk: multi or single stemmed	Chi-squared test	$X^2_2 = 1.69$	0.194

2.3.2 Data analysis:

I calculated species richness, the Shannon-Weiner diversity index (using the Vegan package; Oksanen et al., 2017), and the total number of unique captures for every site in each season. I performed three separate generalized linear models to compare the species richness, Shannon diversity, and total captures (excluding the recaptures) between trees with and without colonies and between seasons (Appendix 2: Tables A2.1-A2.3). I used the variables colony presence/absence, season, and total tree height. I used the lme4 package (Bates et al., 2015) and the lmer function to perform the generalized linear models (Appendix 2: Tables A2.1-A2.3). I took into consideration that the trees were paired and added pair as a random effect into the generalized linear models. The model formula was: Species Richness ~ Colony + Season + Total tree height + (1| Pair). Pair did not have any effect on the results; I therefore only present the non-paired results. I created a new model that did not have pair as a random effect. The model formula without pair as a random effect was: Species Richness ~ Colony + Season + Total tree height. This was repeated for Shannon diversity and total captures.

2.4 Population response

2.4.1 Data Preparation

I quantified how certain tree and weather covariates influence the abundance of the three most frequently detected species: Kalahari tree skink, the Cape thick-toed gecko, and the Cape cobra. The tree covariates assessed were the presence or absence of a colony and total tree height. The weather covariates were air temperature, subsurface temperature, surface temperature, and humidity. I used the Royle-Nichols model (Royle & Nichols, 2003) to estimate mean (latent) abundance while accounting for imperfect detection for the Cape thick-toed gecko and Cape cobra. I used the Royle-Nichols model as it can estimate abundance using presence and absence data without having to physically mark the individuals (Royle & Nichols, 2003). I used the Poisson *N*-mixture model (Royle, 2004) to estimate mean (latent) abundance while accounting for imperfect detection of the Kalahari tree skink. I used the Poisson *N*-mixture model as there is a higher abundance of Kalahari tree skinks at trees with sociable weaver colonies. I considered that the

trees were paired and added pair as a random effect into the models, but it did not have any effect on the results.

In the context of my study, it is essential to consider different methods to estimate the abundance of animal populations (Seber, 1982; Buckland et al., 2001; Williams et al., 2002). The Royle-Nichols model was used to estimate the abundance of the Cape thick-toed gecko and Cape cobra within our study area. The Royle-Nichols model estimates abundance using presence and absence data without having to physically mark the individuals (Royle & Nichols, 2003). In our study, where the size of the study area was large and where complete detection of all reptile species was challenging, the Royle-Nichols model offered an efficient approach (MacKenzie et al., 2006; Duquette et al., 2014).

The Poisson *N*-mixture model was used to estimate the abundance of the Kalahari tree skink , as this was the most abundant reptile species within our study area. The Poisson *N*-mixture model allows the population size to be estimated when the count data is sparse and accounts for detection probability (Royle, 2004; Goldstein & Valpine, 2022). The change in population size can be estimated by calculating the abundance of species at many different sites. The Poisson *N*-mixture model sees site-specific abundance as a random effect. The model uses site-specific abundance parameters and estimates based on the data (Royle, 2004; Royle & Dorazio, 2006). An advantage of the model is that the factors that cause fluctuations in abundance or detection probability can be directly estimated. The model can perform under many different scenarios using point counts (Royle, 2004; Royle & Dorazio, 2006).

2.4.2 Data analysis

I evaluated the Cape thick-toed gecko and Cape cobra abundance using the Royle-Nichols model (Royle & Nichols, 2003), and analysed based on daily detection/non-detection with weather and tree covariates. I performed this test using the occuRN function in the Unmarked package (Fiske & Chandler, 2011) and I used the gridExtra package (Baptiste, 2015) to arrange the plots that were created and draw tables. I used the MuMIn package (Barton, 2020) for the model selection process and I created an unmarked data frame for using the occuRN function. I scaled all the site variables, which included the presence or absence of a colony and total tree height, and observational variables, which included mean air, surface, subsurface temperature, and humidity. I performed a dredge-based model selection using the dredge and pdredge functions in the MuMIn package (Barton, 2020), to fit every possible combination of covariates and ranked them by Akaike information criteria. I used the AIC to assess several models (Appendix 3; Table A3.1-A3.6) to see which model best fits the data (Harrison et al., 2018). I used three tests: sum of squared errors, Pearson's Chi-squared, and Freeman-Tukey Chi-squared to do a best of fit test to evaluate the model. I transformed the values to native scale to estimate the abundance per site and the detection estimate when the observational variables were at a fixed mean value. I plotted the outputs to visualize and estimate interpretations.

Similarly, to the Royle-Nichols analysis above, I evaluated the Kalahari tree skink abundance using the Poisson *N*-mixture model (Royle, 2004) and analysed based on daily detection/nondetection. I performed this test using the function pcount in the Unmarked package, gridExtra package and the MuMIn package. I created an unmarked data frame to use the function unmarkedFramePCount. The process was similar to the Royle-Nichols analysis; I scaled all the site variables, which included the presence or absence of a colony and total tree height. The observational variables were the mean air, surface and subsurface temperature and humidity. I performed a dredge-based model selection using the dredge and pdredge functions in the MuMIn package to fit every possible combination of covariates and ranked them by AIC. I used the AIC to assess several models to see which ones best explained the patterns in the data (Harrison et al., 2018). I used three tests: sum of squared errors, Pearson's Chi-squared, and Freeman-Tukey Chisquared. I transformed the values to native scale to estimate the abundance per site and the detection estimate when the observational variables were at a fixed mean value. I plotted the outputs to visualize and estimate interpretations. This process was repeated for both trapping

seasons.



Chapter 3. Results

During both trapping seasons there were a total of 667 total detections of 19 reptile species, including 151 recaptures. During the breeding season of the sociable weavers, I trapped for 11 days, resulting in 452 total detections of 11 reptile species (Table 2), including 97 recaptures. At sociable weaver colony sites, there were 74 recaptures and 11 different species captured. In contrast, non-colony sites had 23 recaptures and five different species captured. The most abundant lizards observed were the Kalahari tree skink (284 detections at colony sites vs. 95 detections at non-colony sites) and Cape thick toed gecko (41 detections at colony sites vs. wo detections at non-colony sites). There were 57 recaptured Kalahari tree skinks at colony sites and 23 recaptured at non-colony sites. There were 11 recaptured Cape thick-toed geckos at colony sites and no recaptures at non-colony sites. The most common snake, Cape cobra was detected 15 times at colony sites but was not detected at non-colony sites. There were four recaptured Cape tors at colony sites and no recaptures at non-colony sites, giving a ratio of colony to non-colony captures of 3.52:1 (Table 2).

During the non-breeding season of the sociable weaver, I trapped for 11 days, resulting in 215 total detections of eight reptile species (Table 2), including 54 recaptures. There were 43 recaptures at sociable weaver colony sites and 11 recaptures at non-colony sites. The most frequently detected lizards that were found were Kalahari tree skink , (143 detections at colony sites vs. 40 detections at non-colony sites) and Cape thick-toed gecko (17 detections at colony sites vs. three detections at non-colony sites). The Cape cobra was the most common snake, with one detection at colony sites and one at non-colony sites. There were a total of 166 captures at colony sites and 49 captures at non-colony sites, giving the ratio of colony to non-colony captures as 3.39:1 (Table 2).

Table 2: The different number of reptile species and number of recaptures (in brackets) at sociable

 weaver colony sites compared to non-colony sites during the breeding season and non-breeding

 season of the sociable weaver.

