The University of Cape Town

Faculty of Statistical Sciences

Using state space time series analysis on wetland bird species to formulate effective bioindicators in the Barberspan wetland

By

Gareth Edwards

Supervisors

Res Altwegg
Birgit Erni

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Abstract

The Coordinated Waterbird Count dataset (CWAC) is a dataset containing waterbird counts from wetlands across South Africa, going as far back as 1970. These data contain valuable information on population sizes and their trends over time. This information could be used more widely if it was more easily accessible to users. The aim of this report is to bridge the gap between the raw CWAC dataset and the end users (for both experts and non-experts). In so doing the report also provides valuable insight into the state of wetlands in South Africa using various bio indices, starting with Barberspan wetland as the pilot study site. State space time series models were applied to the waterbird counts in the CWAC dataset to determine waterbird population trends over the years. These MCMC based models produced estimated counts for each waterbird per year. Three different indices were applied to the output, namely, exponentiated Shannon's index, Simpson's index and a modified Living Planet Index. These indices aggregate the count data to a measure of effective number of waterbirds in an ecosystem, a measure of evenness of an ecosystem, and an abundance index respectively. Using these three indices, in conjunction with each other, and individual waterbird species as bioindicators for various wetland traits, the end user is presented with a broad overview of the state of the Barberspan wetland. The implication of this research is beneficial to various wetland conservation organisations globally (AEWA, Aichi, RAMSAR) and locally (Working for Wetlands), as it provides valuable insight into the state of wetlands of South Africa. Furthermore, it helps managers at a local level in their decision making to enable more evidence-based approaches to protect South African wetlands and its waterbirds.

Contents

Acknowledgements

Thank you for following this tutorial!

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1 Introduction

1.1 Problem Description

Wetlands are the most threatened and least protected ecosystems globally and in South Africa (Skowno 2019). Wetlands are areas where the land is covered with water such as marshes, sedges, river deltas, edges of lakes or oceans, etc. Wetlands benefit society in many ways. These include flood control, storm buffering and water quality improvement (Clarkson, Ausseil, and Gerbeaux 2013). Wetlands are invaluable to society and their surrounding communities.

The threat to wetlands has only recently been realised locally. Wetland conservation programs for South Africa have been created as late as 2002 despite the severe wetland degradation experienced over the years. As a result of the relative late response, 35-60% of South Africa's wetlands have been severely damaged or destroyed due to bad agricultural practices (Environmental Affairs 2019). As a result, there have been recent programs for wetland rehabilitation. Most notably, the Working for Wetlands, initiated in 2002. Working for Wetlands was initiated by the Water Research Commission, in partnership with the Department of Environmental Affairs, and aims to rehabilitate and protect wetlands in South Africa.

Destruction or degradation of an ecosystem leads to a decrease in species populations and/or a decrease in biodiversity. According to the WWF's 2018 living planet report, it's stated that there has been a 60% decrease in global population biodiversity of mammals, fish, birds, reptiles and amphibians (Grooten and Almond 2018). These views are supported by the Living Planet Index (LPI) (McRae, Deinet, and Freeman 2017; Loh et al. 2005). As a result, there has been a notable increase in effort to preserve and recover global biodiversity. The most notable being The Aichi Biodiversity targets. The Aichi Convention on Biological Diversity presented a strategic plan in 2011 to improve global biodiversity (Convention on Biological Diversity 2010). This plan is made up of 5 goals and 20 targets. The strategic plan needed appropriate metrics to measure its success, and as a result the Living Planet Index (LPI) was created. The LPI measures the progress of Aichi strategic goal C. Aichi strategic goal C states: "To improve the status of biodiversity by safeguarding ecosystems, species and genetic diversity" (Biological Diversity 2020).

Biodiversity is invaluable to our ecosystems and society at large. With loss of biodiversity comes reduced ecosystem resilience (Ritchie and Roser 2021). It has thus imperative to keep track of an ecosystem's biodiversity and species population dynamics to understand the state of an ecosystem. One of the best tools to track biodiversity and species population dynamics are birds (Amat and

Green 2010; Mekonen 2017). Consequently, a citizen scientist initiative, called the Coordinated Waterbird Counts (CWAC), was initiated in 1992 by the Animal Demographic Unit (ADU), to keep track of bird counts in wetlands around South Africa. The CWAC dataset has bird counts of over 200 different bird species from approximately 400 different wetland locations in South Africa. Some of these counts go back as far as the 1970s.

Wetlands and waterbirds are the subject of many conservation projects locally and worldwide. Organisations involved include Agreement on the Conservation of African-Eurasian Migratory Waterbirds (AEWA), Convention on Wetlands of International Importance Especially as Waterfowl Habitat (RAMSAR) and the Working for Wetlands initiative. Regarding the waterbirds in South Africa, there is currently a robust citizen-science based bird monitoring programme in the form of the CWAC dataset. Unfortunately, this is a raw dataset and not very accessible to the broader community. The aim of this project is to use the raw CWAC dataset and produce concise and effective data products, using various statistical techniques, that can be used by experts and non-experts to understand the state of the wetland and waterbird species of South Africa.

1.2 Background to Research

My project forms part of a larger project, The South Africa BiodIveRsity Data pIpelinE for wetlands and waterbirds (BIRDIE) https://www.sanbi.org/biodiversity/building-knowledge/biodiversity-monitoring-assessment/freshwater-programme-birdie-project. BIRDIE is a project that aims to collate all types of wetland data, perform statistical analysis, and make the output available to the public. The data pipeline is to utilise raw wetland data, collate it and produce data that is directly useful for decision making purposes on a local and global scale.

The output will be relevant at national, regional and local levels. At the national level, The data output provides insights of the state of South African wetlands and waterbirds that can be used by international conservation projects like AEWA and Ramsar. At the regional level, the data output supports provincial conservation agencies who need to make a range of decisions about the conservation of sites and species. For example, some species are hunted and quotas need to be set. At the local level, the data output aids wetland site managers decision making regarding the preservation of the wetland and its bird species. Furthermore, the output is also beneficial to bird watchers in helping identify which bird species are present at which wetlands.

The BIRDIE project is being conducted by the South African National Biodiversity Institute (SANBI), in association with FitzPatrick Institute for African Ornithology (FIAO, UCT), the Centre

for Statistics in Ecology, Environment and Conservation (SEEC at the University of Cape Town), Seascape Belgium and the Royal Belgium Institute of Natural Sciences (RBINS). The end goal is to provide automated statistical computing processes on raw data and produce effective visualisations and other data specific output hosted on a web app.

One of the key datasets in the BIRDIE project is the CWAC dataset. The CWAC dataset is well managed and maintains standard protocols for the counters to ensure reliable counts. The census data captured are also presented to international biodiversity contributors such as AEWA and the RAMSAR convention.

CWAC counts usually take place twice a year. Once in summer, traditionally during January and February, and once in winter, traditionally during July. The counting protocol is standardised to increase reliability of the counts and the ability to compare counts across different wetland sites. Counters are encouraged to adhere to these methods as closely as possible. Variables such as number of counters, routes followed, time of day, tide, viewing technique, viewing aids, personnel and counting technique are all kept constant for each wetland. Due to varying terrains and environments, each wetland may require slightly different counting techniques, but these techniques remain constant once established (ADU 2020). Further information on the CWAC counting procedure can be found on the CWAC website (http://www.adu.org.za/docs/cwac-info4.pdf).

The CWAC dataset provides an important insight into the state of wetlands across South Africa. Unfortunately, the data are currently only available in the form of raw counts and difficult to analyse by non-experts. Analysing the count data and identifying pattens in species abundance, biodiversity and population dynamics over the years is an important step in identifying wetland state and to measure if wetland rehabilitation programs have been working.

1.3   State space time series model (SSM)

State space models (SSMs) have become a popular tool used by ecologists to analyse ecological time-series. There is enough evidence to argue that SSMs should be the default tool in analysing time series for ecologists (Auger-Méthé et al. 2021). SSMs have been used in various ecological studies such as fisheries stock assessment (Aeberhard et al. 2020), movement ecology (Patterson et al. 2008) and, most commonly, modelling population dynamics (Newman et al. 2014). These are only a few examples of where SSMs are used. Their application in ecology is vast.

SSMs are able to model temporal autocorrelation in a way that separates observation error from process error (Auger-Méthé et al. 2021). Herein lies the value of SSMs. SSMs are hierarchical models

that essentially model two different time series. One being the state process (latent process or hidden process) which is the unobserved time series that represents the true underlying population dynamics. The other being the observation process that represents the observed counts of that state process. Count data is often prone to observation error, especially when counting large groups of birds. Therefore, separating the observation process from the state process provides a more accurate estimation of the true population. The beauty in this methodology is that variation attributed to population size, population growth rate, environmental stochasticity and any other forms of stochasticity can be estimated from the model (Kéry and Schaub 2011). This allows the ecologist to program the state space time series model such that it accounts for known biological factors that affect the population dynamics. This includes birth rates, death rates, fecundity, immigration, emigration, etc. Figure 1 shows a simple visual illustration of this separation between state and observation processes.
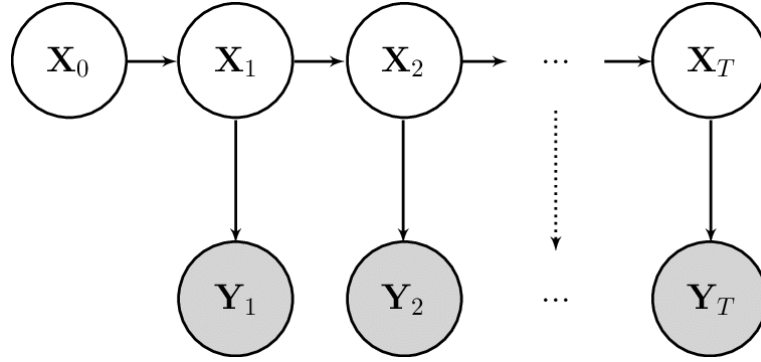
Figure 1: A visual representation of a state space model where X_t is the true population state and Y_t is the observations

When applying SSMs to count data there are two important conditions that must be met for the SSM to produce unbiased estimates of population size. Firstly, false negative (false detections) and false positive (double counting) observations should cancel out on average. Secondly, there should be no temporal patterns in detection probability or false positive rates over time (Kéry and Schaub 2011).

1.4 Bioindicators

Fitting SSMs to population data helps us understand how the population of individual species have fluctuated over the years. But these models don't tell the user much about the biodiversity of the ecosystem. This is where bioindicators and indices come in. In this report, bioindicators refer to biological aspects of an ecosystem that reflect changes in the ecosystem. For example, birds are good

organisms to use as bioindicators as they reflect various environmental changes directly (Mekonen 2017). Indices, in this report, refer to summarised information. The LPI is an example of such an index as it aggregates multiple species trends into a single index value.

Environmental assessments play an important role in environmental decision-making. This has lead to a stark increase in assessment reports that are based on bioindicators (Niemeijer and Groot 2008). According to Niemeijer and Groot (2008), the bioindicators used in these reports often follow a common causal chain. This means that the bioindicator in use directly reflects specific changes in an ecosystem. For example, a decrease in wetland water level would be reflected in the declining population of waterbird species of that wetland (Burgess 1969). Niemeijer and Groot (2008) argue that the bioindicators used are too specific. One should instead use bioindicators that reflect multiple changes in an ecosystem. Bird species are ideal bioindicators to use as they reflect many aspects of an ecosystem (Mekonen 2017)

According to Gregory et al. (2003), effective bioindicators are quantitative, easy to collect, simple to interpret, reflect causes of change in an ecosystem and indicate general patterns of taxa in the ecosystem. Bird count data fits this well. As bird counts are relatively easy to collect (and readily available), quantitative, simple to interpret and they reflect multiple different changes in an ecosystem.

Birds have been used to indicate the eutrophication levels in wetlands in the Mar Menor lagoon of south-eastern Spain (Amat and Green 2010). It was discovered that the Great Crested Grebe abundance increased as the eutrophication levels in the lagoon increased. The increase in eutrophication was a result of nutrient run-off from nearby agricultural practices. Another example from Southern Spain shows the use of Red-Knobbed Coots to indicate the siltation rate in the water and soil in wetlands (Amat and Green 2010). The Red-Knobbed Coot experienced a stark decline in abundance in the 20th century in Southern Spain. This decrease in abundance is attributed to the increased siltation rates in the water and soil in the wetlands in Southern Spain. Caused by invasive agricultural practices. The increased rates of siltation negatively affected the quality of food for the Coots in their wetlands, and thus lead to their demise. Thus, the Red-Knobbed Coots population over time could be indicative of siltation rates in the wetlands in which they are based. These are only two examples of how effective waterbirds are as bioindicators. Other examples show how waterbirds can be indicators for changes in water level in a wetland (Burgess 1969) and species abundance at lower trophic levels (Mekonen 2017).

An important aspect of ecosystem health is biodiversity. Rich biodiversity is indicative of a healthy

ecosystem. Each species has their part to play in the ecosystem with varying degrees of importance. Tracking biodiversity in an ecosystem can also indicate the presence of invasive species (Hooper et al. 2005). Biodiversity indicators are therefore essential in tracking the overall health of a wetland ecosystem.

Biodiversity can be defined by two basic components. That is, how many different species are present in an ecosystem (Magurran 2013) and how many individuals per species is present in an ecosystem (evenness) (Buckland et al. 2005). Based on these components of biodiversity, a community with more species tends to have higher biodiversity than a community with fewer species and a community that displays high levels of evenness is regarded more diverse than a community that displays high levels of unevenness. Regarding the concept of evenness, if two communities have the same species, the one where each species is equally abundant (high degree of evenness) is more diverse than one where there are a few common species and the rest are rare (high degree of unevenness).

Two of the more common biodiversity indices are the Shannon's entropy and the Simpson's index. The exponentiated Shannon's entropy reflect the effective number of species in an ecosystem based on the species counts (Jost 2006). The Simpson's index presents a measure of evenness in a community with 1 being perfect evenness and 0 being very poor evenness. Evenness refers to how similar the species are in their relative frequencies. If a community has equal counts for each species the Simpson's index would be 1 and the community of waterbird species would be perfectly even. If there are one or two species that have significantly higher counts than the rest, then the Simpson's index would be closer to 0 indicating that the community is uneven, and some species are dominant in the ecosystem.

There are currently various indices used, worldwide, that aggregate and measure species trends. These are used to provide an overview of the species health in an ecosystem. The main index in use, globally, is the Living Planet Index (LPI) (Collen et al. 2009). There are other similar indices such as the Australian Threatened Species Index (TSX) (Bayraktarov et al. 2020) and the Wild Bird Index (WBI) (Gregory and Strien 2010). Both the TSX and the WBI are based on the calculations used by the LPI.

Choosing the best index to use proved to be a difficult task as decision science has rarely been applied to these global indices to evaluate their effectiveness and their design (Watermeyer et al. 2021). However, a study by Watermeyer et al. (2021) was conducted that applied decision science techniques to 9 different, commonly used, global environmental indicies, one being the LPI. Based on the study, the LPI performed well in 4 of the 5 criteria used. The criteria being: How well the index

meets its objectives, design, behaviour, methods to test uncertainty, and feasibility. The LPI performed well in all aspects except for feasability.

The LPI was initiated in 1997 by the WWF and the World Conservation Monitoring Centre. It is the most used index that monitors average vertebrate trends around the world. These trend estimates are based on data from as far back as 1970. It uses time-series data from around the world and aims to measure the state of the world's population trends of vertebrate species. The Index covers the terrestrial, freshwater and marine habitats. The time series data is further broken up into its specific biomes and geographic realms or oceans.

1.5   Aim and Objectives

The CWAC dataset is currently a raw and hard to access dataset. The aim of this study is to extract relevant information from the data in the form of time series analysis and bioindicators to track bird species population dynamics and biodiversity. State space time series models (SSM) are used to model the population dynamics. SSMs have become popular amongst ecologists when dealing with population dynamics and is fast becoming the norm (Auger-Méthé et al. 2021). SSMs work well with count data as they separate the observation error from the process error (Kéry and Schaub 2011). This gives the ecologist a better understanding of the true population dynamics. SSMs are also good for forecasting future values or missing values which is suitable for the CWAC dataset as it contains missing counts for some years. The SSM is key to the following aims as the posterior sample is used for further calculations to develop bioindicators.

