



# A Bayesian state-space model for estimating wild boar dynamic population in a hunting estate

J. Solana-Gutiérrez<sup>1,\*</sup>, and L. Thomas<sup>2</sup>

<sup>1</sup> *Escuela Técnica Superior de Ingenieros de Montes. Universidad Politécnica de Madrid. Paseo de las Moreras s/n (Ciudad Universitaria) 28040 Madrid. Spain; joaquin.solana@upm.es*

<sup>2</sup> *Centre for Research into Ecological and Environmental Modelling, School of Mathematics and Statistics, The Observatory, Buchanan Gardens, University of St Andrews, St Andrews, Fife KY16 PLZ Scotland, United Kingdom*

\*Corresponding author

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**Abstract.** *This paper deals with a Bayesian state-space model to estimate wild boar abundance and demographic parameters such as survival rates, intrinsic growth rates and hunting efficiency for a Mediterranean hunting estate. Based on annual wild boar captures from 1995 to 2008, a Bayesian model is built where population abundance is estimated by a reverse-time multinomial Cormack-Jolly-Seber model. In this model, monthly maximum and minimum temperature average, also drought-constrained, frost-constrained and non-constrained bioclimatic intensity are used as predictive factors of the population birth-rate and intrinsic growth. As a result, a wild boar population dynamic model was obtained which simulates hunting activities and estimates hidden demographic parameters. These outcomes are useful to develop better hunting management plans, where future captures are determined according to actual climatic features.*

**Keywords.** *State-space model; Bayesian model; Reverse-time CJS model; Wild boar hunting*

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## 1 Introduction

Knowledge about wildlife populations and their demographic features is essential to accomplish a sustainable hunting management plan. In addition, sampling animal populations is costly in terms of time and effort (Williams et al., 2002). As a consequence, hunting management plans are seldom based on field surveys and frequently ignore changing climatic conditions and current demographic parameters. In addition, Madrilénian environmental administration collects from each hunting estate an annual report where the number of animal captures is registered. Also, forest agents measure weight and age of every wild boar killed in each hunting day. This paper deals with building a Bayesian model that estimates wild boar demographic parameters from hunting administrative reports and other climatic covariates, such as

potential primary productivity and temperatures.

## 2 Location and data resources

The study was conducted in "El Chaparral" a 922 ha extension estate located at 50 miles South West of the Spanish capital and covered of green oak trees and bushes. According to hunting reports, 295 boars were killed at the estate from 1995 to 2008, whose ages were also estimated (Briedermann, 1976; Garzon, 1991; Baubert et al, 1994). Both sources of information allowed us to rebuild an actuarial survival table which shows the wild boar demographic structure conditional on hunted animals.

## 3 Methods

A "reverse time" Cormack-Jolly-Seber (CJS) model (Pradel, 1996; William et al., 2002) was applied to data. In this model, we considered that hunting pressure was similar during the analysis period and hunted animals were representative of the overall population. Indeed, the number of hunters per estate and the available days for practicing hunting are regulated in Spain, thus game pressure is fairly steady over years at each estate. The wild boar population was divided into two subsets: yearlings and adults. For both groups were supposed different abundances (i.e.,  $N_1$  and  $N_a$ ) and demographic parameters, such as survival rate ( $\phi_1$  and  $\phi_a$ ) and capture rate ( $\lambda_1$  and  $\lambda_a$ ). In each season  $i$ , the capture was estimated by  $C_i = N_0 \cdot (1 - \phi)^{i-1} \cdot \lambda$ , and the likelihood conditional on captures ( $C_i$ ) was  $L(N, p | C_i) = \binom{N_i}{C_i} \prod_{i=1}^k N_i \cdot (1 - \phi)^{i-1} \cdot \lambda$ . In addition, 'hunting efficiency' was included in the model as a Binomial variable,  $B(N_a, p)$ . This random variable connected group's captures with their abundances,  $\mathbf{C} = p \cdot \mathbf{N}$ . This means that each capture in the  $t$ th year,  $C_t$ , was considered as an indicator of the true abundance  $N_{a,t}$ , hence  $C_t \sim \text{Binom}(N_{a,t}, p_t)$ . In addition, an age system was built by a Lesley chain, which provides links between annual abundances and animal cohorts, and describes the true population evolution over time (Besbeas et al., 2002; Buckland et al., 2007). For adults, the model abundance at the  $t$ th year was defined by  $N_{a,t} \sim \text{Binom}(N_{1,t-1} + N_{a,t-1}, \phi_{a,t-1})$ , where  $N_{1,t-1}$  denotes the number of animals of age 1 in year  $t - 1$ ,  $N_{a,t-1}$ , denotes the number of adult animals in year  $t - 1$ , and  $\phi_{a,t-1}$  is the adult survival rate in year  $t - 1$ . The number of yearlings in the  $t$ th year is  $N_{1,t} \sim \text{Binom}(N_{a,t-1}, \rho_{t-1} \phi_{1,t-1})$ , where  $\phi_{1,t-1}$  denotes the first-year survival rate in year  $t - 1$  and  $\rho_{t-1}$  denotes the productivity rate in year  $t - 1$  (i.e., the average number of offsprings per adult). The intrinsic growth rate  $\rho_t$  was calculated conditional to abundance estimates:  $\rho_t = \frac{N_{a,t+1} + N_{1,t+1}}{N_{a,t} + N_{1,t}}$

In order to accommodate the survival rates, capture rates and growth rates to seasonal conditions (Besbeas et al., 2002; Brooks et al., 2004; King et al., 2008), a set of logic model were built, where monthly maximum temperature average (Tmax), monthly minimum temperature average (TMin), non-constrained bioclimatic intensity (IBL), drought-constrained bioclimatic intensity (IBS) and frost constrained bioclimatic intensity (IBF) were used as predictive covariates (Montero de Burgos and Gonzalez Rebullar, 1983).