Species	Common names	Breeding season		Non-br seas	-breeding eason	
		Colony	Non-colony	Colony	Non- colony	
Agama aculeata	The ground agama	4 (2)	0	2	2(1)	
Dispholidus typus	Boomslang	0	0	1	0	
Heliobolus lugubris	Bushveld lizard	1		0	1	
Lygodactylus bradfieldi	Bradfield's dwarf	2	0	0	0	
10	gecko	10 1	0.00			
Naja nigricincta woodi	Black spitting cobra	1	0	0	0	
Naja nivea	Cape cobra	15 (4)	0	1	1	
Pachydactylus capensis	Cape thick-toed	41 (11)	2	17 (4)	3 (1)	
	gecko			·		
Philothamnus semivariegatus	Spotted bush snake	ITY	of the	0	0	
Psammophis brevirostris	Short-snouted grass snake	N ¹ C	APE	2	0	
Pseudaspis cana	Mole snake	1	0	0	0	
Stigmochelys pardalis	Leopard tortoise	1	0	0	0	
Trachylepis spilogaster	Kalahari tree skink	284 (57)	95 (23)	143(39)	40 (8)	
Trachylepis punctulata	Speckled skink	0	0	0	2 (1)	
Total		352	100	166	49	

3.1 Diversity

The generalized linear model showed significant differences in reptile species richness due to the presence of a sociable weaver colony (z = 2.934, p < 0.01). There was a greater diversity at colony sites (39 difference reptile species) compared to non-colony sites (16 different reptile species). There was no effect of season (z = -1.424, p = 0.15) or total tree height (z = -0.278, p = 0.78) on the reptile species richness. Species richness was 2.5 times higher at colony trees than non-colony trees during the sociable weaver breeding season (Fig. 3) and there was a significance between colony and non-colony trees. Species richness was 1.6 times higher at colony trees than non-colony trees during the non-breeding season of the sociable weaver (Fig. 3) and there was no significance between between colony and non-colony trees.

There were differences in total captures due to the presence of a sociable weaver colony (z = 10.062, p < 0.001) and season (z = -8.255, p < 0.001). However, there was no effect of total tree height (z = 1.463, p = 0.144) on the total captures. There were 3.71 times more captures at trees with sociable weaver nests than trees without during the breeding season (Fig. 4). There were 3.24 times more captures at trees with sociable weaver nests than trees in Shannon diversity due to the presence of a sociable weaver colony (z = 1.320, p = 0.187), season (z = -0.258, p = 0.796) or total tree height (z = 0.198, p = 0.843).



Figure 3: Species richness at sociable weaver colony trees compared to non-colony trees ($\pm 95\%$ Cl; **p < 0.01).



Figure 4: Total captures at sociable weaver colony trees compared to non-colony trees (±95% Cl; ***p < 0.001).

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3.2 Population responses

3.2.1 Trachylepis spilogaster

During the breeding season, the best model (Table 3) showed the mean abundance of the Kalahari tree skink was significantly influenced by the presence or absence of a colony (log(λ) = 0.591, p < 0.001). The detection probability was influenced by mean temperature of the subsurface (logit(p_i) = 0.666, p < 0.001) and humidity (logit(p_i) = -0.364, p = 0.02). For the non-breeding season, the best model (Table 3) showed that the mean abundance of the Kalahari tree skink was significantly influenced by the presence or absence of a colony (log(λ) = 0.664, p < 0.001), with the detection probability being influenced by mean temperature of the subsurface (logit(p_i) = 0.664, p < 0.001), with

0.444, p < 0.001), mean temperature of the surface (logit(p_i) = 0.483, p < 0.01), and humidity (logit(p_i) = 0.637, p < 0.001).

Table 3: The best models for Kalahari tree skink during the breeding and non-breeding season of the sociable weaver.

Season	Model descriptions	df	logLik	Weight
Breeding season	Abundance ~ colony presence/absence Detection ~ mean subsurface temperature + mean humidity	5	-371.226	0.275
Non-breeding season	Abundance ~ colony presence/absence Detection ~ mean subsurface temperature + mean surface temperature + mean humidity	6	-278.793	0.554

The Kalahari tree skink were 3.2 times more abundant on sociable weaver colony trees than control trees during the breeding season of the sociable weaver (Fig. 5). During the non-breeding season, Kalahari tree skinks were 3.7 times more abundant on sociable weaver colony trees than control trees (Fig. 5). The detection probability of the Kalahari tree skink increased as the subsurface temperatures increased and as the humidity decreased the detection probability decreased during the breeding season (Appendix 4; Figure A4.1). The detection probability of the Kalahari tree skink increased as the subsurface, surface temperatures and humidity increased during the non-breeding season (Appendix 5; Figure A5.1 and A5.2(A)).


Figure 5: Estimated latent abundance of the Kalahari tree skink at colony trees compared to noncolony trees (±95% Cl; ***p < 0.001).

3.2.2 Pachydactylus capensis

During the breeding season, the best model (Table 4) showed the mean abundance of the Cape thick-toed gecko was significantly influenced by the presence or absence of a colony $(\log(\lambda) = 1.201, p < 0.01)$. The detection probability was influenced by the mean temperature of the subsurface $(\log it(p_i) = 0.533, p = 0.03)$ and mean temperature of the surface $(\log it(p_i) = -0.815, p < 0.01)$. For the non-breeding season, the best model (Table 4) showed the mean abundance of the Cape thick-toed gecko was significantly influenced by the presence or absence of a colony $(\log(\lambda) = 0.8773, p = 0.03)$. The detection probability was influenced by the mean temperature of the surface $(\log it(p_i) = 1.08, p < 0.01)$.

Season	Model descriptions	df logLik		Weight	
Breeding season Abundance ~ colony presence/absence Detection ~ mean subsurface temperature + mean surface temperature + mean humidity		5	-72.432	0.167	
Non-breeding season	Abundance ~ colony presence/absence Detection ~ mean subsurface temperature	4	-51.596	0.173	

Table 4: The best models for Cape thick-toed gecko during the breeding and non-breeding season of the sociable weaver.

The Cape thick-toed gecko were 10.5 times more abundant on sociable weaver colony trees than control trees during the breeding season of the sociable weaver (Fig. 6). During the non-breeding season, the Cape thick-toed gecko were 5.6 times more abundant on sociable weaver colony trees than control trees (Fig. 6). The detection probability of the Cape thick-toed gecko increased as the subsurface temperatures increased and as the surface temperature decreased the detection probability decreased during the breeding season (Appendix 4; Figure A4.2). The detection probability of the Cape thick-toed gecko increased as the surface increased during the non-breeding season (Appendix 5; Figure A5.2(B)).



Figure 6: Estimated latent abundance of the Cape thick-toed gecko at colony trees compared to non-colony trees ($\pm 95\%$ Cl; **p < 0.01, *p < 0.05).

3.2.3 Naja nivea

During the breeding season, the best model (Table 5) showed the mean abundance of the Cape cobra was significantly influenced by the presence or absence of a colony $(\log(\lambda) = 1.654, p < 0.01)$. The detection probability was influenced by mean temperature of the subsurface $(\operatorname{logit}(p_i) = 1.63, p < 0.01)$ and mean humidity $(\operatorname{logit}(p_i) = 1.27, p < 0.01)$.

Table 5: The best models for the Cape cobra during the breeding and non-breeding season of the sociable weaver.

Season	Model descriptions	df	logLik	Weight
Breeding season	Abundance ~ colony presence/absence Detection ~ mean subsurface temperature + mean humidity	6	-44.698	0.138
Non-breeding season	N/A	2	-11.766	0.177

The Cape cobra were 13.2 times more abundant on sociable weaver colony trees than control trees during the breeding season (Fig. 7). During the non-breeding season, the null model showed no difference in abundance at sociable weaver colony trees than control trees without colonies (Fig. 7). The detection probability of the Cape cobra increased as the subsurface temperatures and humidity increased during the breeding season (Appendix 4; Figure A4.3).