When formulating bioindicators from data, it's important to first understand what needs to be monitored (Yoccoz, Nichols, and Boulinier 2001). Given the context of wetland and waterbird conservation, multiple types of indices and indicators were necessary to produce a holistic view of the state of the wetland and waterbirds present. The metrics used, in this report, to measure biodiversity were the exponentiated Shannon's entropy and the Simpson's index (as biodiversity indices) and a modified Living Planet Index (LPI) (as a population trend index).

Wetland and waterbird conservationists will be able to utilise these indices and time series models to understand the state of the wetland in terms of its bird species. Furthermore, it can be used as a tool by AEWA, Ramsar and the common bird enthusiast, to monitor the waterbird species in South Africa. The Barberspan wetland is used as pilot study, but if successful, this analysis can be used on all wetland sites represented in the CWAC dataset.

The following are the objectives that, if followed, will lead to successful completion of the aim:

1. Research and develop relevant state space time series model for bird population dynamics in Barberspan. These models can be used for understanding the change of bird counts over time and forecasting future values.

2. Identify species attributes that may affect the population dynamics.

3. Formulate relevant biodiversity indicators using the output of the state space model.

4. Formulate both the state space models and biodiversity indicators such that they display a good overview of wetland state that can be used by both non-experts and experts.

2 Methods

2.1 Study Area

The Barberspan wetland is a protected wetland site known as the Barberspan Bird Sanctuary. It is located in the North West province of South Africa. The 3200ha reserve is centred on a shallow lake that covers about 257 to 2000ha of the reserve, depending on rainfall (Remisiewicz and Avni 2011). The Barberspan wetland is placed on an inland African flyway. As a result, it is a popular stopover location for intra-African and Eurasian migrant waders and waterbirds.

According to RAMSAR reports, the wetland regularly supports approximately 20000 waterbirds with 365 different bird species recorded at the Barberspan wetland (Ramsar 2015). Barberspan is an important location for the migratory waterbirds that it supports. For this reason, it is one of the first RAMSAR sites in South Africa and the only RAMSAR site in the North West province. It also provides ideal conditions for bird watching and is a popular location for keen bird watching enthusiasts.

Barberspan supports thousands of Little Stints and Curlew Sandpipers. It's also a popular location for intra-African nomadic waders such as the Kittlitz's Plover and Crowned Lapwing. The more common species of the wetland include the Red-Knobbed Coot, Egyptian Goose, Yellow Billed Duck, Southern Pochard and the South African Shelduck (Remisiewicz and Avni 2011). Appendix B contains further information regarding the waterbirds in Barberspan.

Barberspan is a well-protected wetland, home to many different waterbird species and rich in bird count data. As a result, it has been adopted by the BIRDIE project as its pilot site for the construction of its data pipeline and is the focus of this study.

2.2 Exploratory Data Analysis

The data used in this report comes from the Coordinated Waterbird Counts (CWAC) initiative (ADU 2020). Counts are conducted twice a year, once every 6 months. One count in January/February (austral summer) and the other in June/July (austral winter). The counting procedure is standardised for each site with a rigorous set of instructions to follow. Counting procedure, however, could not be standardised across wetlands due to differing wetland sizes and terrains. Protocol ensures that each counting session should take place at, more or less, the same time of day, when the sun is either behind or beside the counter, for ideal visibility. The CWAC datasets can be obtained from the CWAC API (http://api.adu.org.za/cwac/).

The CWAC dataset contains waterbird counts from various wetlands across South Africa. Only the Barberspan wetland has been used for this report. There are counts from the year 1993 to 2018 in the CWAC records for the Barberspan wetland. The original dataset omitted the years without counts. These years were inserted into the dataset as missing values. This was done for the sake of completeness and for the benefit of the state space models. A time series of combined waterbird counts in the Barberspan wetland can be seen in figure 2.
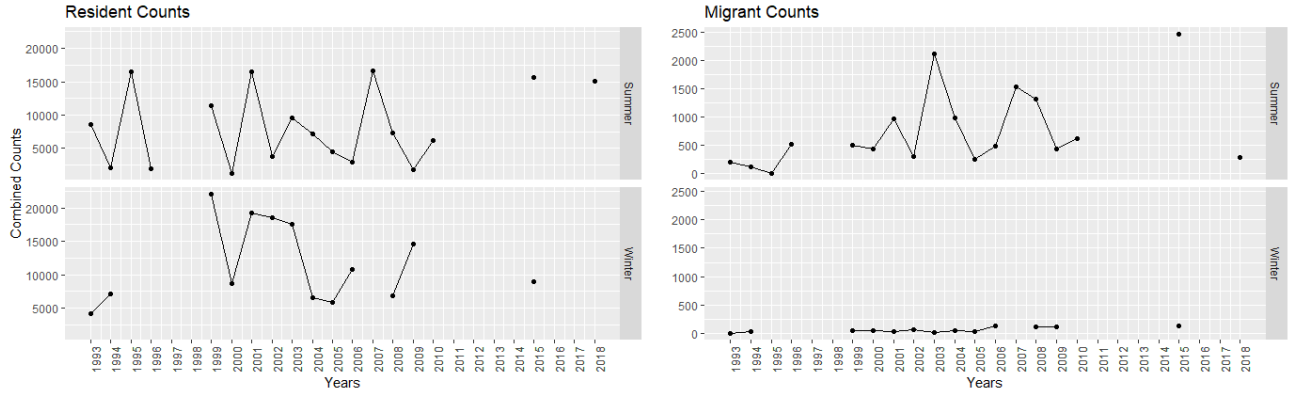
Figure 2: Combined counts of waterbirds per year at Barberspan wetland separated by migratory status

Figure 2 shows a large difference between the number of residents and migrants in Barberspan. For this reason the resident and migrant species were modelled and analysed separately. Modelling and analysing migrants and residents together would lead to the resident species dominating the model.

The residents and migrant have also been analysed separately to account for their differences in seasonal abundance patterns. These patterns present themselves in the data and are evident in figure 2. There are clearly more migrant species present in Barberspan during summer than winter. This is due to their migratory pattern as these waterbirds often migrate to the south for the southern summer. The resident counts don't display this pattern. The resident counts tend to fluctuate randomly throughout the year with no clear reason for these fluctuations.

The CWAC dataset, unfortunately, doesn't have recorded counts for every year since its inception. The following time periods contained no counts: The winter of 1995, the winter of 1996 to the winter of 1998, the winter of 2007, the winter of 2010 to the winter of 2014, the summer of 2016 to the winter of 2017 and the winter of 2018.

2.3 State Space Model

State space time series models (SSMs) have been used for modelling population dynamics in this study. SSMs are flexible models that allow one to modify population models to account for known biological processes that affect population variation. This works well when modelling migratory avian species (Barshep et al. 2017; Camp et al. 2016; Wilson et al. 2011). State space models are also able to separate the observation and state error. By removing the observation error from the state error, the model is able to predict population trends more accurately (Kéry and Schaub 2011). Bird count data is often affected by observation error as counters are prone to missing or double counting individuals. This makes SSMs ideal in the current situation.

There have been two studies which applied SSMs to waterbird counts in Southern Africa (Barshep et al. 2017; Simmons et al. 2015). Barshep et al. (2017) used two different SSMs. A univariate model for resident species, "sedentary residents with limited or no seasonal movement between sites" and a bivariate model (with summer and winter as the two variables) for the migrant species, "Palaearctic migrants and intra-African migrants". Both studies utilised the same model for the migrant species. Both models are fitted to the logarithm of the counts.

Model 1 is a univariate model that treats summer/winter as a covariate. The observation process is modelled as followed:

$$ln(y_t) = \mu_t + \gamma_t + \alpha_t, \quad \alpha_t \sim N(0, \sigma_\alpha^2) \tag{1}$$

Where $ln(y_t)$ is the logarithm of the summer and winter counts, μ_t is the true population, α_t is the observation error with variance σ_α^2. γ_t is the summer/winter variable represented as follows:

$$ln(seasonal\ effect): \gamma_t = -\gamma_{t-1} + \zeta_t, \quad \zeta_t \sim N(0, \sigma_\zeta^2) \tag{2}$$

Where a positive γ_t represents the summer variable.

The state process was modelled as a linear trend model as the resident species tend to remain in the same place all year round. The state process is represented as follows:

$$ln(relative\ population\ size\ at\ time\ t): \mu_t = \mu_{t-1} + \beta_{t-1} + w_t, \quad w_t \sim N(0, \sigma_w^2) \tag{3}$$

Where β_t is the rate of change of the population over time and is modelled as follows:

$$ln(population\ change) : \beta_t = \beta_{t-1} + \epsilon_t, \quad \epsilon_t \sim N(0, \sigma_\epsilon^2) \tag{4}$$

The variables α_t, w_t, ϵ_t and ζ_t are all serially independent with variances σ_α^2, σ_w^2, σ_ϵ^2 and σ_ζ^2 respectively. This concludes model one that is applied to resident species. See figure 3 for a visual illustration of model 1.

Model 2 is applied to the migrants and considers their migratory movement. The migrant species in South African wetlands tend to breed in the northern hemisphere (during the southern winter) then migrate south for the southern summer. The young birds tend to remain in the south during the subsequent southern winter period. Model 2 was thus formulated as a bivariate time series model treating summer counts and winter counts as separate variables with the summer population as the main focus. The proportion of birds that stay over for the subsequent southern winter was modelled as the second variable. Figure 3 shows a visual description of this model. The mathematical representation of model 2 is as follows:

observation process

$$ln(summer\ count) : s_t = \mu_{t-1} + \alpha_t, \quad \alpha_t \sim N(0, \sigma_\alpha^2) \tag{5}$$

$$ln(winter\ count) : w_t = \mu_t + \lambda_t + e_t, \quad e_t \sim N(0, \sigma_e^2) \tag{6}$$

state process

$$ln(summer\ population\ change) : \mu_t = \mu_{t-1} + \beta_{t-1} + w_t, \quad w_t \sim N(0, \sigma_w^2) \tag{7}$$

$$ln(population\ change) : \beta_t = \beta_{t-1} + \zeta_t, \quad \zeta_t \sim N(0, \sigma_\zeta^2) \tag{8}$$

$$ln(summer\ to\ winter\ ratio) : \lambda_t = \lambda_{t-1} + \epsilon_t, \quad \epsilon_t \sim N(0, \sigma_\epsilon^2) \tag{9}$$

Where, s_t is the summer count at time t and w_t is the winter count at time t. μ_t is the latent summer population, β_t is the rate of change at time t and λ is the winter to summer ratio. α_t, e_t, w_t,

ζ_t and ϵ_t are all normally distributed, serially independent and independent of each other with variance σ_α^2, σ_e^2, σ_w^2, σ_ζ^2 and σ_ϵ^2 respectively.

Model 2 has been used in this study and applied to both migrant and resient species. The 2 species differ in migratory patterns but there is reason to believe that observation error may be dependent on the season. For example, in winter there may be thicker foliage than in summer. There may also be less light available, on average, due to increased cloud cover during winter months. Separating the winter and summer counts allows the model to account for season specific observation error. Therefore, the same state space model was applied to both the residents and the migrants.

(a) Model 1

(b) Model 2
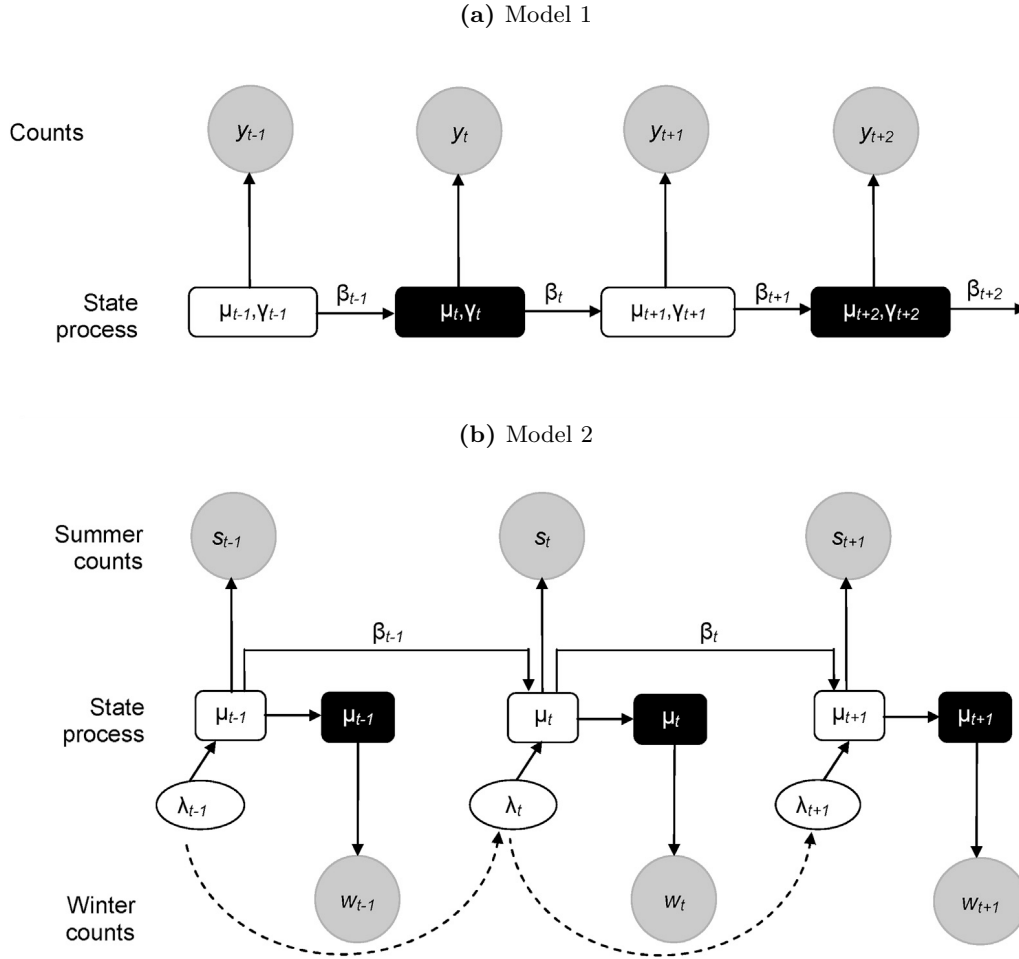
Figure 3: Visual illustrations of State Space Model 1 and 2 to model resident waterbirds and migrant waterbirds respectively (Barshep et al. 2017). The symbol representation is as follows:

y_t = summer and winter count observations for the univariate model
s_t = summer count
w_t = winter count
γ_t = seasonal effect
μ_t = population level
β_t = slope
λ_t = winter to summer ratio

2.3.1 Inferential approaches to SSMs

There are 2 fundamentally different ways to fit SSMs. That is a frequentist approach or a Bayesian approach (Auger-Méthé et al. 2021).

Frequentist approach

The frequentist, or classical, approach is common in most statistical analysis. When fitting SSMs according to the frequentist framework, we essentially perform maximum likelihood estimation on the joint likelihood of the parameters, θ, and the states, z. The mathematical structure can be illustrated as follows:

$$L(\theta, z_{1:T}|y_{1:T}) = \prod_{t=1}^{T} g(y_t|z_t, \theta_0) f(z_t|z_{t-1}, \theta_p) \tag{10}$$

Where θ_0 and θ_p represent the observation process parameters and the state process parameters respectively. And T representing the length of the time series. To simplify the maximum likelihood process, one would first maximise the marginal likelihood and integrate out the hidden states (z) (Auger-Méthé et al. 2021). Thus, only having to maximise the marginal likelihood with respect to the parameters (θ). The parameter estimates produced from maximising the marginal likelihood have the necessary statistical properties (consistency and asymptotic normality) to estimate the hidden states (Valpine 2012; Douc et al. 2011). One would use the predicted parameters and calculate the conditional distribution of the hidden states given the observations (y) and the estimated parameters ($\widehat{\theta}$). Calculating the maximum marginal likelihood with respect to the parameters is a computationally expensive problem. This is the common pitfall for SSMs in general, for both the frequentist and Bayesian approach (Auger-Méthé et al. 2021).

There are two common methods one can use to evaluate the maximum marginal likelihood. Namely the Kalman Filter and the Laplace approximation method (which approximates the maximum marginal likelihood as opposed to evaluating it).

Bayesian approach

The Bayesian approach takes into account previous information that is summarised into a quantitative model known as the prior distribution (Ellison 2004). Bayesian modelling provides a platform to incorporate external evidence or expert knowledge with evidence presented by the study (Goodman 2005).