From a Bayesian point of view, this state-space abundance model depends on the  $\rho_t, \lambda_t, \phi_{1,t}, \phi_{a,t}, \sigma_C$  parameters and the underlying population levels  $N_1, N_a$ , which are considered as missing values (Brooks et al., 2004) along with the capture variance  $\sigma_C$ . Under the assumption of independence between the observed system and the state-space system, the likelihood of observed data can be expressed as

$f(\mathbf{C}|N_1, N_a, \rho, \lambda, \phi_1, \phi_a, \sigma_C) = f(\mathbf{C}|N_1, N_a) \cdot f(N_1, N_a|\rho, \lambda, \phi_1, \phi_a, \sigma_C)$ . That is, the observational likelihood of  $\mathbf{C}$  was split in an abundance component,  $f(\mathbf{C}|N_1, N_a)$  and a multinomial state-space component  $f(N_1, N_a|\rho, \lambda, \phi_1, \phi_a, \sigma_C)$  expressed by a Lesley model. Both systems, observed and state-space, have common parameters,  $\rho, \lambda, \phi_1, \phi_a$ , and a joint stochastic simulation can provide matched parameter estimations. For prior abundances  $N_1$  and  $N_a$  Gaussian distributions with equal means and variances were selected. All models and analysis was made with OpenBUGS (Spiegelhalter et al., 2002) applying 25,000 iterations with a burn-in phase of 5,000 iterations.

## 4 Result

The MCMC convergence was achieved, although this was slow to be achieved in the two first years of the series caused by autocorrelation problems. Wild boar abundances for young and adults,  $N_{1,i}$  and  $N_{a,i}$ , intrinsic growth rates,  $\rho_i$ , and survival rates,  $\phi_{1,i}, \phi_{a,i}$ , were obtained for each  $i$ th year. Logic regressions were calculated for different bioclimatic variables. According to the Deviance Information Criterion (DIC), monthly minimum temperature average (TMin) was the most appropriate covariate among the candidate variables. Although, annual heterogeneity was supposed at a first stage for survival and capture rates,  $\phi_{1,t}, \phi_{a,t}, \lambda_t$ , outcomes showed that some regression parameters were non-significant (i.e.,  $\beta_{\phi_1}, \alpha_\lambda, \beta_\lambda$ ). Particularly, a constant coefficient  $\alpha_1$  generated a unique survival rate for yearling animals and capture rate regardless of year. In addition,  $\beta_a$  coefficient was negative for monthly minimum temperature average, therefore the warmer the year, the lower the survival rate. Finally, a sensitivity analysis was conducted for comparing three different a priori distributions: a non-informative Gaussian, a non-informative Beta, and a non-informative Uniform. As a result, the Gaussian distribution was the most appropriate prior according to the DIC.

## 5 Discussion

First of all, the final state-space model for estimating wild boar abundance produced feasible and useful estimates for population demographic parameters. Adult survival rates  $\phi_a$  were similar to survival rates obtained from non state-space models. For instance, results from a previous non state-space model considering individual animal history (Royle et al., 2007) produced a constant adult survival rate  $\phi = 0.64$ , similarly our Bayesian model yielded an average of 0.586 with a 95% confident interval from 0.464 to 0.704. Young survival rates  $\phi_1$  calculated under homogeneity assumption produced a survival rate of 0.714, and the same under heterogeneity but with a 95% confidence interval from 0.333 to 0.926. Moreover, the high mortality rate obtained, 28.6%, is matched with figures extracted from other wild boar demographic studies (Saez-Royuela, 1989). For the analysed period, the intrinsic growth rate was  $\rho = 1.068$ , it means that the wild boar population increased annually by 6.8% in spite of the fact that wild boars had a high hunting pressure. This agrees with other authors who expressed a steady increment and spread of wild boar across all Spain (Sainz-Royuela, 1985; Fernandez-Llario, 2006) from the sixties until today. The Bayesian state-space model estimated a total abundance of 30 wild boars, 22 adults and 8 young animals. In summary, the state space model produced acceptable estimates of the survival rate, the intrinsic growth rate and the hunting efficiency. Based on our outcomes, after a 3-year burn-in period, the demographic rate estimates are trustable and the abundance predictions very useful for building wild boar hunting management plans and monitoring hunting estates over time.

## 6 Conclusion

In this study a CJS reverse-time method was applied to analyse the abundance and demographic parameters of wild boar populations under hunting pressure. The outcomes were similar to figures obtained in other statistical descriptive studies, however, Bayesian models provide estimates of parameters needed for a better simulation of the population dynamics.

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