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Chapter 4. Discussion

The results of this study indicate important effects of sociable weaver colonies on reptile species richness, total captures, and the species abundance measures, but abundance measures were not consistent across seasons for all species. Kalahari tree skink and Cape thick-toed gecko were abundant during both breeding and non-breeding seasons of the sociable weaver, whereas the Cape cobra were more abundant during the breeding season of the sociable weaver (Lowney et al., 2022).

During the breeding season of the sociable weaver, there were more detections, more reptile species and approximately three times more unique captures at colony sites than at non-colony sites. During the non-breeding season of the sociable weaver, there were fewer total detections and reptile species but there were still approximately three times more captures at colony sites than at non-colony sites. The species richness was higher at colony trees than control trees during the sociable weaver breeding season and non-breeding season. This shows that there is greater diversity at sociable weaver colonies compared to non-colony trees (Lowney et al., 2021; Lowney et al., 2022).

The abundance of the Kalahari tree skink, Cape thick-toed gecko and Cape cobra were higher at sociable weaver colony sites than non-colony sites, and the two lizards showed no seasonal effect while the snake showed a seasonal effect. These results suggest that the two lizards potentially use colony trees for both food and shelter (Lowney et al. 2022) whereas cobras preferentially use colonies for food only.

Multiple studies (Brain, 1969; Rymer et al. 2014) corroborate my results, including Lowney et al. (2022), who found a higher abundance of reptiles at trees with sociable weaver colonies. This is

attributed to the colonies' enhanced resource availability, characterized by increased food resources and the provision of shelter to reptiles (Lowney et al. 2022). Lowney et al. (2022) also found a higher abundance of invertebrates at trees with sociable weaver colonies, due to the sociable weavers depositing faeces and nest material below the colony, thus providing more food for insects, which in turn positively affects other taxa including reptiles. This is likely one of the main reasons for the higher abundance of reptiles at these sociable weaver colony sites.

Similarly, my study aligns with the findings of Brain (1969) and Rymer et al. (2014), who found a higher abundance of the Kalahari tree skink on trees that contained sociable weaver colonies compared to trees without colonies. Sociable weaver nests provide multiple benefits to the skinks, including food and shelter. Cooper & Whiting (2000) found that certain variables, including air temperature, size of the tree and ground cover, influenced the abundance of Kalahari tree skink on trees that contained sociable weaver colonies. In contrast, my study found that, presence or absence of a colony, mean subsurface and surface temperature, and humidity all had a significant effect on the detection of the Kalahari tree skink. Our results differed to Cooper & Whiting (2000), as our sampling methods were different as Cooper & Whiting (2000) visually searched for the lizards while I used traps. The models that were used were different as well, Cooper & Whiting (2000) did a multiple regression analysis while I used the Royle Nichols model.

Many studies have documented the seasonally shifting foraging patterns of snakes, especially in environments where the availability of prey varies by microhabitat (Madsen & Shine, 1996; Arnold & Wasersug, 1978; Fitzgerald et al., 2002). Natusch et al. (2020) found similar results in the foraging behaviour of snakes in relation to bird nests. They observed that rainforest pythons (*Simalia amethistina*) remained proximate to metallic starling (*Aplonis metallica*) nesting sites during breeding season. When the starlings stopped breeding, the pythons moved away from the

colony trees and searched for food elsewhere. This was similar to the pattern I observed with Cape cobras and the sociable weaver nests, as the Cape cobra used the sociable weaver colonies more frequently during the breeding season. Once the birds stopped breeding, the snakes moved away, likely to search for an alternative source of food. These observations underscore the influence of sociable weaver colonies on the Cape cobras behaviour, impacting both their foraging strategies and movement patterns.

Natusch et al. (2016) found a similar trend to Lowney et al. (2022). There were more reptiles abundant at trees with metallic starling nests than trees without these nests. It is known that a high biomass of birds attracts a range of animals, including predatory species (Robinson, 1984; Covas, 2002). Natusch et al. (2016) further revealed that most of the predators, including snakes, gathered under trees with these birds' nests. The high abundance of predators can discourage other animals that use these nests during the breeding season. Snakes can indirectly affect other animals; an example is Mazzotti et al. (2022), who studied raccoons predating on crocodile eggs in Florida. The introduction of Burmese pythons (*Python bivittatus*) led to a decline in raccoon abundance and prolonged the survival of crocodile eggs. In another example, snakes decreased nest predation on turtle eggs in Southern Florida (Wilson, 2017; Mazzotti et al., 2022).

There were differences in detection probability for the Kalahari tree skink and Cape thick-toed gecko. The detection probability for the Kalahari tree skink increased as the subsurface temperatures increased but as the humidity decreased the detection probability for the Kalahari tree skink decreased. The detection probability for the Cape thick-toed gecko increased as the subsurface temperatures increased but as the surface temperatures decreased the detection probability for the Cape thick-toed gecko the detection probability for the Cape thick-toed gecko the detection probability for the Cape thick-toed gecko decreased. It is necessary to recognize that conducting surveys introduces variability in detection probability (Fiske & Chandler, 2011; Duquette et al.,

2014), which must be considered when interpreting the results. The detection variability was accounted for in my results.

Expecting differences in detection probability and mitigating its effects, though the study design and to collect the covariates to account for detection variation is important for the effectiveness of models (MacKenzie et al. 2018). In surveys the likelihood of detection can differ due to various factors like environmental variables (such as weather conditions), seasonal behavioural patterns, or distinctions among observers (MacKenzie et al. 2018). Detection probability can also differ due to habitat features (MacKenzie et al. 2018).

This research reveals that sociable weavers are ecosystem engineers and affect their surrounding habitat (Romero et al., 2015; Coggan et al., 2018), and adds to existing literature about birds that act as ecosystem engineers (Lowney et al., 2021). Sociable weaver colonies can influence reptile communities though non-exclusive mechanisms such as microhabitat engineering and through food resource allocation (Lowney et al., 2021). This work builds on existing literature that highlights the importance of sociable weaver colonies for all animals (Romero et al., 2015; Coggan et al., 2018; Lowney et al., 2022).

Further research could investigate how different animals find sociable weaver colony trees, how far the animals travel to reach them. The high abundance of animals around these sociable weaver colonies shows that taking advantage of this nutritional subsidy has certain benefits. Sociable weaver colonies could enhance the number of species that can be sustained by the ecosystem, making these trees with nests valuable for conservation in the future (Kennedy & Kennedy, 2014). The remarkable nature of these animal concentrations and predator-prey interactions provides a chance to educate the public about the ecology of Tswalu Kalahari Reserve, which will aid

conservation efforts. Inspiring and educating the public about animals, and the changing dynamics of ecosystems, can help to develop support for conservation efforts.

Overall, sociable weaver nests have a positive effect on reptiles. The nests provide food for snakes and lizards as well as shelter from environmental conditions. The sociable weaver nests are important for all animals including reptiles. The interaction between birds and reptiles shows how complex ecological relationships are, and that multiple species are of importance when studying or managing ecosystems. These findings have implications for the management and conservation of ecosystems, since the fact that different species interact with each other is important for decisions about habitat management.



Chapter 5. Conclusion

In conclusion, this study sheds light on the dynamics of reptile populations, particularly focusing on the influence of sociable weaver colonies on reptile abundance and species richness. The research reveals that during the breeding season of the sociable weaver, there is a notable increase in reptile detections, species richness, and captures at colony sites compared to non-colony sites. This trend persists even during the non-breeding season, with colony sites still exhibiting higher captures.