Bayesian statistics revolves around Bayes' rule. The Bayes rule is a way to calculate unknown

conditional probability. That is, to calculate the probability of the parameters of a model given the data (Clyde et al. 2021). The mathematical expression of the Bayes Rule is as follows:

$$p(\theta|y) = \frac{p(y|\theta)p(\theta)}{y} \tag{11}$$

Where y represents the observed data and θ represents the model parameters. $p(y|\theta)$ represents the probability of observing the data given a set of parameters (the likelihood) and $p(\theta)$ represents the prior probability of experiencing those parameters (Clyde et al. 2021).

The need to specify priors is considered to be an advantage by some and critisized by others (Dennis 1996). However, if the expert knowledge is sound, it would greatly benefit the model and will lead to more biologically sound outcomes. However, using different priors for the same experiment may yield different conclusions.

Given the criticism of subjective priors (Lele and Dennis 2009), the least controversial way for choosing priors is, therefore, to use non-informative priors as far as possible. However, it is also believed that using only non-informative priors limits the benefits the Bayesian approach has to offer (Banner, Irvine, and Rodhouse 2020).

Besides the use of priors being a contentious topic, the Bayesian approach still holds a vast array of benefits. Hierarchical models are conceptually easier to understand when cast within a Bayesian framework (Kéry and Schaub 2011). Count data is observations that are based on the true population of monitored species. The observations and true population relate to each other in a hierarchical manner and are subject to both observation and process error. Given this hierarchical structure, the Bayesian approach is a more intuitive method to use.

When applying SSMs in a Bayesian context, the main goal is to determine the posterior distribution for the states and the parameters based on data and the prior distributions. The mathematical representation of this approach is as follows:

$$p(\theta, z_{1:T}|y_{1:T}, \kappa) = \frac{L_J(\theta, z_{1:T}|y_{1:T})\pi(\theta|\kappa)}{\int \int L_J(\theta, z_{1:T}|y_{1:T})\pi(\theta|\kappa)dz_{1:T}d\theta} \tag{12}$$

Where $L_J(\theta, z_{1:T}|y_{1:T})$ is the joint likelihood and $\pi(\theta|\kappa)$ is the prior distribution(s). The denominator of equation 12 represents the probability of the data for all possible values of the states and parameters. Equation 12 forms the basic structure of Bayes' theorem as seen in equation 11.

The posterior distribution is the focus in the Bayesian approach. This is most commonly done by

obtaining samples from the posterior distribution, known as a Markov Chain Monte Carlo (MCMC) approach. This is a computationally expensive task that is nearly impossible to do by hand. There are various MCMC algorithms that approximate the posterior distribution. Namely, Metropolis Hastings samplers, Hamiltonian Monte Carlo and the Gibbs sampler, amongst many (Auger-Méthé et al. 2021).

Another important aspect in the Bayesian approach is to apply convergence tests on the MCMC outcome, regardless of the sampler used. Testing convergence ensures that the sampler used, after approximating the probabilistic distribution many times, has converged to a common interval across all MCMC chains. This can often be viewed on a trace plot of MCMC outcomes (Auger-Méthé et al. 2021). A more formal approach would be the Gelman-Rubin metric (Gelman and Rubin 1992), which is a popular metric to measure convergence in an MCMC context.

A Bayesian approach was used to fit the SSM to the data in this study. The model was fit using the Just Another Gibbs Sampler (JAGS) package in R [Plummer (2003); R Core Team (2020); Kellner (2019);]. A Gibbs sampler is an MCMC method that samples variables sequentially from a multivariate distribution while keeping all other variables constant (Coro 2017). The JAGS package uses an internally specified variation of a Gibbs sampler to estimate the model states and parameters. In the immediate case, the probability distribution will take on the form of equation 12 which will be based on equations 5 to 9. Uniform priors were used for all variance variables (α, e, w, ζ and ϵ) and MCMC trace plots and the Gelman-Rubin metric were used to test convergence of the estimated states and parameters.

2.3.2   Model selection

A major drawback for SSMs is the issue of model selection. Model selection for SSM is still an area of active research (Jonsen et al. 2013). SSM model selection becomes difficult as the computation power needed to run an SSM is so large. As a result, ecologists end up using only one SSM model in the study because of limited computational power.

Model comparison methods differ depending on whether the SSM is conducted in a Frequentist framework or a Bayesian framework. The most used model selection method for a frequentist SSM is the Akaike Information Criterion (AIC). The AIC is a popular model selection method in many statistical models. The AIC measures how well the model fits the data and penalizes models with a higher number of parameters. AIC, however, does not work well for SSMs, even in a frequentist framework, for various reasons (Auger-Méthé et al. 2021).

For SSMs in a Bayesian context, AIC is not well defined (Hooten and Hobbs 2015). There are 3 notable model selection methods used for Bayesian SSMs. These are the WAIC, DIC and BIC. Many sources of literature have proven DIC and BIC to not be very good at all in Bayesian model selection (Auger-Méthé et al. 2021; Gelman, Hwang, and Vehtari 2014; Hooten and Hobbs 2015). Sources have found WAIC to be more effective than DIC and BIC, even though it still fails in many cases (Gelman, Hwang, and Vehtari 2014). The method most of the literature agreed upon was a cross validation method. In this cross-validation method, the SSM would be fit with a training set of the data, while an unused subset of the data (the test set) is used to determine the effectiveness of the SSMs forecasting ability. The SSM that forecasts values closest to the corresponding test set values is then considered the "best" model. This method works well but has its limitations when data is sparse. In the case of sparsity, splitting the data into a training and test set becomes difficult as the training set may not be sufficient to produce an accurate model. Furthermore, splitting time series data into training and test set becomes difficult because of the serial dependence between the data points.

Yoccoz (1991) and Cox et al. (1977), state that, at times, ecologists tend to overemphasize the use of statistical measures for model selection and fail to prioritise biological or ecological factors. Given the contentious issues regarding model selection for SSMs, it is beneficial to choose the SSM that is based on sound ecological fundamentals rather than contentious model selection statistics. More time and effort should be focused on the modelling process and ensuring the correct ecological processes are modelled into the SSM.

The model selection process in this study was based on ecological background and knowledge rather than traditional model selection metrics for SSMs such as DIC, AIC or WAIC, thus following the philosophy of Cox et al. (1977) and Yoccoz (1991). This approach was also used given that the sparsity and dependent nature of data inhibited the ability to create training and test sets for cross-validation.

2.4   Biodiversity Indicators

There are multiple different ways one can formulate biodiversity indices. The first, and main task, however, is to identify what must be monitored and how (Yoccoz, Nichols, and Boulinier 2001). In the South African wetland's context, one would want to monitor species that directly reflect changes in the ecosystem. In other words, it follows the pressure – state – response causal change (Niemeijer and Groot 2008). As discussed in the introduction, species like the Great Crested Grebe (eutrophication level indicator) and Red-Knobbed Coots (siltation rate indicator) provide known

causal links to environmental changes.

Biodiversity is an important aspect of any ecosystem (Duffy 2009) and subject to large scale conservation efforts such as the Aichi convention. Biodiversity has many definitions. According to Magurran (2013), biodiversity is the "variety and abundance of species in a defined unit of study". Buckland et al. (2005) defines biodiversity as how the abundance is distributed across species, otherwise known as evenness. Evenness refers to the level of homogeneity of the ecosystem, regarding its species. For example, if an ecosystem contains 5 different bird species, with each bird species containing an equal number of individuals, then that ecosystem's bird population would be displaying perfect evenness. Whereas, if the ecosystem contains one or two dominant bird species then it would be displaying an uneven bird population. The research thus exhibits two different types of indicators that reflect the state of a wetland. Ones to monitor the variety of waterbirds in a wetland and one to monitor the abundance of waterbirds in a wetland.

The two most common indices used to measure population abundance and evenness is the exponentiated Shannon's entropy and the Simpson's index, respectively. The Shannon's entropy obtains a value that describes the entropy of a community. According to Jost (2006), this entropy measure should ideally be transformed to obtain a true diversity measure. This is done by taking the exponent of the entropy. By doing so, one transforms the Shannon's entropy to a true measure of diversity which is also defined by Jost as the effective number of species in a community. The Simpson's index need not be treated the same as its output is already an index value. The Simpson's index presents a value between zero and one with 1 representing perfect evenness and values closer to 0 representing a more uneven population.

Abundance Index

A popular population abundance index is the Living Planet Index (LPI) that is designed to track changes in population sizes over time. The LPI is used as an aggregated abundance index. It calculates the percentage change from a reference year (1970) to all subsequent years. This is done by averaging the rate of change (from reference year to current year) across all species of a species group (McRae, Deinet, and Freeman 2017).

A criticism of the LPI is that it tends to over represent birds and mammals and temperate realms as they are more intensely monitored (Collen et al. 2009). In response, the LPI was modified to include a proportionally weighted index (McRae, Deinet, and Freeman 2017). The weighted LPI tackles the problem of taxonomic and geographical bias. The weighted LPI is applied to the problem of bias that presents itself on a global level.

The LPI is calculated as follows:

$$\overline{d_t} = \frac{1}{n_t} \sum_{i=1}^{n_t} d_{it} \tag{13}$$

Where $\overline{d_t}$ is the average annual trend if there were multiple population time series of the same species. n_t refers to the number of populations. d_t is the annual rate of change for a population at time t, given by:

$$d_t = log_{10}(\frac{N_t}{N_{t-1}}) \tag{14}$$

Here, N_t refers to the population at year t.

The LPI is conducted using two different methods. One being the LPI-U (unweighted LPI) and the LPI-D (proportionally weighted LPI). In the LPI-U, the data is divided into 6 subsets. Based on region (tropical or temperate) and three realms (terrestrial, freshwater and marine). The index for each system is calculated by averaging the species trends within each system. The systems being (tropical terrestrial, tropical freshwater, temperate terrestrial, etc.). The index for each region (tropical or temperate) is then calculated by averaging the trends for each system. The tropical and temperate trends are then averaged to form a global trend which is converted into an index as follows:

$$I_t = I_{t-1} * 10^{\overline{d_t}}, \quad I_0 = 1 \tag{15}$$

Where $\overline{d_t}$, in this case, is the average trend within a region, realm, system or globally.

The LPI-D approach is similar. Only it applies proportional weights to species when averaging the trends. For example, if birds represent 43.3% of terrestrial vertebrate species in the Palearctic realm, then this value is used in weighting the bird species when calculating the weighted average of the Palearctic realm trend for terrestrial species. The mathematical representation is as follows:

$$\overline{d_{t,realm.region}} = \frac{1}{N_t} \sum_{j=1}^{N_t} d_{jt} w_j \tag{16}$$

Where d_t is the average trend of a given realm and region. N_T is the number of taxonomic groups within a realm, d_{jt} is the average trend of taxonomic group j at time t and w_j is the proportional weighting of that taxonomic group (0.43 according to the previous example).

Understanding waterbirds population change over time in South African wetlands can tell us a lot about the wetland. As discussed previously, some species populations may indicate certain wetland

characteristics such as eutrophication levels and siltation rates. Monitoring the combined number of waterbird species can indicate when there are sharp declines or increases in species abundance. These sharp turning points could indicate that the wetland is changing in some way and thus alert wetland managements to further assess the wetland and take necessary action.

A modified LPI approach was used to form an abundance indicator in this study. The modified LPI used calculates percentage change from each year to the next for a trait specific group of waterbirds.

The modified LPI calculations were applied to the mean summer population posterior value, per year, estimated by the state-space model. The SSM was first applied to each species in a trait specific group separately. The percentage change for each year was calculated for each species, then the average percentage change across all species in the group was calculated, per year. The calculations used are as follows:

$$d_t = \frac{\mu_t - \mu_{t-1}}{\mu_{t-1}} \tag{17}$$

Where d_t is the population percentage change at year t for a single waterbird species and μ_t is the mean value of the true summer population at time t, obtained from the state-space output (see equation 5). The average percentage change per year, for a trait specific group, was calculated by taking the average d_t across all waterbirds in the trait specific group per year. The mathematical representation is as follows:

$$\overline{d_{tg}} = \frac{1}{N} \sum_{i=1}^{N} d_{ti} \tag{18}$$

Where $\overline{d_{tg}}$ is the average population percentage change for trait group g at year t. N is the total number of waterbirds in group g. d_{ti} is the percentage change of species i at year t.

Unlike the LPI, it does not convert the percentage change to an index value. Converting percentage change from a reference year to an index value resulted in high levels of uncertainty in the index value. Using percentage change only was still subject to high levels of uncertainty but less than if it were converted to an index value after.

It would be technically possible to produce credible intervals for the modified LPI if it were applied to the whole posterior distribution. As it would propagate the error around the species-specific population trends. However, when attempted, the credible intervals produced are too wide to be of any use. This is partly because the SSM assumes that the observation errors are independent when

in fact all species were counted during the same survey. Incorporating the observation process more realistically could help solve this problem but was beyond the scope of this report. As a result the bioindicators used in this report were applied to the mean values of the posterior distribution.

The modified LPI can be applied to any groupings of waterbird species. One could group the waterbirds based on different traits and calculate the percentage change per year on that specific group. The waterbirds could be grouped together based on traits such as habitat, body size, brood size, food type, etc. For this report migrant status, nest site and the number of different foraging sites used by a waterbird were used as examples of how the modified LPI can be used for trait specific groups (figure 4 and 5).
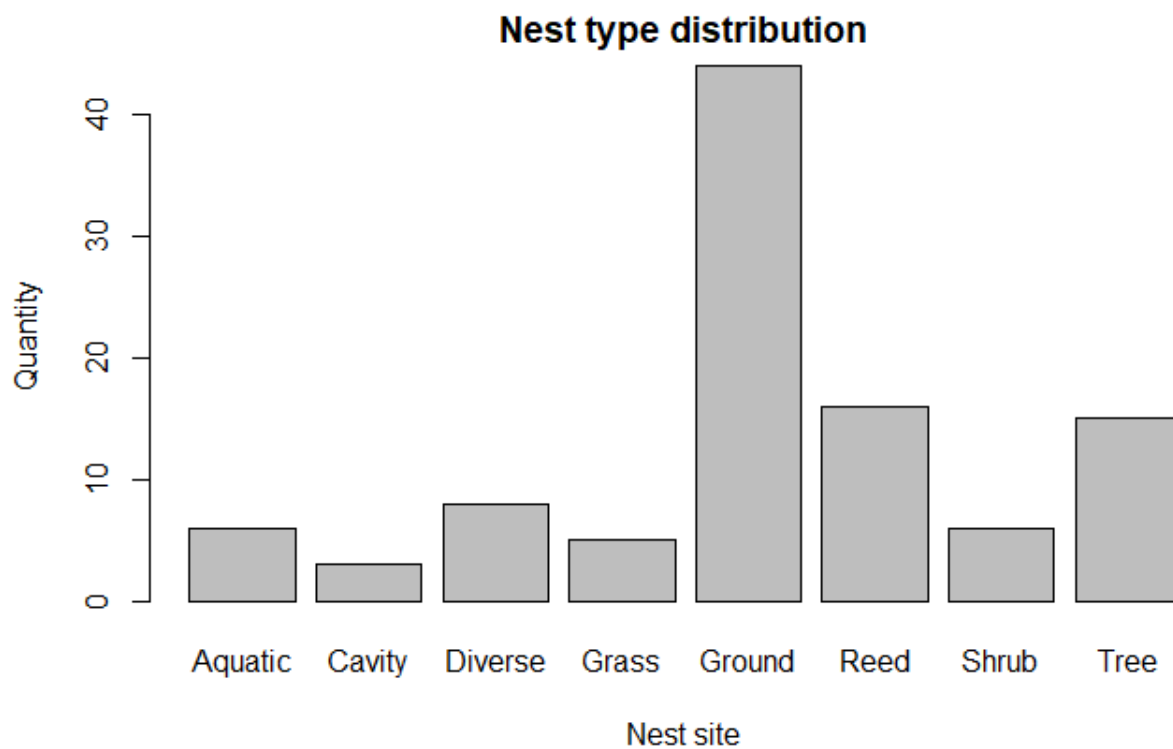
Figure 4: Number of species that use each nest site type

Number of foraging type distribution
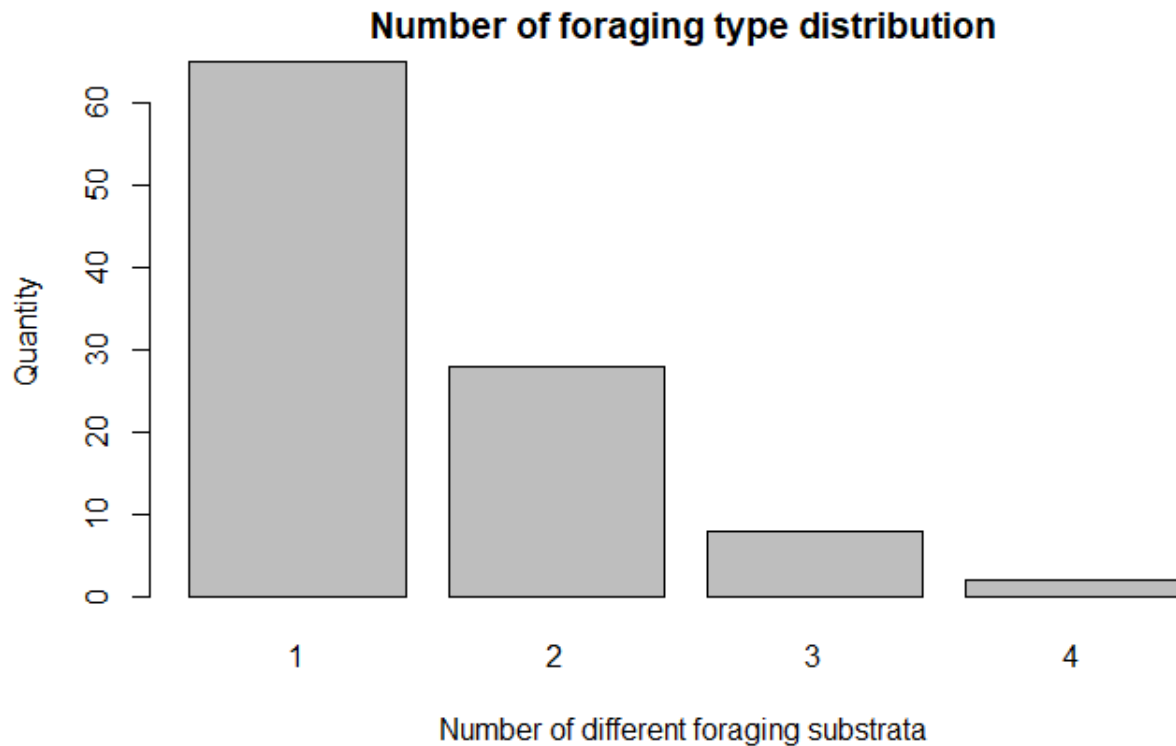
Figure 5: Quantity of species that make use of one, two, three or four different types of foraging sites

The majority of species in Barberspan nest on the ground. These nests are commonly built by creating a depression in the ground lined with grass or feathers. 44 different waterbird species predominantly build their nest on the ground. 16 different species build their nest in the reeds and 15 species use trees to nest. The cavity, grass, aquatic and shrub nest type are attributed to the fewest species (20 different species in total).

There are five different foraging sites represented in the above plot. These sites are: aquatic, ground, off-ground, aerial and mud. Most species in Barberspan only make use of one of these sites (65 different species). 28 different species utilise at least two different foraging sites and only 10 species utilise 3 or more foraging sites.

The modified LPI used in this report was applied to each of the groups represented by the above plots. For each group the SSM was applied to the combined counts of that group. The SSM was then applied to each individual species of the group and the average percentage population change, per year, was calculated across all species in the group to determine the annual percentage population change for the group.

Diversity indices

22

The diversity of species in an ecosystem is a very important aspect of a healthy ecosystem (Duffy 2009). Richer species diversity, or higher levels of evenness, is indicative of a healthy ecosystem (Hooper et al. 2005). Quantifying diversity has been a contentious measure in ecology (Peet 1974). The literature emphasizes that diversity is dependent on the research questions and the task at hand and there is no universally agreed upon definition of what diversity is (Hurlbert 1971).

In the context of this report, which focuses on South African wetlands and waterbirds, the aim is to monitor the biodiversity of the waterbird species in a wetland over time. The popular indices used to measure species biodiversity is the Shannon Entropy and the Simpson Index. There have been studies aimed at finding the best index for species diversity. The result being that one can't identify one all-encompassing index, but using a few together gives one a better overview of the ecosystem (Morris et al. 2014).

The closest framework there is to an all-encompassing diversity index is the Hill Numbers model (Hill 1973). The Hill Numbers framework provides a range of measures of the effective number of species in a system. Each one differing in their propensity to add more, or less emphasis on the rarer species. The Hill Numbers general formula is as follows:

$$N_\alpha = (p_1^\alpha + p_2^\alpha + \ldots + p_n^\alpha)^{\frac{1}{1-\alpha}} \tag{19}$$

Where N_α is the diversity number of order alpha. These diversity numbers reflect an estimate of the effective number of species present in a sample. The p's refer to the proportions of species in the sample and n represents the number of species in the sample. The most commonly used values for alpha are 0, 1 and 2. N_0 refers to the number of species in a sample. N_1 results in an exponent $\frac{1}{1-1}$ but, according to Hill, the N_1 diversity number approximates to the exponential of the Shannon's Entropy (proof is supplied by Hill). The more general formula for the Shannon Entropy is as follows:

$$x = -\sum_{i=1}^{S} p_i ln(p_i) \tag{20}$$

Where x is the index, p_i is the proportion of species i in the sample and S is the number of species in the sample.

N_2 is the inverse Simpson's Index. The more common general formula for the Simpson's Index is as follows:

$$x = \sum_{i=1}^{S} p_i^2 \qquad (21)$$

Different indices measure different aspects of diversity (Hill 1973). The Simpson's Index is more sensitive to the abundance of common species in an ecosystem. For this reason, it is also referred to as the measure of dominance concentration. Whereas the Shannon entropy index measures the entropy of an ecosystem (Jost 2006).

According to Jost (2006), the problem with some diversity indices is the way in which researchers use them. For example, the Shannon's entropy index is not a diversity measure but rather a measure of entropy in the ecosystem (Jost 2006). Thus, it becomes more intuitive and easy to work with when converted to a true diversity (effective number of species in an ecosystem) before any comments can be made regarding evenness in the ecosystem. Jost, uses the example of other fields such as physics, economics and information theory. It's common practice in all these fields to convert entropy values to the effective number of elements in a system instead of reporting on the entropy index value. One simply needs to exponentiate the Shannon Entropy value to determine the effective number of species in the ecosystem.

The Simpson's index can be used without any conversion as it already is an index value and is immediately intuitive and easy to use without any conversions. As a result no transformations were made on the Simpson's index in this report. The Simpson's index is a measure of dominance with values ranging from 0 (lowest level of evenness) to 1 (highest level of evenness) and can be used directly to determine dominance in an ecosystem without any conversion.

Further problems are addressed regarding diversity indices in ecology. Measuring diversity in a system has many differing semantic and technical aspects. Given the different aspects of diversity, and the plethora of possible indices to measure them, some have argued that diversity measures are a "nonconcept" (Hurlbert 1971). However, given the variety of measures one can use, the issue is perhaps not the indices but how to choose which ones to use.

The best way to use diversity indices is to use various indices simultaneously (Whittaker 1965), as each index can tell the user different aspects of the diversity in the system. In terms of the Shannon entropy and Simpson index, the Shannon entropy, when converted gives a value of the effective number of species in an ecosystem while The Simpson index tells the user about the dominance concentration of the ecosystem. The Simpson's index will also be able to identify species over-population in an ecosystem.

Biodiversity has many definitions and applications. The use of more than one biodiversity indicator is important to cover as many aspects of biodiversity as possible. This gives the user a more complete understanding of the wetland and waterbird state. This is the reason three different biodiversity indicators were used in the report. When a user analyses these indices in conjunction with one another they are able to see a more clear picture of waterbird and wetland state.

3 Results

The first and foremost objective was to develop and fit a relevant State Space Model to the waterbird counts in the Barberspan wetland. The model discussed in the methods section was developed and fitted using the JAGS framework in R. This model was able to account for seasonal fluctuations in the count data. This applies specifically to the palearctic and intra-African migrants. The same model was applied to the resident species to fit potential seasonal patterns caused by the observation process.

The model was applied to 69 resident species and 34 migrant species. The model was applied to each individual resident and migrant species and then to the summed resident counts and summed migrant counts. Applying the SSM to the combined counts gives an overview of the population dynamics of the Barberspan wetland. When applied to individual species, it provides a more in depth analysis of the population dynamics on the species level. This is done with the user in mind. It is important to display as much information as possible for the user. Displaying only aggregated metrics often hides finer details that may be of importance.

3.1 State Space Model Output

The SSM was applied to the combined counts of resident species and then applied to the combined migrant species. The SSM models two time series, one for summer and one for winter. Figure 6 and 7 displays the output of the SSM on the combined waterbird counts at the Barberspan wetland.

Figure 6: SSM output applied to the combined resident counts at Barberspan wetland, separated by season. The grey area surrounding the black dotted line is the 95% credible interval around the mean true population produced by the MCMC output.
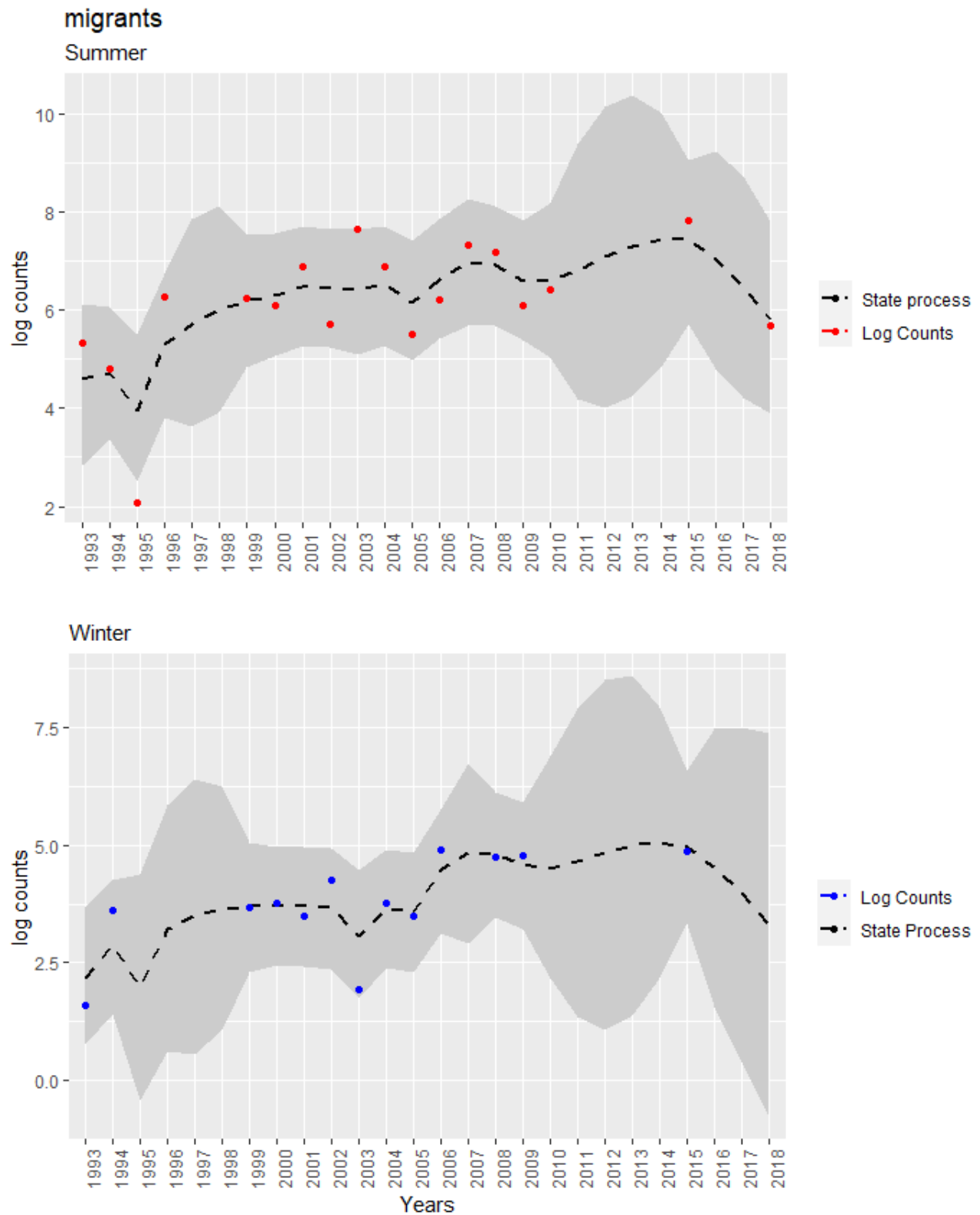
Figure 7: SSM output applied to the combined migrant counts at Barberspan wetland, separated by season. The grey area surrounding the black dotted line is the 95% credible interval around the mean true population produced by the MCMC output.

Both models exhibit no sign of significant change over time. The migrant population seems to increase gradually from 1993 till around 2014. After which it experiences drop in counts. The resident summer population, on average, displays a positive rate of change over time. The average rate of change for the migrant population is [-1.23, 1.28]. The model only focuses on rate of change in the summer counts and models the winter counts as the proportion of species that remain from summer. The average rate of change for the resident population is [-1.19, 1.32].

Appendix B shows the state space models applied to the individual waterbird species. When considering average trends from 1993 to 2018, 38 out of the 69 resident species analysed in Barberspan show positive trends. The other 31 exhibit negative trends. However, none of these trends are statistically significant. The 4 bird species showing the strongest increasing trends are the Southern Pochard, Black-necked Grebe, White-faced Duck and the Common Moorhen. The four strongest decreasing trends are attributed to the African Jacana, White-Backed Duck, Maccoa Duck and the Marsh Owl.

The migratory species display more negative trends than positive. 26 out of the 34 analysed migratory species exhibit decreasing trends while only 8 display positive trends. The Hottentot Teal, Common Greenshank, Common black-headed GUll and the Marsh Sandpiper are the 4 species with the strongest negative trend. The Whiskered Tern, Little Stint, Curlew Sandpiper, Common Sandpiper, Common Ringed Plover, Ruff, Squacco Heron and Black Crake are the only migrant species in Barberspan that display a positive trend.

It is interesting to note that when the model is applied to the combined migrant counts, a positive average rate of change is seen. This shows how aggregating species count data can hide important aspects at the individual species level. This is one of the criticisms of indices that are based on species aggregation such as the Living Planet Index (LPI) (Ritchie and Roser 2021). The LPI tends to be very sensitive to sharp population increases or decreases. For example, if 2 out of 5 waterbirds increase drastically while the other 3 decrease gradually; the LPI will aggregate the trends in such a way that it will indicate a sharp increase for all 5 species which is misleading (Ritchie and Roser 2021). To create an effective data dashboard (as the BIRDIE project aims to do) it's essential to have information on individual species and information on an aggregated level.

3.2   Abundance Indices

Dispite the crticism of abundance indices such as the LPI, it is still the most popular abundance index. The LPI was developed to track global species population change over time (Collen et al.

2009). This was in response to the Convention on Biological Diversity targets set out in 2010, which aims to reduce the loss of biodiversity on the planet. Due to the popularity of the LPI, a modified LPI was used in this report to track aggregated population change over time for the waterbirds.