The study highlights that both Kalahari tree skinks and Cape thick-toed geckos show consistently higher abundances at sociable weaver colony sites, suggesting that these reptiles potentially benefit from the food and shelter provided by the colonies. On the other hand, the Cape cobra displays a seasonal difference, indicating a preference for sociable weaver colonies during the breeding season, possibly due to shifts in foraging behaviour.

Comparison with existing studies, including Brain (1969), Rymer et al. (2014), Natusch et al. (2016), and Lowney et al. (2022) corroborates the findings of this research, highlighting the positive impacts of sociable weaver colonies on reptile abundance and diversity. The presence of colonies provides food availability and shelter, attracting a variety of species, including predators. Moreover, the study underscores the broader ecological implications of such relationships, emphasizing the importance of understanding complex interactions for effective ecosystem management and conservation.

The employed methods, namely drift fences, funnel traps, and *N*-mixture models, have proven effective in this study, aiding in estimating abundance and detection probability for reptile

populations. While each approach has its advantages and limitations, they collectively contribute to a more comprehensive understanding of reptile community dynamics in the Kalahari.

Overall, this research underscores the significant role of sociable weaver colonies as ecosystem engineers, influencing reptile communities through various mechanisms. By creating habitats and providing nutritional subsidies, these colonies enhance the ecosystem's capacity to sustain diverse species. The implications extend to conservation efforts, with the potential to educate the public about ecological relationships, inspire support for conservation, and influence habitat management decisions. The intricate interplay between birds and reptiles serves as a reminder of the interconnectedness of species within ecosystems, emphasizing the need for holistic approaches to biodiversity conservation and management.



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Appendices

Appendix 1: Non-target species

Table A1.1. Non-target species that were captured in the traps

Scientific name	Common name
Mus indutus	Desert pygmy mouse
Steatomys krebsii	Krebs fat mouse
Crocidura sp.	Musk shrews
Kassina senegalensis	Common bubbling kassina
Gerbilliscus leucogaster	Bushveld gerbil
Tomopterna cryptotis	Common sand frog
Parabuthus granulatus	Granulated thick-tailed scorpion
Breviceps adspersus	Common rain frog
Rhabdimys pumilio	Four-striped grass mouse
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Appendix 2: Generalized linear models

Coefficients				
	Estimate	Standard error	Z value	P value
Intercept	0.58979	0.62737	0.940	0.34717
Colony	0.72611	0.24752	2.934	0.00335
Season	-0.29376	0.20633	-1.424	0.15452
Total tree height	-0.03077	0.11081	-0.278	0.78127

 Table A2.1. The generalized linear model for the species richness:

Table A2.2. The generalized linear model for the total captures:

Coefficients	100.000	NUL TIN	100 100	
	Estimate	Standard error	Z value	P value
Intercept	1.45862	0.29830	4.890	1.01e-06
Colony	1.18948	0.11821	10.062	< 2 e-16
Season	-0.78506	0.09510	-8.255	< 2 e-16
Total tree height	0.07468	0.05105	1.463	0.144

 Table A2.3. The generalized linear model for Shannon diversity:

Coefficients	UNIX	FRSIT	Voft	ha	
	Estimate	Standard error	Z value	P value	
Intercept	-1.76703	1.55437	-1.137	0.256	
Colony	0.78454	0.59414	1.320	0.187	
Season	-0.12518	0.48480	-0.258	0.796	
Total tree height	0.05306	0.26857	0.198	0.843	

Appendix 3: Model lists

Table A3.1. The model list for *Trachylepis spilogaster* during the breeding season of the sociable weaver

p(Int)	lam(Int)	p(mean_humidity)	p(mean_temp_subsurface)	p(mean_temp_surface)	lam(colony_pres_abs)	lam(total_tree_height)	df	logLik	AIC	delta	weight
-2.21	2.25	-0.36	0.67	NA	0.59	NA	5.00	-371.23	752.45	0.00	0.27
-2.20	2.24	-0.33	0.85	-0.16	0.59	NA	6.00	-370.42	752.84	0.39	0.23
-2.21	2.25	-0.36	0.67	NA	0.55	0.10	6.00	-370.76	753.53	1.08	0.16
-2.20	2.24	-0.33	0.85	-0.16	0.55	0.10	7.00	-369.96	753.92	1.46	0.13
-2.20	2.25	NA	1.19	-0.22	0.59	NA	5.00	-372.51	755.01	2.56	0.08
-2.21	2.26	NA	0.99	NA	0.59	NA	4.00	-373.88	755.76	3.31	0.05
-2.20	2.24	NA	1.19	-0.22	0.55	0.10	6.00	-372.04	756.09	3.64	0.04
-2.21	2.26	NA	0.98	NA	0.55	0.10	5.00	-373.42	756.83	4.38	0.03
-2.17	2.26	-0.78	NA	0.15	0.59	NA	5.00	-377.65	765.30	12.85	0.00
-2.16	2.26	-0.89	NA	NA	0.59	NA	4.00	-378.74	765.48	13.03	0.00
-2.18	2.25	-0.78	NA	0.15	0.55	0.10	6.00	-377.19	766.37	13.92	0.00
-2.16	2.25	-0.89	NA	NA	0.55	0.10	5.00	-378.28	766.56	14.11	0.00
-1.90	2.09	-0.38	0.69	NA	NA	0.35	5.00	-386.58	783.15	30.70	0.00
-1.89	2.08	-0.35	0.89	-0.18	NA	0.35	6.00	-385.70	783.41	30.95	0.00
-1.89	2.09	NA	1.24	-0.23	NA	0.35	5.00	-387.84	785.69	33.24	0.00
-1.90	2.09	NA	1.02	NA	NA	0.35	4.00	-389.30	786.60	34.15	0.00
-1.85	2.10	-0.39	0.69	NA	NA	NA	4.00	-394.01	796.03	43.57	0.00
-1.86	2.09	-0.82	NA	0.15	NA	0.35	5.00	-393.05	796.10	43.65	0.00
-1.84	2.09	-0.35	0.89	-0.18	NA	NA	5.00	-393.13	796.25	43.80	0.00
-1.85	2.09	-0.93	NA	NA	NA	0.35	4.00	-394.13	796.27	43.82	0.00
-1.83	2.10	NA	1.25	-0.23	NA	NA	4.00	-395.28	798.56	46.11	0.00
-1.84	2.10	NA	1.03	NA	NA	NA	3.00	-396.75	799.50	47.05	0.00
-1.81	2.10	-0.83	NA	0.16	NA	NA	4.00	-400.50	808.99	56.54	0.00
-1.79	2.10	-0.94	NA	NA	NA	NA	3.00	-401.58	809.16	56.70	0.00
-2.21	2.38	NA	NA	0.66	0.59	NA	4.00	-400.88	809.75	57.30	0.00
-2.22	2.38	NA	NA	0.66	0.55	0.09	5.00	-400.41	810.82	58.36	0.00
-1.85	2.18	NA	NA	0.70	NA	0.35	4.00	-417.14	842.28	89.83	0.00
-1.78	2.17	NA	NA	0.70	NA	NA	3.00	-424.78	855.56	103.11	0.00
-2.44	2.73	NA	NA	NA	0.58	NA	3.00	-453.63	913.26	160.81	0.00
-2.45	2.74	NA	NA	NA	0.55	0.09	4.00	-453.13	914.26	161.81	0.00
-1.98	2.42	NA	NA	NA	NA	0.34	3.00	-472.30	950.59	198.14	0.00
-1.87	2.38	NA	NA	NA	NA	NA	2.00	-480.59	965.18	212.73	0.00