The modified LPI has been applied to the resident and migrant waterbirds separately. The output is seen in figure 8.
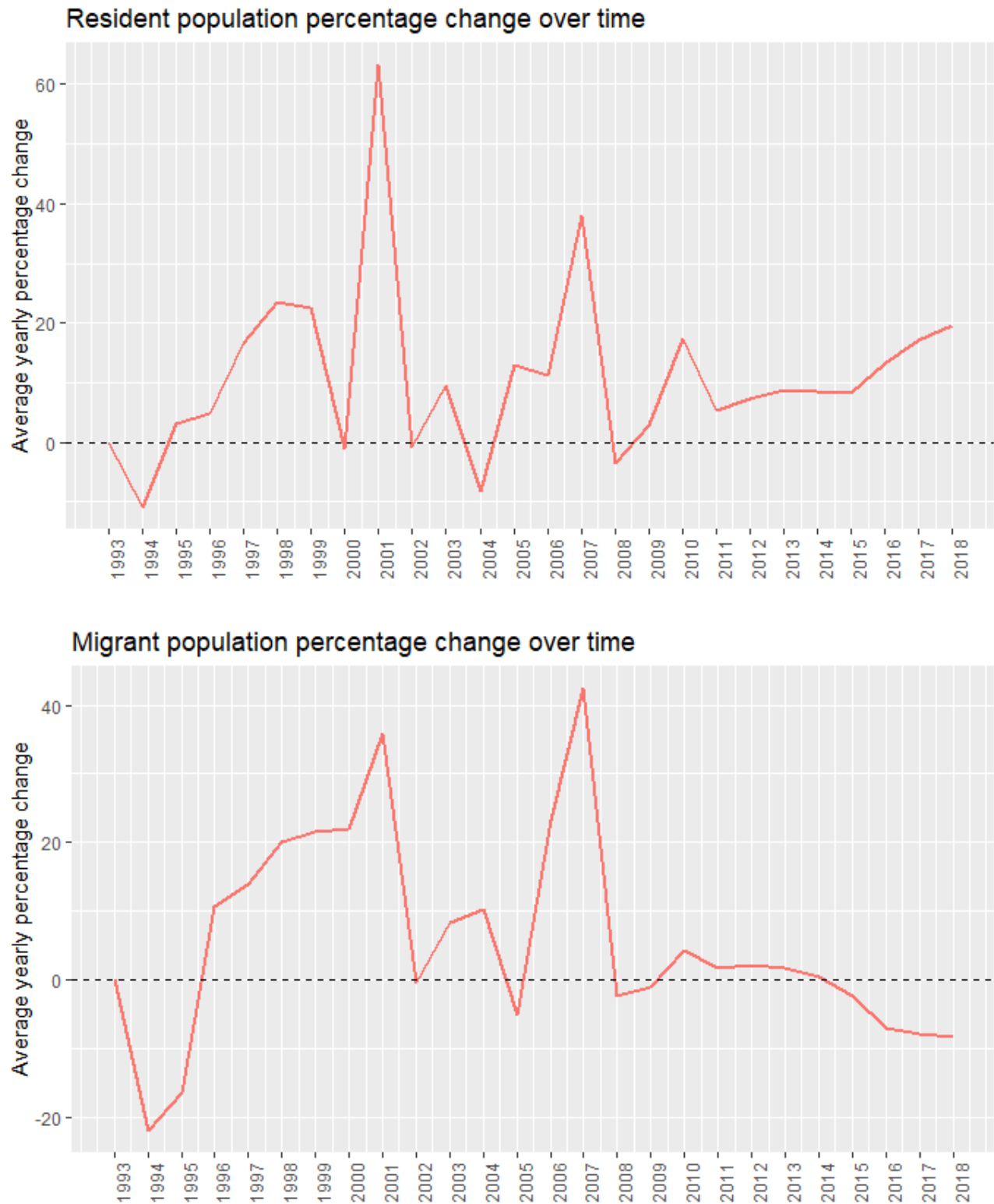
Figure 8: Average yearly percentage change for resident and migrant waterbirds at Barberspan wetland based on trend estimates produced by a state-space time series model.

The uncertainty produced for the modified LPI was unreasonably large when applied in JAGS.

Therefore, only the mean population counts obtained from the MCMC output was used to calculate the yearly percentage increase. The average yearly percentage increase, displayed by the modified LPI, displays only minor changes in the resident and migrant populations over time. This agrees with the modelled counts produced by the SSM. The migrant population has an average yearly percentage increase of 5.81%. The resident population has an average yearly increase of 11.71%. The positive percentage change for the residents and migrants again agree with the SSM output of the summer counts. Both resident and migrant summer counts show slight positive trends.

The benefit of this abundance index is that it can be applied to groups of species and present an aggregated rate of change for that type of species. Currently the focus has been on migrant and resident species but other waterbird traits can also be taken into account. Different species traits may result in different population trends for those species. Therefore, a certain amount of disaggregation is necessary to account for more specific species traits. Two further traits have been taken into account in this study. Namely, nest site and foraging substratum.

3.2.1   Nest Site Trait

Eight different nest sites were considered. Namely, aquatic, cavity, grass, ground, reed, shrub, tree and diverse. The SSM was applied to each individual waterbird species in each group. The percentage change was averaged across species in the group to determine aggregated percentage change of that group. The plots showing the abundance indices for each of the nest site traits and the SSM output applied to the combined counts of each group are displayed in figure 9-16.
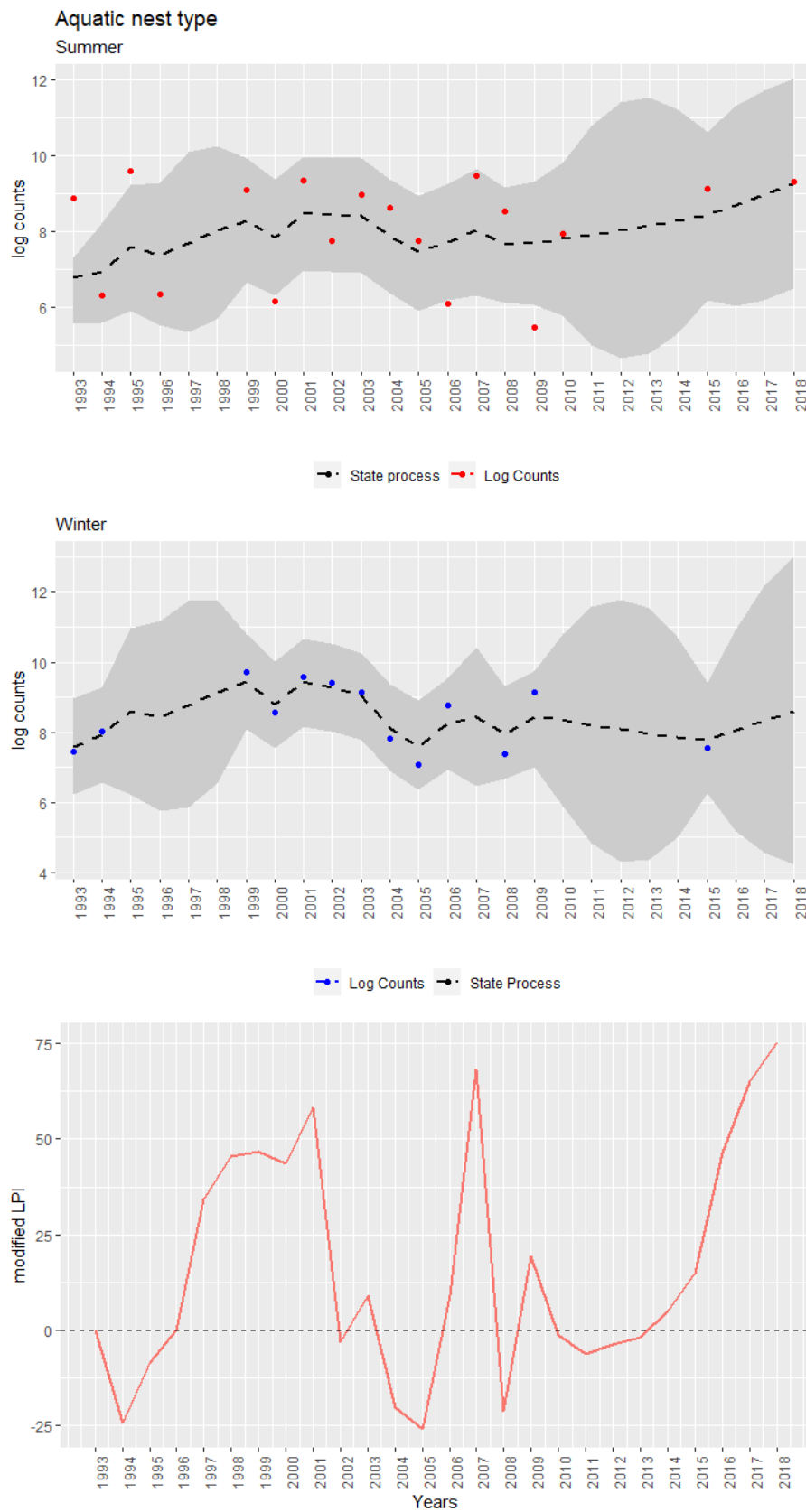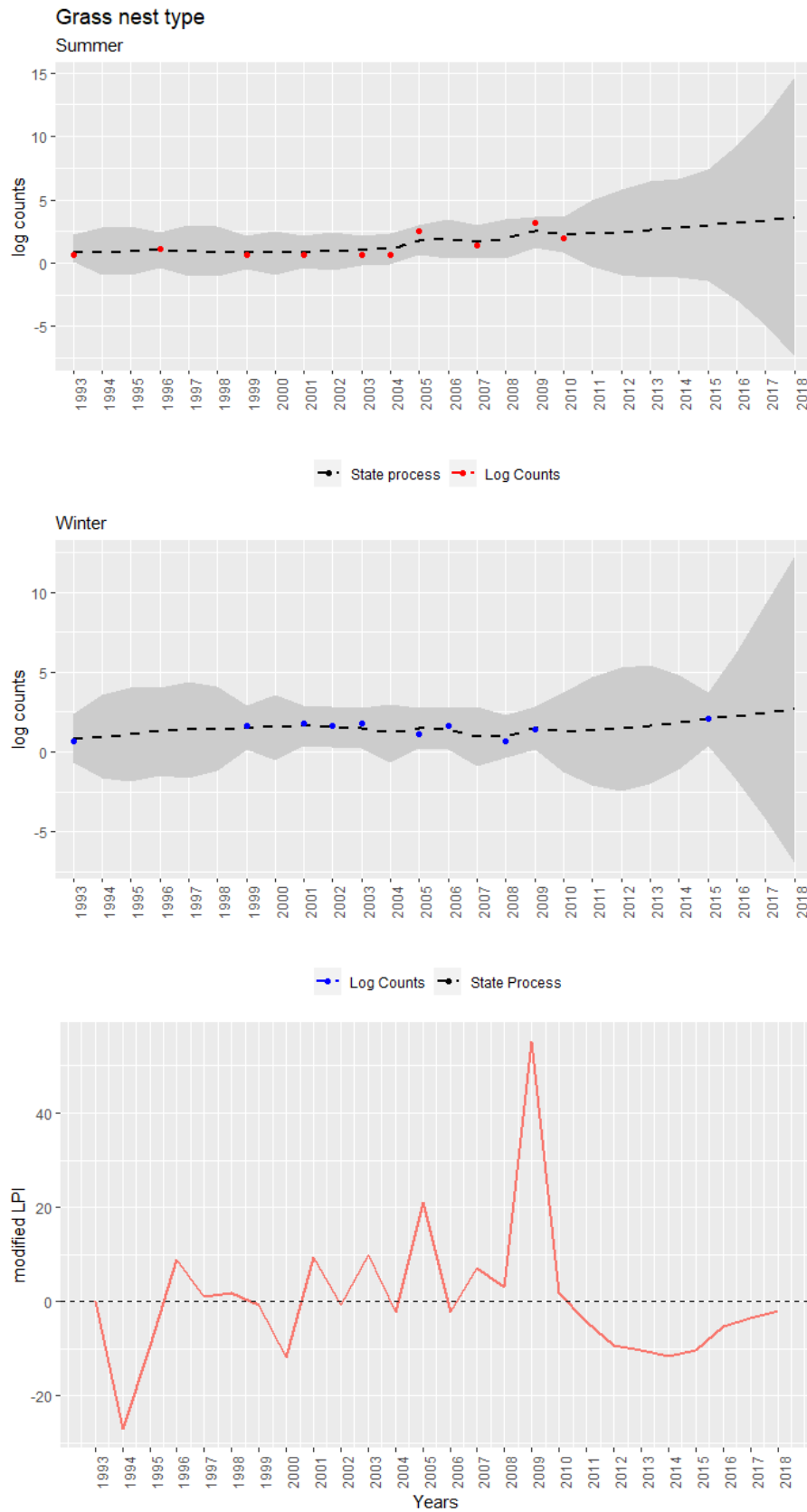
Figure 9: The first two plots is the SSM output applied to the combined counts of the waterbirds that nest in an aquatic environment, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.
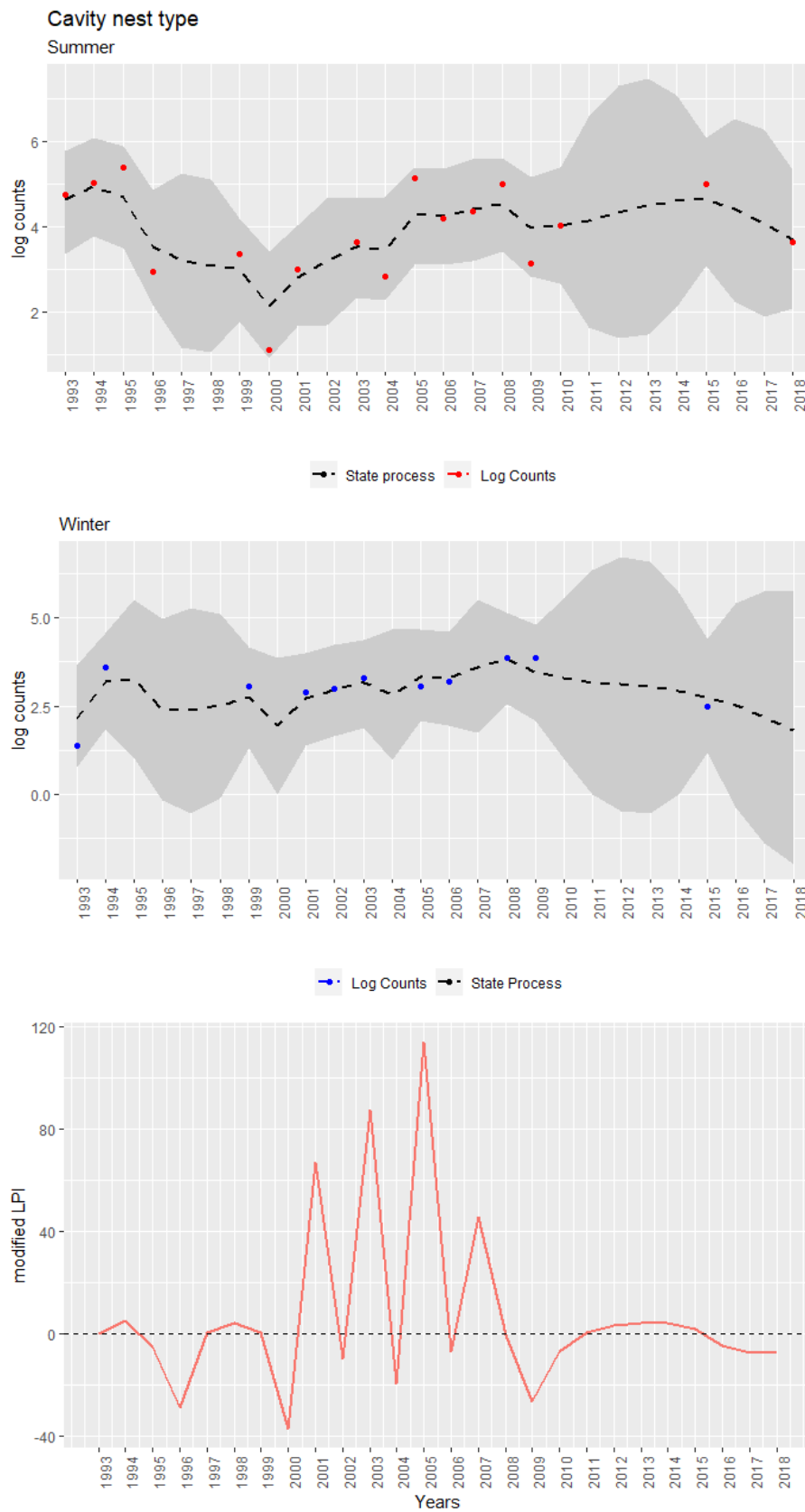
Figure 10: The first two plots is the SSM output applied to the combined counts of the waterbirds that nest in cavities, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.
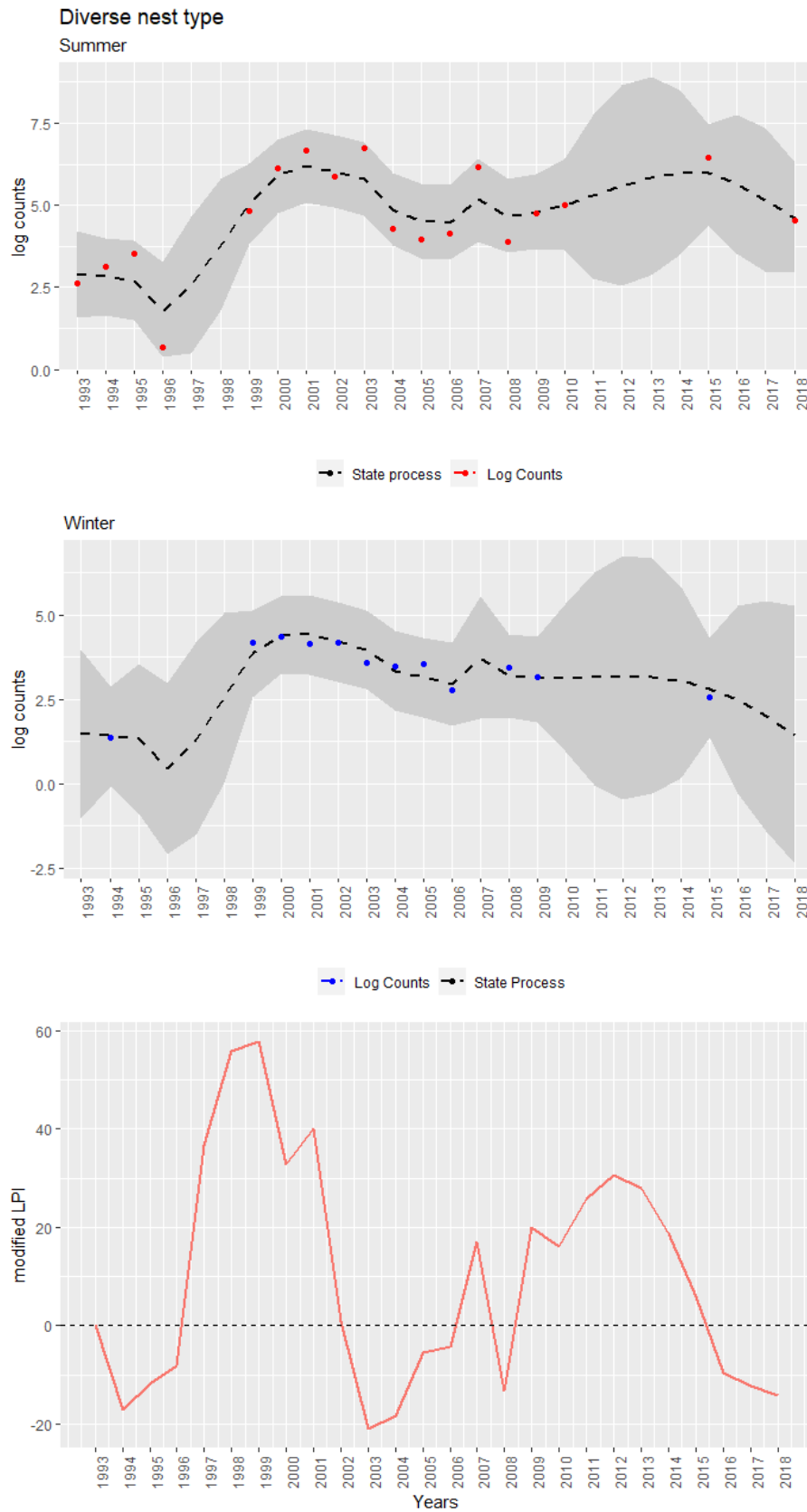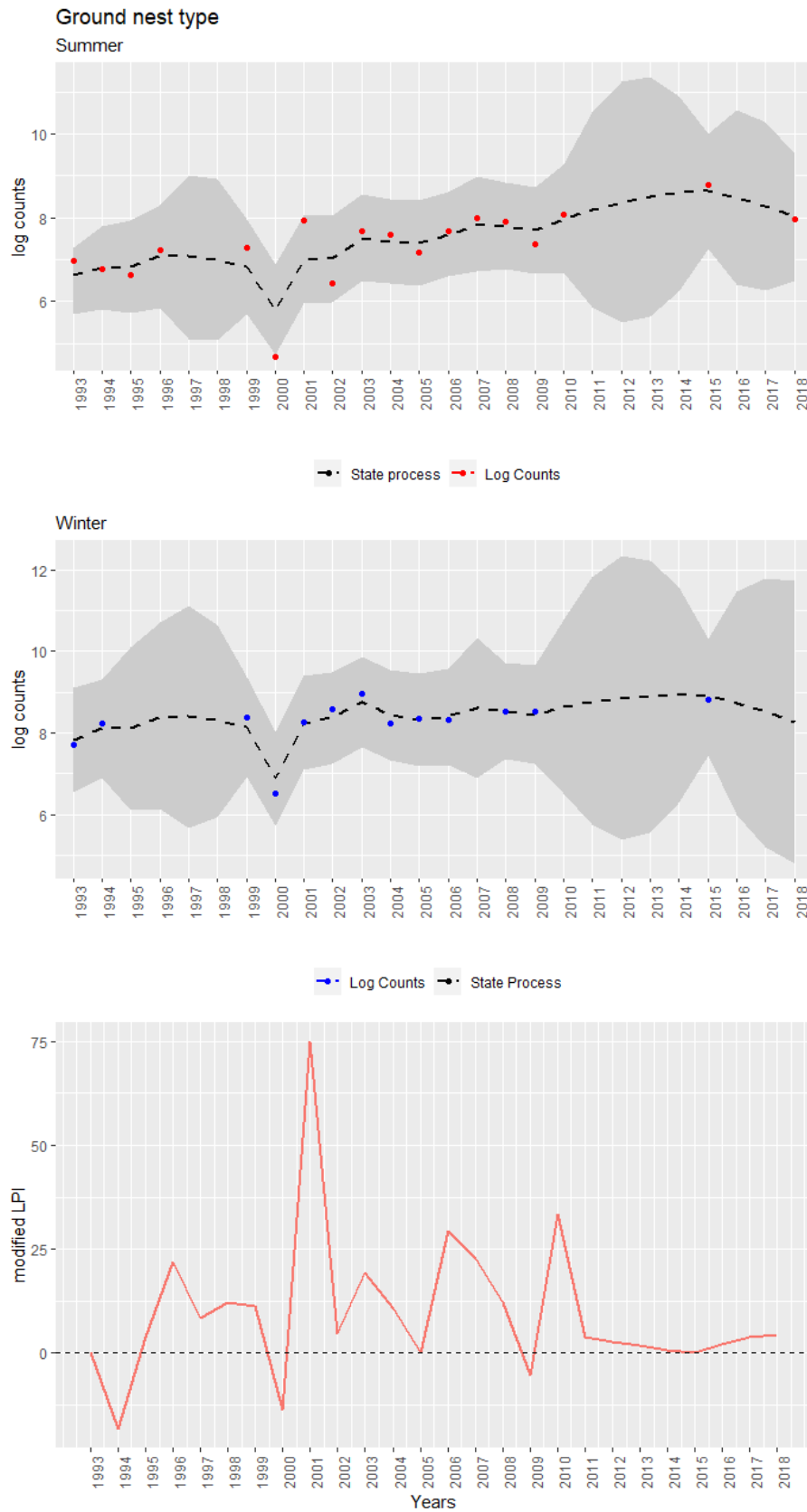
Figure 11: The first two plots is the SSM output applied to the combined counts of the waterbirds that make their nests in diverse environments, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.
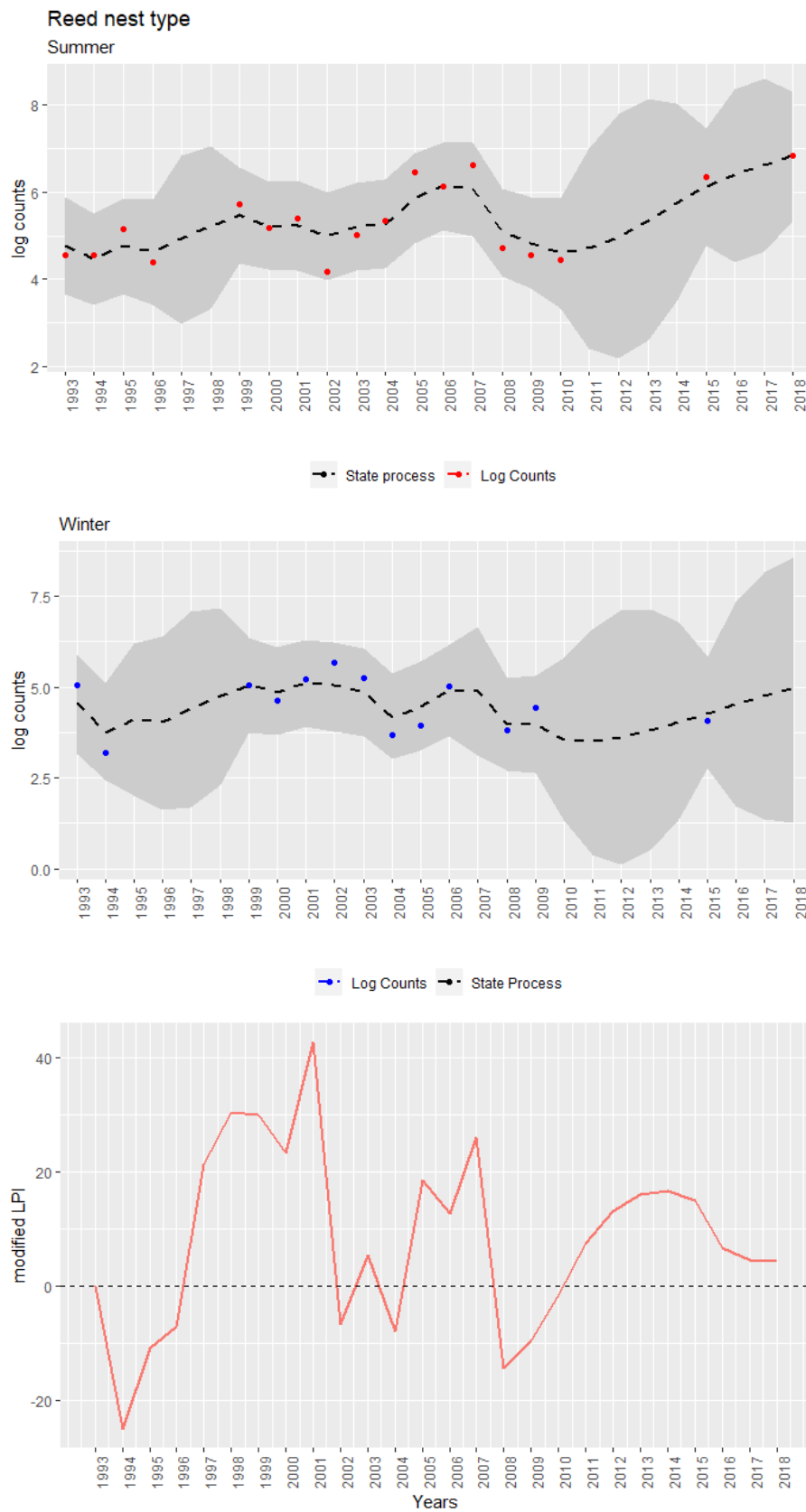
Figure 12: The first two plots is the SSM output applied to the combined counts of the waterbirds that nest in grassy environments, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.
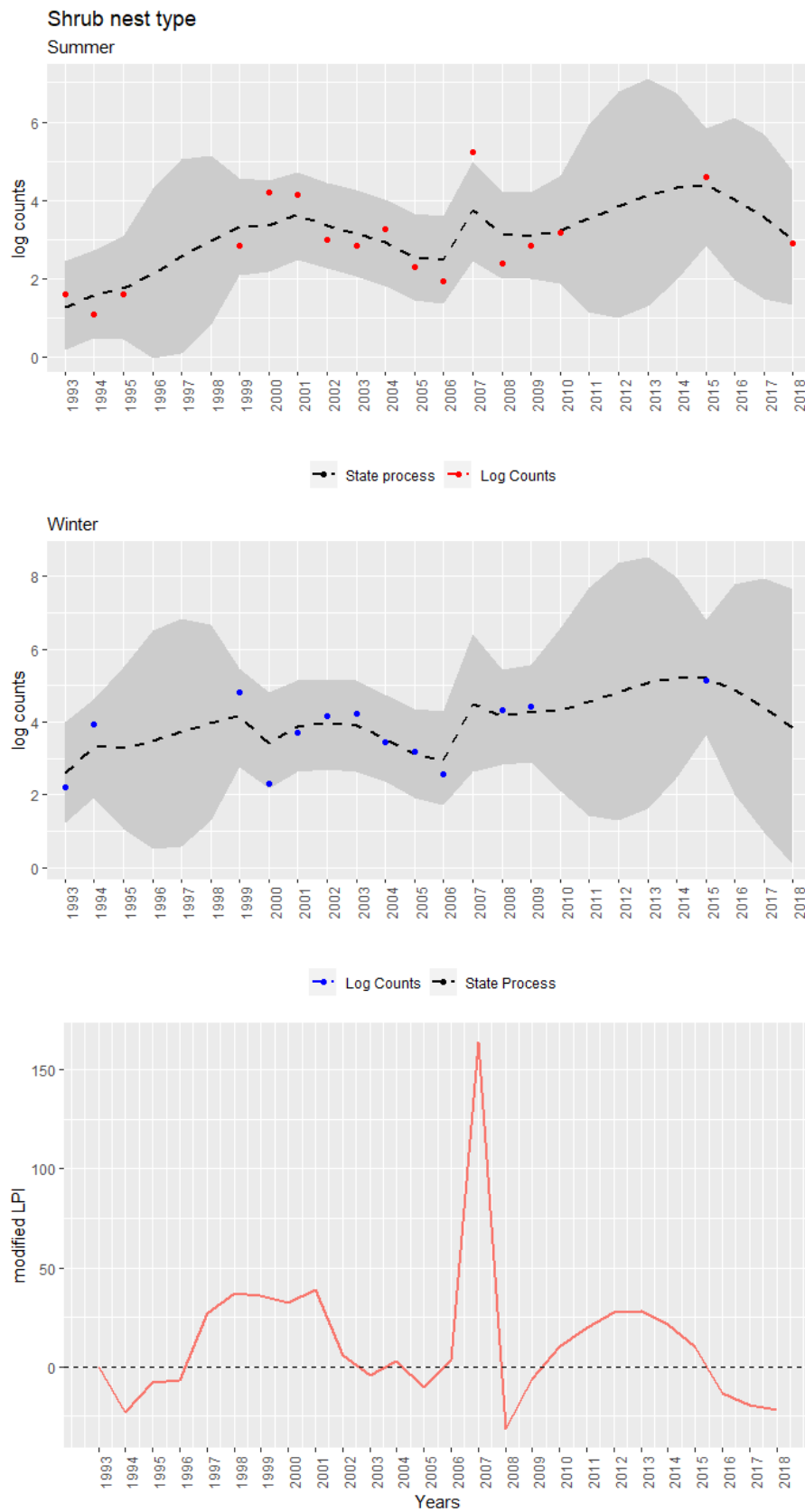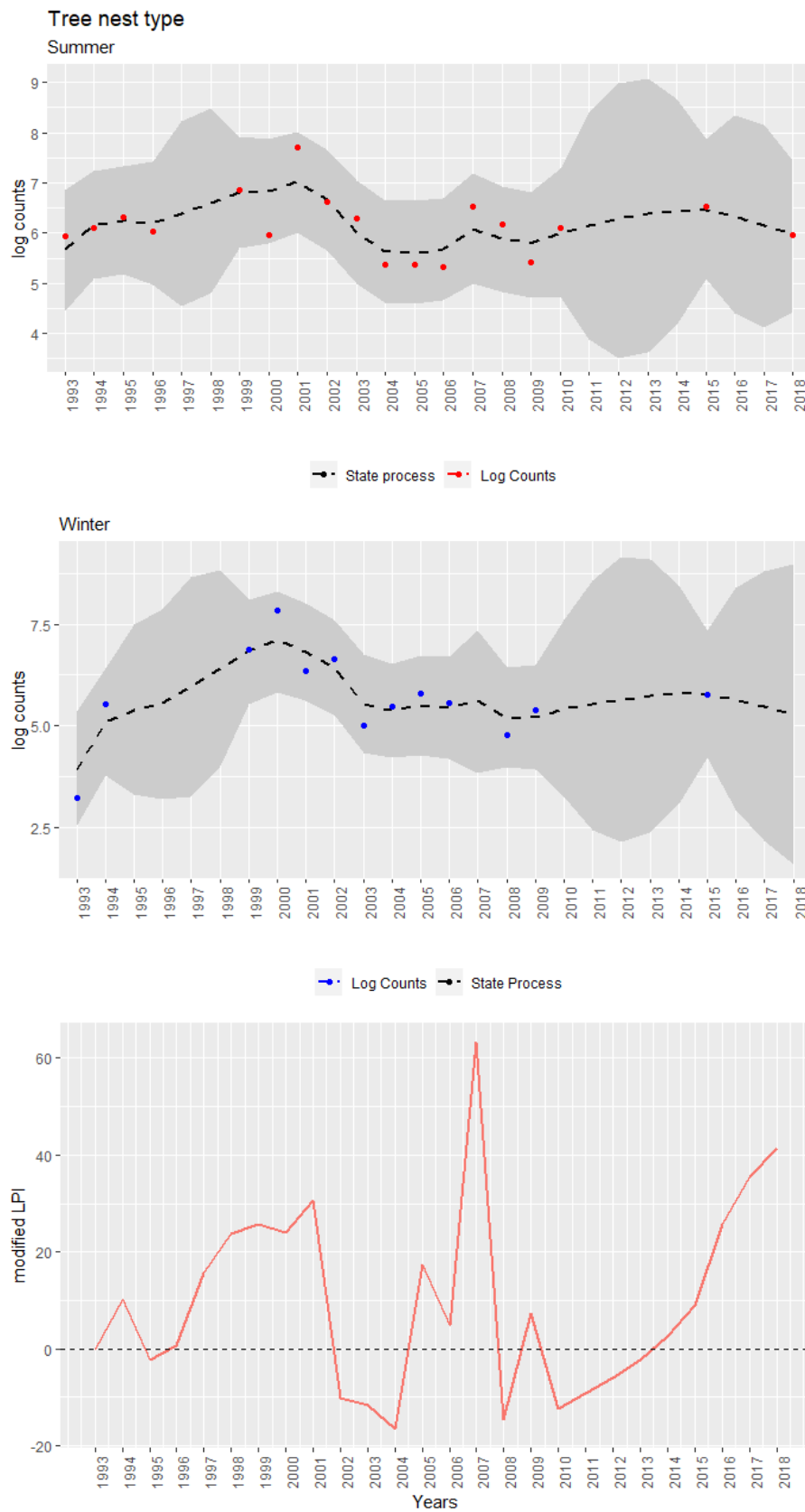
Figure 13: The first two plots is the SSM output applied to the combined counts of the waterbirds that nest by creating recessions in the ground, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.