p(Int)	lam(Int)	p(mean_humidity)	p(mean_temp_subsurface)	p(mean_temp_surface)	lam(colony_pres_abs)	lam(total_tree_height)	df	logLik	AIC	delta	weight
-3.00	2.38	0.64	0.44	0.48	0.66	NA	6.00	-278.79	569.59	0.00	0.55
-3.11	2.47	0.63	0.44	0.48	0.60	0.14	7.00	-278.16	570.32	0.73	0.38
-3.04	2.44	0.36	0.62	NA	0.66	NA	5.00	-282.72	575.44	5.85	0.03
-3.15	2.54	0.36	0.61	NA	0.60	0.14	6.00	-282.06	576.13	6.54	0.02
-3.05	2.46	0.62	NA	0.81	0.66	NA	5.00	-284.44	578.88	9.29	0.01
-3.16	2.56	0.62	NA	0.80	0.60	0.14	6.00	-283.78	579.55	9.97	0.00
-3.11	2.53	NA	0.38	NA	0.66	NA	4.00	-288.20	584.40	14.81	0.00
-3.24	2.64	NA	0.38	NA	0.60	0.14	5.00	-287.51	585.02	15.44	0.00
-3.11	2.53	NA	0.41	-0.03	0.66	NA	5.00	-288.16	586.33	16.74	0.00
-3.23	2.64	NA	0.41	-0.03	0.60	0.14	6.00	-287.48	586.95	17.37	0.00
-2.43	1.98	0.67	0.46	0.51	NA	0.39	6.00	-291.43	594.86	25.28	0.00
-3.17	2.61	NA	NA	0.27	0.66	NA	4.00	-293.51	595.02	25.44	0.00
-3.30	2.74	NA	NA	0.26	0.60	0.14	5.00	-292.80	595.59	26.01	0.00
-2.45	2.02	0.37	0.64	NA	NA	0.39	5.00	-295.52	601.05	31.46	0.00
-3.23	2.70	NA	NA	NA	0.66	NA	3.00	-298.95	603.89	34.31	0.00
-3.38	2.84	NA	NA	NA	0.60	0.14	4.00	-298.20	604.41	34.82	0.00
-2.45	2.03	0.65	NA	0.84	NA	0.39	5.00	-297.28	604.57	34.98	0.00
-2.21	1.85	0.68	0.47	0.52	NA	NA	5.00	-297.40	604.80	35.21	0.00
-3.22	2.70	-0.04	NA	NA	0.66	NA	4.00	-298.78	605.56	35.97	0.00
-3.38	2.84	-0.04	NA	NA	0.60	0.14	5.00	-298.04	606.07	36.49	0.00
-2.48	2.07	NA	0.40	NA	NA	0.39	4.00	-301.24	610.48	40.90	0.00
-2.22	1.88	0.38	0.66	NA	NA	NA	4.00	-301.59	611.17	41.59	0.00
-2.48	2.07	NA	0.42	-0.04	NA	0.39	5.00	-301.20	612.40	42.82	0.00
-2.21	1.88	0.67	NA	0.86	NA	NA	4.00	-303.37	614.74	45.16	0.00
-2.24	1.92	NA	0.41	NA	NA	NA	3.00	-307.45	620.89	51.31	0.00
-2.49	2.11	NA	NA	0.28	NA	0.39	4.00	-306.75	621.51	51.92	0.00
-2.23	1.91	NA	0.43	-0.04	NA	NA	4.00	-307.40	622.81	53.22	0.00
-2.51	2.16	NA	NA	NA	NA	0.39	3.00	-312.40	630.79	61.20	0.00
-2.24	1.95	NA	NA	0.28	NA	NA	3.00	-313.08	632.16	62.57	0.00
-2.51	2.15	-0.05	NA	NA	NA	0.39	4.00	-312.22	632.44	62.85	0.00
-2.25	1.98	NA	NA	NA	NA	NA	2.00	-318.84	641.68	72.09	0.00
-2.25	1.98	-0.05	NA	NA	NA	NA	3.00	-318.66	643.32	73.74	0.00

Table A3.2. The model list for *Trachylepis spilogaster* during the non-breeding season of the sociable weaver

p(Int)	lam(Int)	p(mean_humidity)	p(mean_temp_subsurface)	p(mean_temp_surface)	lam(canopy_height)	lam(colony_pres_abs)	lam(total_tree_height)	df	logLik	AIC	delta	weight
-2.37	-0.25	NA	0.53	-0.81	NA	1.20	NA	5.00	-72.43	154.86	0.00	0.17
-2.36	-0.33	NA	0.55	-0.83	NA	1.02	0.46	6.00	-71.61	155.23	0.36	0.14
-2.34	-0.32	NA	0.55	-0.83	0.38	1.00	NA	6.00	-71.81	155.62	0.75	0.11
-2.36	-0.26	-0.13	0.45	-0.84	NA	1.20	NA	6.00	-72.31	156.62	1.76	0.07
-2.36	-0.33	-0.14	0.46	-0.86	NA	1.02	0.47	7.00	-71.47	156.95	2.09	0.06
-2.34	-0.24	-0.38	NA	-0.70	NA	1.20	NA	5.00	-73.49	156.99	2.12	0.06
-2.38	-0.32	NA	0.55	-0.83	-0.17	1.04	0.62	7.00	-71.60	157.19	2.33	0.05
-2.33	-0.33	-0.14	0.46	-0.86	0.39	1.00	NA	7.00	-71.67	157.34	2.47	0.05
-2.34	-0.32	-0.40	NA	-0.72	NA	1.02	0.45	6.00	-72.71	157.43	2.56	0.05
-2.31	-0.31	-0.40	NA	-0.72	0.38	1.00	NA	6.00	-72.88	157.76	2.90	0.04
-2.33	-0.22	NA	NA	-0.46	NA	1.19	NA	4.00	-74.95	157.91	3.04	0.04
-2.32	-0.29	NA	NA	-0.47	NA	1.02	0.42	5.00	-74.27	158.55	3.68	0.03
-2.29	-0.29	NA	NA	-0.47	0.35	1.00	NA	5.00	-74.42	158.85	3.98	0.02
-2.37	-0.33	-0.14	0.46	-0.86	-0.16	1.04	0.62	8.00	-71.46	158.92	4.05	0.02
-2.34	-0.31	-0.40	NA	-0.72	-0.12	1.04	0.56	7.00	-72.70	159.41	4.55	0.02
-1.87	-0.44	NA	0.56	-0.85	0.85	NA	NA	5.00	-75.10	160.20	5.34	0.01
-2.33	-0.29	NA	NA	-0.46	-0.12	1.04	0.53	6.00	-74.26	160.53	5.67	0.01
-1.87	-0.44	NA	0.57	-0.86	NA	NA	0.86	5.00	-75.48	160.97	6.10	0.01
-2.32	-0.18	NA	NA	NA	NA	1.19	NA	3.00	-77.94	161.88	7.01	0.00
-1.87	-0.44	-0.15	0.46	-0.89	0.85	NA	NA	6.00	-74.95	161.90	7.04	0.00
-1.87	-0.44	NA	0.56	-0.85	0.72	NA	0.14	6.00	-75.09	162.18	7.32	0.00
-1.83	-0.44	-0.41	NA	-0.74	0.84	NA	NA	5.00	-76.14	162.27	7.41	0.00
-2.31	-0.24	NA	NA	NA	NA	1.03	0.40	4.00	-77.31	162.62	7.76	0.00
-1.86	-0.44	-0.15	0.47	-0.89	NA	NA	0.86	6.00	-75.34	162.68	7.81	0.00
-2.28	-0.24	NA	NA	NA	0.33	1.01	NA	4.00	-77.46	162.92	8.05	0.00
-1.83	-0.44	-0.41	NA	-0.74	NA	NA	0.85	5.00	-76.55	163.09	8.23	0.00
-1.81	-0.43	NA	NA	-0.48	0.83	NA	NA	4.00	-77.67	163.34	8.47	0.00
-2.32	-0.18	NA	0.06	NA	NA	1.19	NA	4.00	-77.88	163.77	8.91	0.00
-2.32	-0.18	0.02	NA	NA	NA	1.19	NA	4.00	-77.93	163.87	9.01	0.00
-1.87	-0.45	-0.15	0.47	-0.89	0.73	NA	0.14	7.00	-74.94	163.88	9.02	0.00
-1.80	-0.43	NA	NA	-0.48	NA	NA	0.83	4.00	-78.08	164.16	9.30	0.00
-1.84	-0.44	-0.41	NA	-0.74	0.75	NA	0.11	6.00	-76.13	164.26	9.40	0.00