Figure 14: The first two plots is the SSM output applied to the combined counts of the waterbirds that make their nests amongst the reeds, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.

Figure 15: The first two plots is the SSM output applied to the combined counts of the waterbirds that nest in shrubs, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.
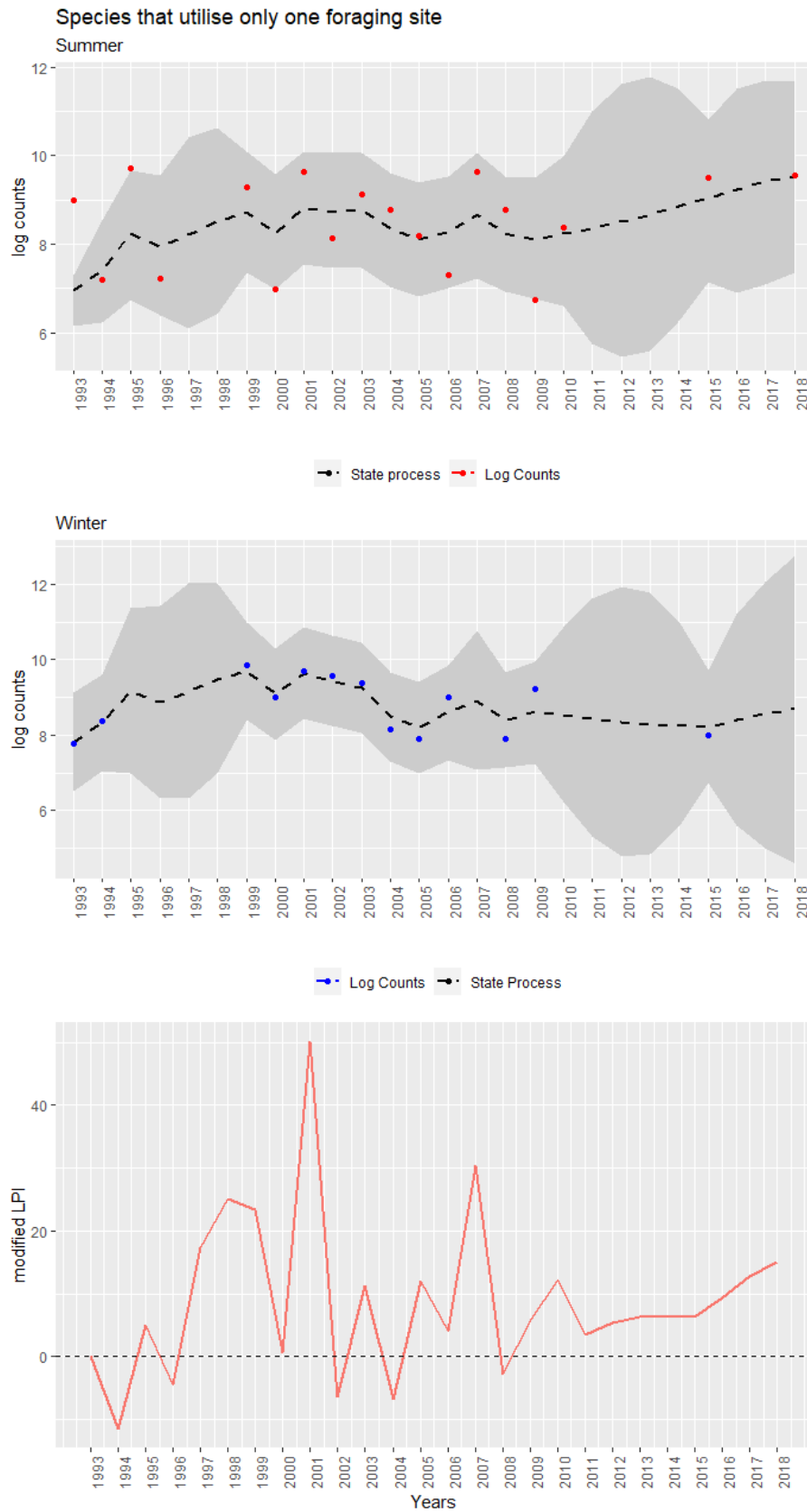
Figure 16: The first two plots is the SSM output applied to the combined counts of the waterbirds that nest in trees, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.

All nest site traits show a positive yearly increase on average. The species with the aquatic or shrub nest type showed the greatest yearly percentage change with an average yearly increase of 16.86% and 12.70% respectively. The species with the grass nest site increases the least with a yearly average of 0.35%. All these values are subject to high levels of uncertainty, as discussed previously. However, there is still very little evidence to show that the nest site of a waterbird negatively affects their population.

3.2.2 Foraging Site Trait

There are 5 different foraging sites used by the waterbirds in Barberspan. Some species use only one site type such as the wader species that often only forage in an aquatic environment. Other species show more diversity in their foraging such as the Cape Wagtail which forages on ground, off-ground, in mud and in aquatic environments. There are many different combinations of foraging sites across the waterbird species. The abundance index was thus applied to species groups based on how many different foraging sites they utilise. Most species only exhibited one foraging substratum but some exhibited 2, 3 or 4 different foraging substrata.

The abundance index was applied to each group the same way as it was applied to the nest site groups. Figure 17-20 shows the abundance index for each foraging site group and their combined counts.

Figure 17: The first two plots is the SSM output applied to the combined counts of the waterbirds that utilise only one foraging site, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.
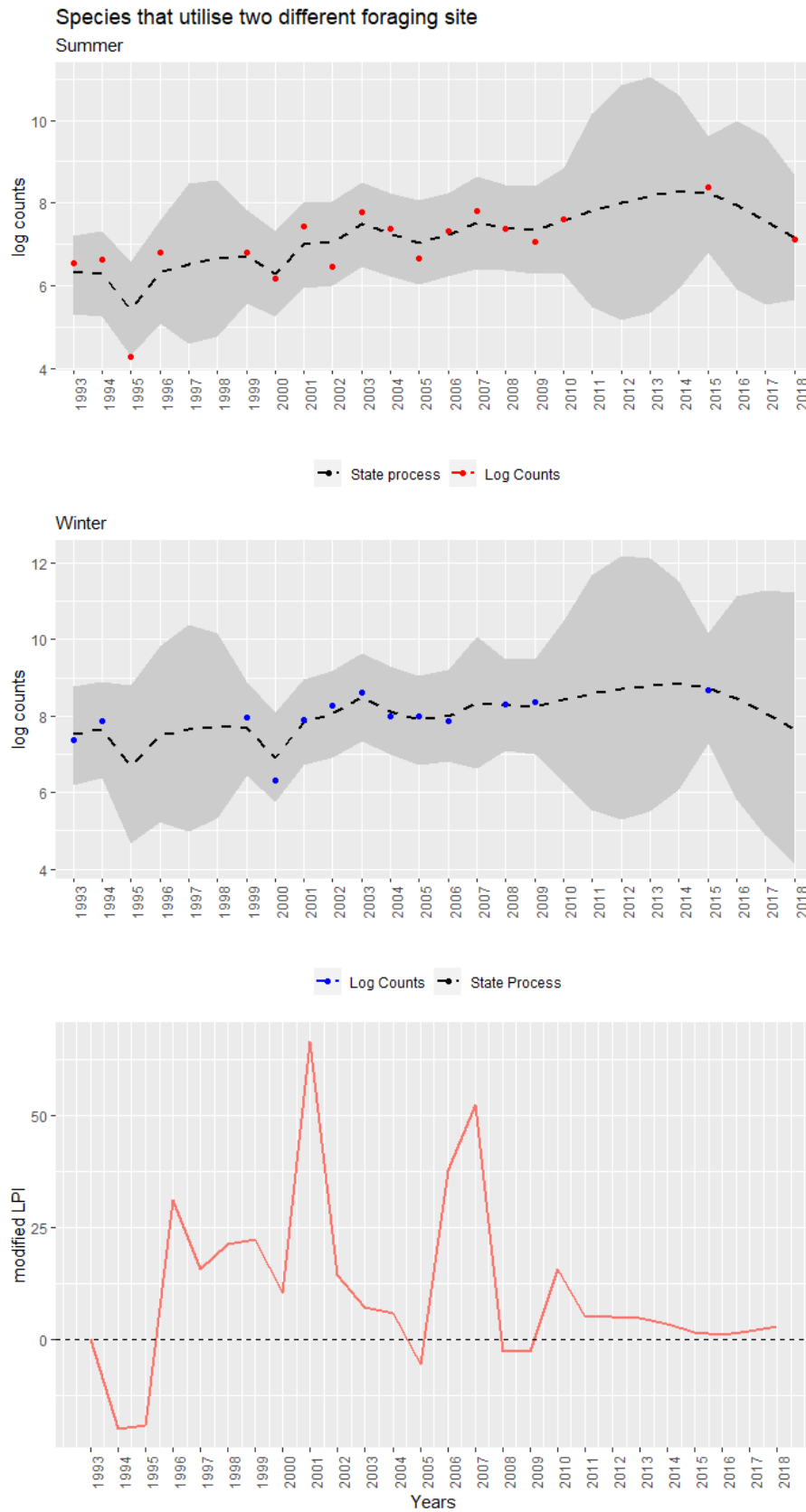
Figure 18: The first two plots is the SSM output applied to the combined counts of the waterbirds that utilise two different foraging sites, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.
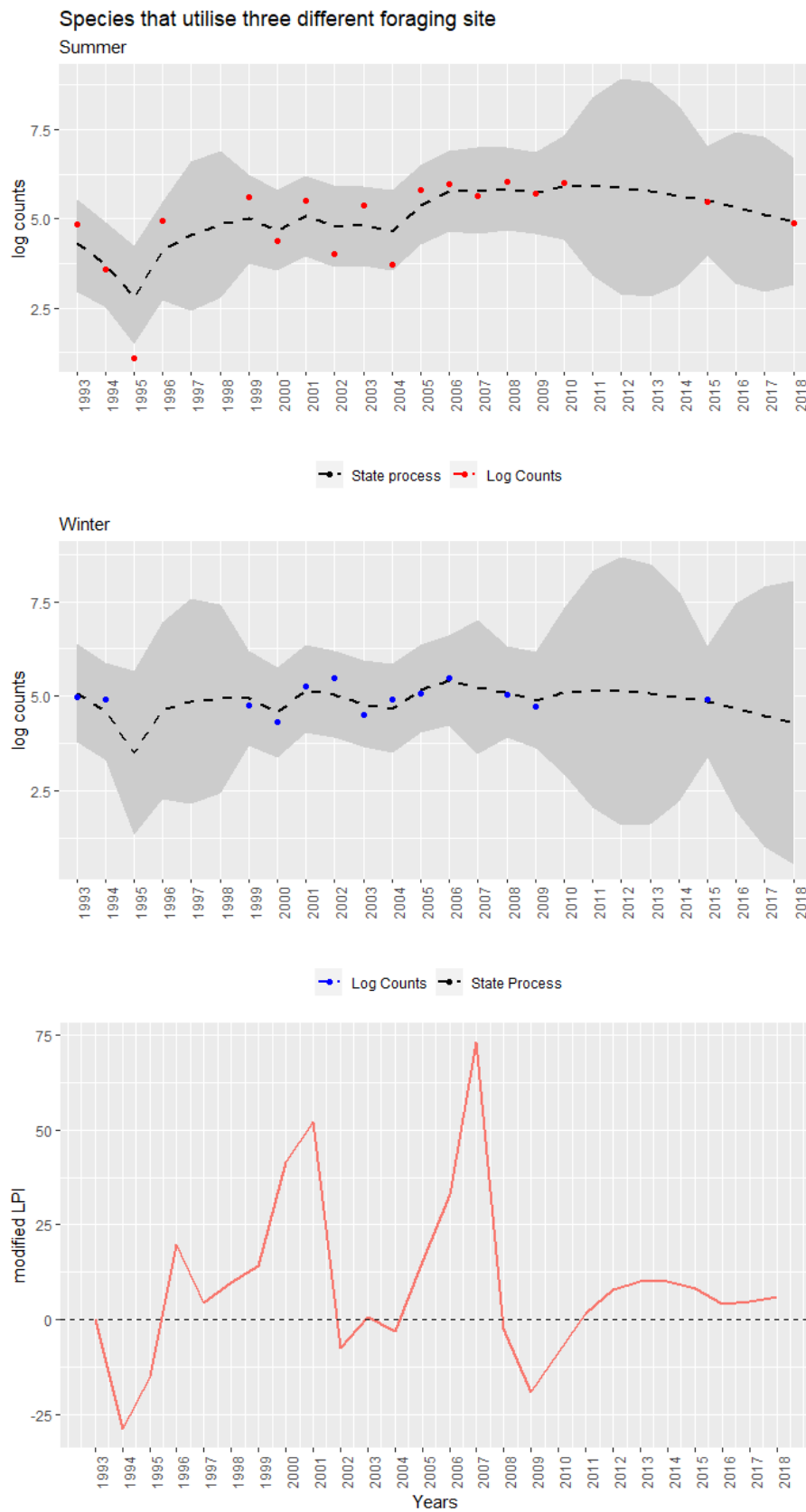
Figure 19: The first two plots is the SSM output applied to the combined counts of the waterbirds that utilise two different foraging sites, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.