Table A3.3. The model list for *Pachydactylus capensis* during the breeding season of the sociable weaver

-2.31	-0.24	NA	0.07	NA	NA	1.03	0.40	5.00	-77.25	164.50	9.64	0.00
-2.32	-0.24	NA	NA	NA	-0.15	1.05	0.54	5.00	-77.30	164.59	9.73	0.00
-2.30	-0.24	0.02	NA	NA	NA	1.03	0.40	5.00	-77.31	164.61	9.75	0.00
-2.28	-0.24	NA	0.06	NA	0.34	1.01	NA	5.00	-77.40	164.80	9.94	0.00
-2.28	-0.24	0.02	NA	NA	0.33	1.01	NA	5.00	-77.46	164.91	10.05	0.00
-1.81	-0.44	NA	NA	-0.48	0.75	NA	0.09	5.00	-77.66	165.33	10.47	0.00
-2.32	-0.18	0.11	0.13	NA	NA	1.19	NA	5.00	-77.80	165.60	10.74	0.00
-1.70	-0.30	NA	0.55	-0.84	NA	NA	NA	4.00	-78.91	165.81	10.95	0.00
-2.31	-0.25	0.11	0.13	NA	NA	1.03	0.40	6.00	-77.17	166.33	11.47	0.00
-2.32	-0.24	NA	0.07	NA	-0.15	1.05	0.54	6.00	-77.24	166.47	11.61	0.00
-2.32	-0.24	0.02	NA	NA	-0.15	1.05	0.54	6.00	-77.29	166.59	11.72	0.00
-2.28	-0.25	0.11	0.13	NA	0.33	1.01	NA	6.00	-77.32	166.64	11.78	0.00
-1.76	-0.41	NA	NA	NA	0.81	NA	NA	3.00	-80.73	167.47	12.60	0.00
-1.70	-0.30	-0.14	0.46	-0.87	NA	NA	NA	5.00	-78.78	167.57	12.70	0.00
-1.67	-0.30	-0.39	NA	-0.73	NA	NA	NA	4.00	-79.91	167.81	12.95	0.00
-1.75	-0.41	NA	NA	NA	NA	NA	0.82	3.00	-81.13	168.25	13.39	0.00
-2.32	-0.24	0.11	0.14	NA	-0.16	1.05	0.55	7.00	-77.15	168.30	13.44	0.00
-1.65	-0.30	NA	NA	-0.48	NA	NA	NA	3.00	-81.30	168.59	13.73	0.00
-1.76	-0.42	NA	0.07	NA	0.81	NA	NA	4.00	-80.68	169.35	14.49	0.00
-1.76	-0.42	NA	NA	NA	0.74	NA	0.09	4.00	-80.73	169.46	14.59	0.00
-1.76	-0.41	0.02	NA	NA	0.81	NA	NA	4.00	-80.73	169.46	14.60	0.00
-1.75	-0.41	NA	0.07	NA	NA	NA	0.82	4.00	-81.07	170.13	15.27	0.00
-1.75	-0.41	0.02	NA	NA	NA	NA	0.82	4.00	-81.12	170.25	15.38	0.00
-1.76	-0.42	0.11	0.14	NA	0.81	NA	NA	5.00	-80.59	171.19	16.32	0.00
-1.76	-0.42	NA	0.07	NA	0.73	NA	0.09	5.00	-80.67	171.34	16.48	0.00
-1.76	-0.42	0.02	NA	NA	0.74	NA	0.09	5.00	-80.73	171.45	16.59	0.00
-1.76	-0.41	0.11	0.14	NA	NA	NA	0.82	5.00	-80.98	171.96	17.09	0.00
-1.60	-0.29	NA	NA	NA	NA	NA	NA	2.00	-84.27	172.54	17.68	0.00
-1.76	-0.42	0.11	0.14	NA	0.73	NA	0.10	6.00	-80.59	173.17	18.31	0.00
-1.60	-0.29	NA	0.06	NA	NA	NA	NA	3.00	-84.22	174.44	19.58	0.00
-1.60	-0.29	0.02	NA	NA	NA	NA	NA	3.00	-84.27	174.53	19.67	0.00
-1.60	-0.29	0.11	0.14	NA	NA	NA	NA	4.00	-84.13	176.26	21.40	0.00

p(Int)	lam(Int)	p(mean_humidity)	p(mean_temp_subsurface)	p(mean_temp_surface)	lam(canopy_height)	lam(colony_pres_abs)	lam(total_tree_height)	df	logLik	AIC	delta	weight
-3.50	0.08	NA	NA	1.08	NA	0.88	NA	4.00	-51.60	111.19	0.00	0.17
-3.66	0.16	NA	NA	1.08	NA	0.75	0.39	5.00	-51.09	112.18	0.99	0.11
-3.57	0.10	NA	NA	1.08	0.34	0.73	NA	5.00	-51.20	112.40	1.21	0.09
-3.49	0.07	0.06	NA	1.10	NA	0.88	NA	5.00	-51.59	113.18	1.99	0.06
-3.50	0.08	NA	0.01	1.08	NA	0.88	NA	5.00	-51.60	113.19	2.00	0.06
-3.17	-0.09	NA	NA	1.10	0.64	NA	NA	4.00	-52.97	113.94	2.74	0.04
-3.68	0.17	NA	NA	1.08	-0.16	0.77	0.54	6.00	-51.08	114.16	2.96	0.04
-3.65	0.15	0.06	NA	1.11	NA	0.75	0.39	6.00	-51.08	114.16	2.97	0.04
-3.66	0.16	NA	0.01	1.08	NA	0.75	0.39	6.00	-51.09	114.18	2.99	0.04
-3.56	0.09	0.06	NA	1.10	0.34	0.73	NA	6.00	-51.19	114.39	3.20	0.03
-3.58	0.10	NA	0.01	1.08	0.34	0.73	NA	6.00	-51.20	114.40	3.21	0.03
-3.20	-0.05	NA	NA	1.10	NA	NA	0.63	4.00	-53.20	114.41	3.21	0.03
-3.51	0.08	0.09	0.05	1.10	NA	0.88	NA	6.00	-51.58	115.17	3.98	0.02
-2.95	-0.13	NA	NA	1.11	NA	NA	NA	3.00	-54.79	115.59	4.40	0.02
-3.16	-0.09	0.07	NA	1.13	0.64	NA	NA	5.00	-52.96	115.92	4.73	0.02
-3.17	-0.09	NA	0.00	1.10	0.64	NA	NA	5.00	-52.97	115.94	4.74	0.02
-3.17	-0.09	NA	NA	1.10	0.64	NA	0.00	5.00	-52.97	115.94	4.74	0.02
-3.67	0.17	0.06	NA	THAT TATE	-0.16	0.77	0.54	7.00	-51.07	116.14	4.95	0.01
-3.66	0.16	0.09	0.04	1.10	NA	0.75	0.39	7.00	-51.08	116.15	4.96	0.01
-3.69	0.18	NA	0.01	1.08	-0.15	0.77	0.54	7.00	-51.08	116.15	4.96	0.01
-3.58	0.10	0.09	0.05	1.10	0.34	0.73	NA	7.00	-51.19	116.38	5.19	0.01
-3.19	-0.06	0.07	NA	1.13	NA	NA	0.63	5.00	-53.19	116.38	5.19	0.01
-3.19	-0.05	NA	-0.01	1.11	NA	NA	0.63	5.00	-53.20	116.40	5.21	0.01
-2.94	-0.13	0.07	NA	1.14	NA	NA	NA	4.00	-54.78	117.57	6.38	0.01
-2.94	-0.13	NA	-0.02	1.12	NA	NA	NA	4.00	-54.79	117.59	6.40	0.01
-3.17	-0.09	0.08	0.03	1.12	0.64	NA	NA	6.00	-52.96	117.91	6.72	0.01
-3.16	-0.09	0.07	NA	1.13	0.64	NA	0.00	6.00	-52.96	117.92	6.73	0.01
-3.17	-0.09	NA	0.00	1.10	0.64	NA	0.00	6.00	-52.97	117.94	6.74	0.01
-3.69	0.18	0.09	0.04	1.11	-0.15	0.77	0.54	8.00	-51.07	118.13	6.94	0.01

Table A3.4. The model list for *Pachydactylus capensis* during the non-breeding season of the sociable weaver

-3.20	-0.05	0.08	0.02	1.13	NA	NA	0.63	6.00	-53.19	118.38	7.19	0.00
-2.94	-0.13	0.08	0.01	1.14	NA	NA	NA	5.00	-54.78	119.57	8.38	0.00
-3.43	0.28	NA	0.66	NA	NA	0.88	NA	4.00	-55.84	119.69	8.50	0.00
-3.17	-0.09	0.08	0.03	1.12	0.64	NA	0.00	7.00	-52.96	119.91	8.72	0.00
-3.56	0.34	NA	0.66	NA	NA	0.75	0.36	5.00	-55.40	120.81	9.61	0.00
-3.48	0.28	NA	0.66	NA	0.32	0.73	NA	5.00	-55.48	120.96	9.76	0.00
-3.42	0.31	-0.60	NA	NA	NA	0.87	NA	4.00	-56.67	121.34	10.15	0.00
-3.45	0.27	-0.22	0.54	NA	NA	0.88	NA	5.00	-55.71	121.43	10.24	0.00
-3.55	0.37	-0.60	NA	NA	NA	0.75	0.36	5.00	-56.23	122.47	11.27	0.00
-3.58	0.34	-0.22	0.54	NA	NA	0.75	0.36	6.00	-55.27	122.54	11.35	0.00
-3.03	0.04	NA	0.67	NA	0.64	NA	NA	4.00	-57.28	122.55	11.36	0.00
-3.47	0.30	-0.60	NA	NA	0.32	0.73	NA	5.00	-56.31	122.62	11.43	0.00
-3.50	0.28	-0.22	0.54	NA	0.32	0.73	NA	6.00	-55.35	122.70	11.50	0.00
-3.57	0.35	NA	0.66	NA	-0.06	0.76	0.42	6.00	-55.40	122.80	11.61	0.00
-3.05	0.08	NA	0.67	NA	NA	NA	0.61	4.00	-57.55	123.10	11.91	0.00
-3.37	0.38	NA	NA	NA	NA	0.87	NA	3.00	-58.60	123.19	12.00	0.00
-3.01	0.06	-0.61	NA	NA	0.63	NA	NA	4.00	-58.09	124.18	12.99	0.00
-2.76	-0.04	NA	0.67	NA	NA	NA	NA	3.00	-59.12	124.23	13.04	0.00
-3.05	0.04	-0.22	0.54	NA	0.64	NA	NA	5.00	-57.14	124.29	13.10	0.00
-3.49	0.44	NA	NA	NA	NA	0.75	0.35	4.00	-58.17	124.34	13.15	0.00
-3.57	0.38	-0.60	NA	NA	-0.07	0.76	0.42	6.00	-56.23	124.46	13.27	0.00
-3.41	0.37	NA	NA	NA	0.32	0.73	NA	4.00	-58.25	124.49	13.30	0.00
-3.59	0.35	-0.22	0.54	NA	-0.07	0.76	0.42	7.00	-55.27	124.54	13.35	0.00
-3.02	0.03	NA	0.67	NA	0.70	NA	-0.07	5.00	-57.27	124.55	13.36	0.00
-3.04	0.10	-0.61	NA	NA	NA	NA	0.61	4.00	-58.36	124.72	13.53	0.00
-3.07	0.07	-0.22	0.54	NA	NA	NA	0.61	5.00	-57.42	124.83	13.64	0.00
-2.74	-0.03	-0.61	NA	NA	NA	NA	NA	3.00	-59.91	125.81	14.62	0.00
-2.78	-0.05	-0.23	0.54	NA	NA	NA	NA	4.00	-58.98	125.96	14.77	0.00
-2.93	0.11	NA	NA	NA	0.63	NA	NA	3.00	-60.04	126.08	14.89	0.00
-3.00	0.05	-0.61	NA	NA	0.69	NA	-0.06	5.00	-58.09	126.18	14.99	0.00
-3.04	0.03	-0.22	0.54	NA	0.70	NA	-0.06	6.00	-57.14	126.28	15.09	0.00
-3.51	0.45	NA	NA	NA	-0.06	0.75	0.41	5.00	-58.17	126.34	15.15	0.00

-2.96	0.15	NA	NA	NA	NA	NA	0.61	3.00	-60.31	126.62	15.43	0.00
-2.65	0.00	NA	NA	NA	NA	NA	NA	2.00	-61.85	127.70	16.51	0.00
-2.92	0.10	NA	NA	NA	0.69	NA	-0.07	4.00	-60.04	128.07	16.88	0.00