Figure 20: The first two plots is the SSM output applied to the combined counts of the waterbirds that utilise four different foraging sites, separated into summer and winter counts. The last plot is the average yearly percentage change across those waterbird species.
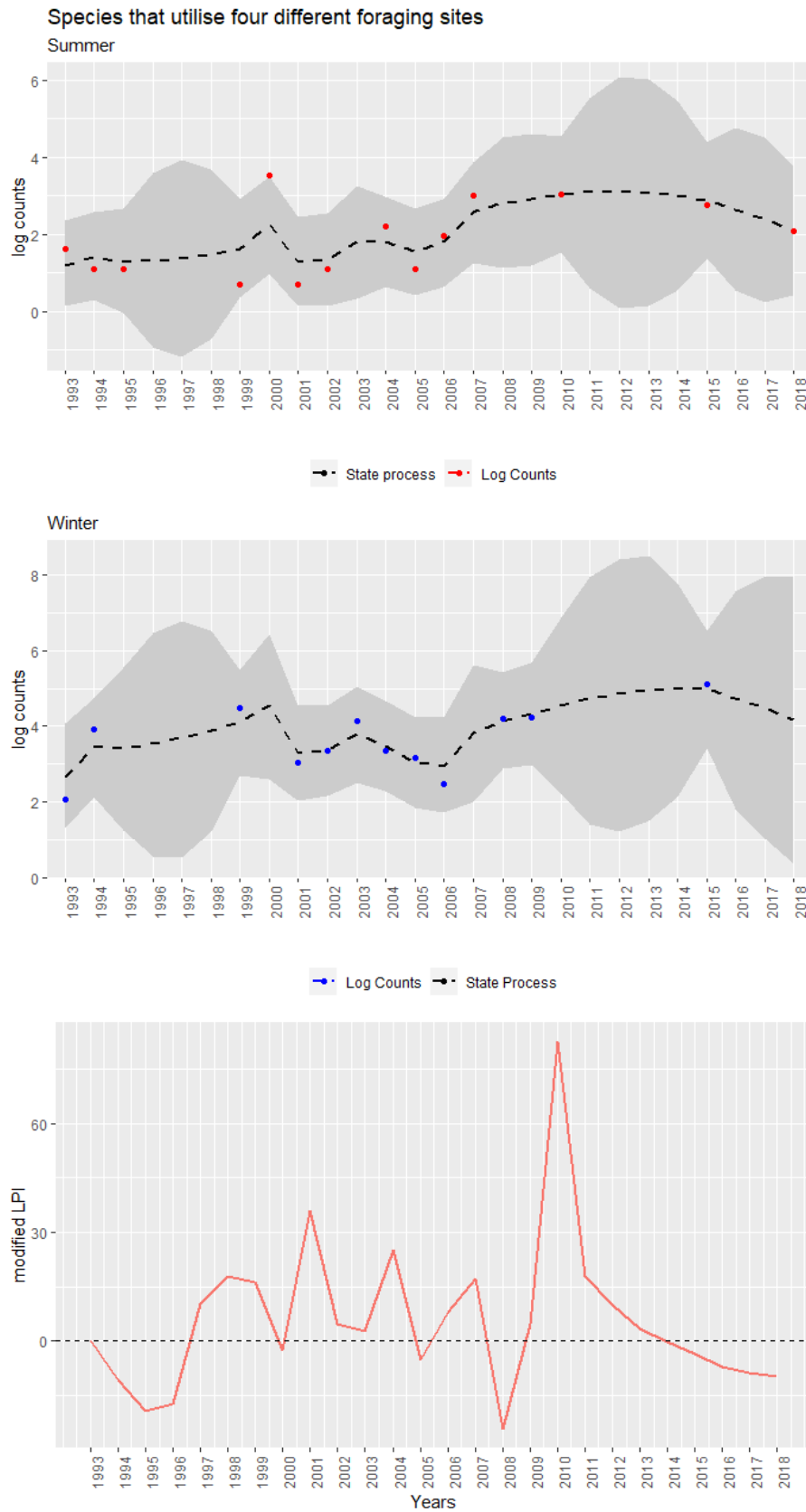
The average percentage change for each foraging substratum group is very similar. There is no evidence to show that a waterbird species that forages in more locations, increases in population faster than waterbirds with few foraging sites.

Not all waterbird traits will be indicators that determine population dynamics but some are useful. It was useful to analyse the waterbirds separately based on migrant status as the fluctuations in the counts are different due to their migratory patterns. However, the number foraging substrata and nest site doesn't seem to play an important role in describing population dynamics for the waterbirds.

3.3 Bioindicators

The underlying levels of the state space models, once generated, are assumed to be the true underlying population of the analysed bird species. Bioindicators are formulated using these values. Again, these indicators are subject to high levels of uncertainty as discussed previously. The indicators used here are the Simpson's index and the exponentiated Shannon's index. The Simpson's index provides a value representing the evenness of the ecosystem. The value of the Simpson's index varies from 0 to 1. 0 being very little evenness and 1 being perfect evenness. The exponentiated Shannon index gives the value of the effective number of species in an ecosystem. The Shannon and Simpson's index are often used together. The Shannon index shows the effective number of species in an ecosystem while the Simpson's index provides a measure of evenness. Figure 21 displays the Shannon and Simpson index each year for Barberspan. The 95% error bands have been omitted in these plots for better visualisation.
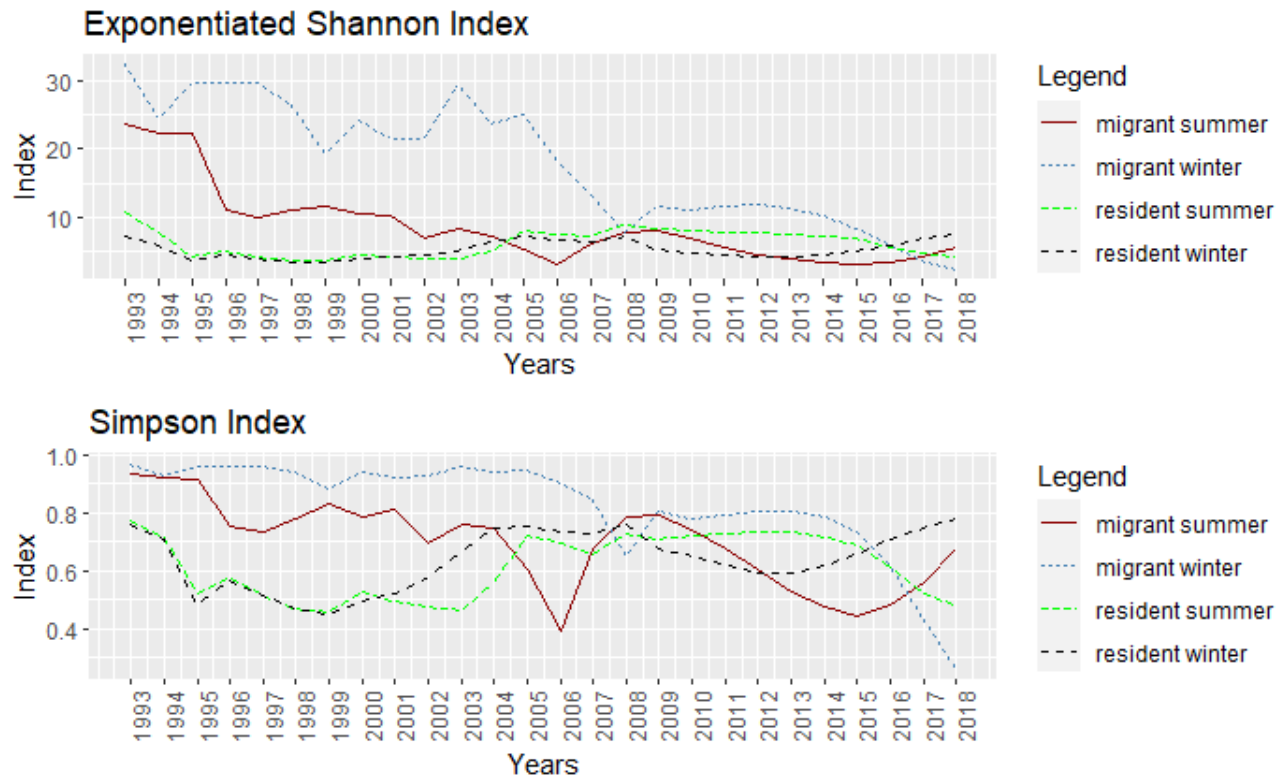
Figure 21: The Shannon and Simpson's indices for resident and migrant species in winter and summer

Due to the high levels of uncertainty of the index, it's difficult to state anything concrete based on these index values. However, it's evident that, on average, there is an overall decrease in the effective number of migratory waterbirds at Barberspan from 1993 compared to 2018 as displayed by the exponentiated Shannon's index. In 1993 we see an effective number of migrants at Barberspan to be greater than 20; by 2018 we see that number drop to below 10. Given that migrant population has not changed significantly over time (as seen in figure 7), we can determine that the decrease in effective number of species is not an even decrease across the migrants at Barberspan. The Simpson's index, accordingly, suggests a trend toward lower evenness for the migrants at Barberspan over time.

4 Discussion

Wetlands are valuable ecosystems for society. Unfortunately, there has been global wetland degradation with about half of the global wetlands being lost to accommodate for agricultural practices and urbanisation. The loss of wetlands has a negative impact on biodiversity, human well-being and has negative long-term impacts on economies (Clarkson, Ausseil, and Gerbeaux 2013). This has given rise to many wetland conservation projects, both locally and globally.

Waterbirds serve as good indicators of the state of the wetland they occupy (Gregory et al. 2003; Mekonen 2017). Appendix B shows state space time series plots for each waterbird species recorded in Barberspan wetland from 1993 till 2018. Based on the state space model applied to the counts, 26 out of 34 migratory waterbirds experienced declining trends. This agrees with similar reports on waterbirds in Southern Africa. A study on migrant waterbirds in South Africa reported that 11 of the 16 palearctic migrants investigated experienced negative trends from 2005-2009 (Barshep et al. 2017). A paper analysing palearctic migrants in Sandwich Harbour and Walvis Bay, Namibia, reported similar findings; Four of the 12 palearctic migrants studied experienced declines while only one species experienced an increasing trend (Common Whimbrel) from 1990-2013 (Simmons et al. 2015). Further studies show that Palearctic-Afrotropical migratory waterbirds are experiencing declines in abundance globally (Kirby et al. 2008; Deniau et al. 2022).

Out of the three waterbird attributes investigated in this study (migratory status, nest site and number of foraging sites used), the migratory status proved to be the most likely to affect population declines, as proportionally more migratory waterbirds displayed declining trends (76.5%) compared to resident waterbirds (55%). The other attributes investigated provided no significant evidence to suggest that they are drivers for population change among the waterbirds in Barberspan. More waterbird traits could be used and investigated in future research to identify their relation to waterbird population dynamics.

Upon further investigation, we see that the effective number of waterbird species in Barberspan is decreasing over time, this is displayed in the exponentiated Shannon's index. This could be due to various aspects such as bad agricultural practices, increased foot traffic, climate change, lack of rainfall, etc. Further investigation could be made to identify which factors are affecting the fluctuation of waterbirds in South African wetlands. To aid such an investigation, various auxiliary variables can be monitored and/or obtained such as water level, temperature, climate, foot traffic frequency, etc. These variables could be incorporated into the SSM for a deeper insight into how these variables affect waterbird population fluctuation and, consequently, the state of the wetland.

The SSM can be altered to incorporate various variables into the model by using a multivariate auto-regressive state space model (MARSS). A similar approach has been taken by Elghafghuf et al. (2018) to model the abundance of sea lice on Atlantic salmon over time. Incorporating temperature (or similar climate change indicators) as a covariate in the analysis of the CWAC data could be beneficial, as an overwhelming number of studies state that climate change is likely the main driver in the declining waterbird populations (Maclean et al., n.d.; Kirby et al. 2008; Pavón-Jordán et al. 2015). As a start, one could use a MARSS model and incorporate average seasonal temperature as a covariate in the time series analysis of the CWAC data. This follows a similar approach followed by Oedekoven et al. (2017) in attributing changes in the distribution of species abundance of British breeding birds.

The Simpson index displays some evidence that the waterbirds of Barberspan are becoming less even over time. This means that there are some waterbirds that are dominating while other species are leaving Barberspan. This is most notable for the migratory waterbirds. Investigating the SSM output on the individual migratory waterbirds (Appendix B) we see 6 out of the 34 migratory waterbirds make up, approximately, 83% of the total counts for all migratory waterbirds at Barberspan. These are the Little Stint, Ruff, Curlew Sandpiper, White-winged tern, Whiskered tern and Common Ringed Plover. These 6 waterbirds all displayed fairly positive trends up until year 2013 - 2015, while the rest of the migratory waterbirds displayed decreasing trends or no discernible trend at all. This leads to an increasingly uneven community of waterbirds over time and a decrease in effective number of species over time. After the declining period between the year 2013 and 2015, only the Curlew Sandpiper recovered and started displaying a positive trend again. This leads to further unevenness in the community and a further decrease in the effective number of migratory waterbirds in Barberspan. We see these aspects reflected in the Simpson's and exponentiated Shannon's index. The Shannon's index displays a decrease in effective number of species over time until it reaches an effective number of 4 to 6 migratory waterbirds in Barberspan from 2013 onward. Similarily, the Simpson's index displays a decrease in evenness over time until it reaches a value of 0.17 for the winter counts and 0.66 for the summer counts in 2018. There are generally more migratory waterbirds at Barberspan in the summer due to their migratory pattern, thus we see higher evenness in summer than winter.

High measures of unevenness among migratory waterbird species were also presented in a study conducted in the wetlands of Northeastern Algeria. Ali, Ismahan, and Moussa (2016), discovered a high dominance in Eurasian Coots in the wetland studied. The Eurasian Coots made up about 53% of the 39 migratory waterbird species found in the wetland. Similarily, A study conducted in a South African riverine habitat, the Shamvura stretch of the Okavango River, also found high levels of

dominance among the waterbirds present in the wetland (Kopij and Paxton 2018). In this study there were 6 out of the 84 recorded waterbirds that were classified as dominant: African reed cormorant, African openbill, cattle egret, wattled lapwing, African darter and white-faced duck. Among the waterbirds in Barberspan it was also found that resident species were most dominant. The Egyptian Goose and the Red-Knobbed Coot made up 70% of all waterbird counts at Barberspan with the Red-Knobbed Coot being most dominant making up 58% of all counts.

A pitfall within this study is the absence of credible intervals for the modified LPI, exponentiated Shannon's index and the Simpson's index. The LPI is commonly displayed using confidence intervals created by bootstrap sampling (McRae, Deinet, and Freeman 2017; Collen et al. 2009; Loh et al. 2005). The Simpson's index and the Shannon's index is also commonly displayed using bootstrapped confidence intervals (Fontana et al. 2011; Buckland et al. 2005). These studies all conducted their analysis within a frequentist framework. Literature is limited regarding biodiversity analysis and applying biodiversity indices to SSM output in a Bayesian framework, as was done in this study. The initial approach was to apply the modified LPI, exponentiated Shannon's index and the Simpson's index to the full posterior distribution produced by the Gibbs sampler to obtain credible intervals. However, the state space model models each individual waterbird species with it's own observation error, thus when performing operations between the posterior output of individual species we experience an accumulative effect on the error values. When the index calculations were applied to aggregate each species posterior output we were faced with very large error values which rendered the credible intervals useless. The state space model should ideally be altered to incorporate an observation error per counting session instead of per species. This would be a more realistic model and would, theoretically, produce smaller, and more realistic, credible intervals.

The outcome of this report is a first step in displaying what can be done using the CWAC dataset. The aspects of biodiversity to monitor were selected based on analysing what needs to be monitored, who needs to monitor it and why it needs to be monitored, thus following the instruction of Yoccoz, Nichols, and Boulinier (2001). The individual indices were selected based on best practices in quantifying biodiversity (Buckland et al. 2005, 2012). The three indices used in conjunction with one another provide a good overview of the waterbird and wetland state. For example, if The LPI displays alarming negative percentage changes for a year or two the user can use the other indices and time series plots to investigate. One could check the exponentiated Shannon's index to see if the effective number of species types has decreased or has all types of species been leaving the wetland at the same rate. One could also check the Simpson's index to identify if there are any dominant species that are using up resources of other species and driving them away as a result. If the Simpson's index

displays strong unevenness, the user can then analyse the individual time series plots to identify which species are increasing and which are decreasing. Knowing exactly which waterbird species are decreasing and which are increasing provides valuable insight into which aspects of the wetland may be a problem. For example, increases in Great Crested Grebe can be indicative of increased eutrophication levels (Amat and Green 2010) and decreases in Red-Knobbed Coots can be indicative of increased siltation rates in the water and soil of a wetland (Amat and Green 2010).

5 Conclusion

The CWAC dataset proves to be beneficial in displaying the state of waterbirds and wetlands in South Africa. State space time series models both the migrant and resident population dynamics well. Using the modified LPI, exponentiated Shannon's entropy and Simpson's index in conjunction provides good insight into the state of the waterbirds and wetland in question. These 3 indicators can help conservationists develop more targeted approaches in their efforts to conserve waterbirds and wetlands.

Unfortunately the method of calculating the modified LPI, exponentiated Shannon's entropy and the Simpson's index resulted in high levels of uncertainty. Future work should go into applying these bioindicators to the SSM output in a way that minimises uncertainty.

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