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p(Int)	lam(Int)	p(mean_humidity)	p(mean_temp_subsurface)	p(mean_temp_surface)	lam(colony_pres_abs)	lam(total_tree_height)	df	logLik	AIC	delta	weight
-4.41	0.58	1.27	1.63	NA	1.65	-0.61	6.00	-44.70	101.40	0.00	0.14
-4.77	1.06	1.24	1.58	NA	1.32	NA	5.00	-45.93	101.85	0.46	0.11
-4.37	0.63	NA	0.48	NA	1.63	-0.58	5.00	-46.12	102.24	0.84	0.09
-4.31	0.67	NA	NA	NA	1.61	-0.57	4.00	-47.25	102.50	1.10	0.08
-4.77	1.14	NA	0.46	NA	1.32	NA	4.00	-47.29	102.57	1.18	0.08
-4.71	1.17	NA	NA	NA	1.31	NA	3.00	-48.36	102.72	1.33	0.07
-4.34	0.64	NA	NA	0.39	1.63	-0.58	5.00	-46.38	102.77	1.37	0.07
-4.74	1.14	NA	NA	0.37	1.32	NA	4.00	-47.54	103.09	1.69	0.06
-4.42	0.58	1.31	1.93	-0.27	1.65	-0.60	7.00	-44.64	103.28	1.88	0.05
-4.77	1.06	1.28	1.89	-0.28	1.32	NA	6.00	-45.87	103.73	2.34	0.04
-4.32	0.66	-0.20	NA	NA	1.62	-0.57	5.00	-46.99	103.97	2.58	0.04
-4.36	0.62	0.53	NA	0.82	1.64	-0.59	6.00	-46.06	104.11	2.72	0.04
-4.37	0.63	NA	0.54	-0.06	1.63	-0.58	6.00	-46.11	104.23	2.83	0.03
-4.72	1.16	-0.20	NA	NA	1.31	NA	4.00	-48.12	104.23	2.84	0.03
-4.76	1.14	0.51	NA	0.79	1.32	NA	5.00	-47.23	104.46	3.06	0.03
-4.76	1.14	NA	0.53	-0.07	1.32	NA	5.00	-47.28	104.56	3.16	0.03
-3.06	0.04	1.29	1.64	NA	NA	NA	4.00	-51.15	110.29	8.90	0.00
-3.03	0.09	NA	0.47	NA	NA	NA	3.00	-52.53	111.07	9.67	0.00
-2.98	0.12	NA	NA	NA	NA	NA	2.00	-53.59	111.17	9.78	0.00
-3.01	0.10	NA	NA	0.38	NA	NA	3.00	-52.79	111.58	10.19	0.00
-3.04	0.01	1.29	1.64	NA	NA	0.19	5.00	-50.99	111.97	10.58	0.00
-3.07	0.04	1.33	1.96	-0.29	NA	NA	5.00	-51.08	112.17	10.77	0.00
-2.98	0.11	-0.20	NA	NA	NA	NA	3.00	-53.35	112.71	11.31	0.00
-3.01	0.06	NA	0.47	NA	NA	0.19	4.00	-52.37	112.74	11.35	0.00
-2.96	0.08	NA	NA	NA	NA	0.19	3.00	-53.42	112.85	11.45	0.00
-3.02	0.09	0.52	NA	0.80	NA	NA	4.00	-52.48	112.95	11.56	0.00
-3.03	0.09	NA	0.54	-0.08	NA	NA	4.00	-52.53	113.05	11.66	0.00
-2.99	0.06	NA	NA	0.38	NA	0.19	4.00	-52.63	113.26	11.86	0.00
-3.05	0.01	1.33	1.96	-0.29	NA	0.19	6.00	-50.92	113.85	12.45	0.00
-2.96	0.07	-0.20	NA	NA	NA	0.19	4.00	-53.19	114.38	12.99	0.00
-3.00	0.05	0.52	NA	0.81	NA	0.19	5.00	-52.32	114.63	13.24	0.00
-3.01	0.06	NA	0.54	-0.08	NA	0.19	5.00	-52.36	114.73	13.33	0.00

Table A3.5. The model list for Naja nivea during the breeding season of the sociable weaver
p(Int)	lam(Int)	p(mean_humidity)	p(mean_temp_subsurface)	p(mean_temp_surface)	lam(colony_pres_abs)	lam(total_tree_height)	df	logLik	AIC	delta	weight
-7.19	2.31	NA	NA	NA	NA	NA	2.00	-11.77	27.53	0.00	0.18
-6.70	1.67	NA	NA	NA	NA	0.59	3.00	-11.50	29.00	1.47	0.08
-7.27	2.31	NA	-0.40	NA	NA	NA	3.00	-11.59	29.18	1.65	0.08
-7.21	2.31	0.22	NA	NA	NA	NA	3.00	-11.71	29.43	1.90	0.07
-7.19	2.31	NA	NA	-0.10	NA	NA	3.00	-11.76	29.51	1.98	0.07
-7.19	2.31	NA	NA	NA	0.00	NA	3.00	-11.77	29.53	2.00	0.07
-6.78	1.67	NA	-0.40	NA	NA	0.59	4.00	-11.33	30.65	3.12	0.04
-7.36	2.31	NA	-0.97	0.69	NA	NA	4.00	-11.43	30.86	3.33	0.03
-6.48	1.43	NA	NA	NA	-0.26	0.70	4.00	-11.44	30.89	3.36	0.03
-6.72	1.67	0.22	NA	NA	NA	0.59	4.00	-11.45	30.90	3.37	0.03
-6.70	1.67	NA	NA	-0.10	NA	0.59	4.00	-11.49	30.98	3.45	0.03
-7.27	2.31	-0.14	-0.50	NA	NA	NA	4.00	-11.58	31.16	3.63	0.03
-7.27	2.31	NA	-0.40	NA	0.00	NA	4.00	-11.59	31.18	3.65	0.03
-7.23	2.31	0.52	NA	0.35	NA	NA	4.00	-11.68	31.36	3.83	0.03
-7.20	2.30	0.22	NA	NA	0.00	NA	4.00	-11.71	31.43	3.90	0.03
-7.19	2.31	NA	NA	-0.10	0.00	NA	4.00	-11.76	31.51	3.98	0.02
-6.87	1.67	NA	-0.97	0.69	NA	0.59	5.00	-11.17	32.33	4.80	0.02
-6.56	1.43	NA	-0.40	NA	-0.26	0.70	5.00	-11.27	32.54	5.01	0.01
-6.79	1.67	-0.14	-0.50	NA	NA	0.59	5.00	-11.32	32.63	5.10	0.01
-7.43	2.31	0.67	-1.06	1.35	NA	NA	5.00	-11.33	32.66	5.13	0.01
-6.51	1.43	0.22	NA	NA	-0.26	0.70	5.00	-11.39	32.78	5.25	0.01
-6.74	1.67	0.53	NA	0.35	NA	0.59	5.00	-11.42	32.83	5.30	0.01
-7.36	2.31	NA	-0.97	0.69	0.00	NA	5.00	-11.43	32.86	5.33	0.01
-6.49	1.43	NA	NA	-0.10	-0.26	0.70	5.00	-11.43	32.87	5.34	0.01
-7.27	2.31	-0.14	-0.50	NA	0.00	NA	5.00	-11.58	33.16	5.63	0.01
-7.23	2.31	0.52	NA	0.35	0.00	NA	5.00	-11.68	33.36	5.83	0.01
-6.94	1.67	0.67	-1.06	1.35	NA	0.59	6.00	-11.06	34.13	6.60	0.01
-6.65	1.43	NA	-0.97	0.69	-0.26	0.70	6.00	-11.11	34.22	6.68	0.01
-6.57	1.43	-0.14	-0.50	NA	-0.26	0.70	6.00	-11.26	34.52	6.99	0.01
-7.43	2.31	0.67	-1.06	1.35	0.00	NA	6.00	-11.33	34.66	7.13	0.01
-6.52	1.43	0.52	NA	0.35	-0.26	0.70	6.00	-11.36	34.72	7.18	0.00
-6.72	1.43	0.67	-1.06	1.35	-0.26	0.70	7.00	-11.01	36.01	8.48	0.00

Table A3.6. The model list for *Naja nivea* during the non-breeding season of the sociable weaver

Appendix 4: Detection probability graphs for *T. spilogaster*, *P. capensis* and *N. nivea* during the breeding season of the sociable weaver.



Figure A4.1 The subsurface temperature and humidity graphs affecting the detection probability for *T. spilogaster*.



Figure A4.2 The surface and subsurface temperature graphs affecting the detection probability for *P. capensis*.



Figure A4.3 The subsurface temperature and humidity graphs affecting the detection probability for *N. nivea*.

Appendix 5: Detection probability graphs for *T. spilogaster* and *P. capensis* during the non-breeding season of the sociable weaver.



Figure A5.1 The surface and subsurface temperature graphs affecting the detection probability for *T. spilogaster*.



Figure A5.2 (A) The humidity graph affecting the detection probability for *T. spilogaster*. **(B)** The surface temperature graphs affecting the detection probability for *P. capensis*.