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13th Scientific Meeting of the Classification and Data Analysis Group
Firenze, September 9-11, 2021

edited by

Giovanni C. Porzio

Carla Rampichini

Chiara Bocci



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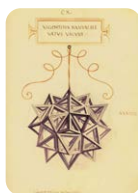
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MODEL-BASED CLUSTERING FOR ESTIMATING CETACEANS SITE-FIDELITY AND ABUNDANCE

Gianmarco Caruso¹, Greta Panunzi¹, Marco Mingione¹, Pierfrancesco Alaimo di Loro¹, Stefano Moro², Edoardo Bompiani¹, Caterina Lanfredi¹, Daniela Silvia Pace², Luca Tardella¹ and Giovanna Jona Lasinio¹

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ABSTRACT: Estimating the size of animal populations in a given area is of particular interest in ecological studies on wildlife conservation, and this task is commonly handled via capture-recapture methods. A recent work (Pace *et al.*, 2021) adopts a two-step approach for identifying groups of animals with similar site-fidelity patterns - according to specific metrics - and estimating the abundance of bottlenose dolphins between 2017 and 2020 at the Tiber Estuary (Mediterranean Sea, Rome, Italy). In this work, we aim at simultaneously classifying individuals and estimating their abundance in the study area, by introducing finite mixtures within the *Open-Population Jolly-Seber* framework. In capture-recapture analyses, finite mixture models allow to account for groups heterogeneity and to reduce the bias in the final abundance estimates (Pledger, 2005).

KEYWORDS: Capture-recapture analysis, Wildlife population, Finite mixture models, Unsupervised classification, Applied statistics

1 Introduction

Capture-recapture methods are widely employed in estimating the size of wildlife populations, whose units are subject to multiple captures across several occasions. We will use the terms *capture* and *recapture* in accordance with the classical literature (Seber, 1986), but animals are not necessarily *captured*: nowadays, non-invasive ways of keeping trace of a wild animal over time are successfully employed. In that spirit, for example, Pace *et al.* (2021) employs

photo-identification for identifying bottlenose dolphins from natural markings present on their bodies. In the same paper an interesting characteristic of this type of animals is illustrated: marked individuals may show a different level of *site-fidelity*. This point introduces the need of defining a statistical protocol or a specific model accounting for the different probabilities of *capture* among the categories. Here, we propose a method that allows both to differentiate between *resident* and *non-resident* individuals and to estimate the population abundance in a common modelling framework. This improves on the original multi-step protocols (see Pace *et al.*, 2021) in guaranteeing the correct uncertainty propagation of the two estimation processes.

2 The model

We consider the Schwarz & Arnason (1996)'s formalization of the Jolly-Seber model, which assumes the existence of a *super-population*, representing the set of individuals potentially available in the study area between the first and the last sampling period. In Jolly-Seber-type models, captures are assumed to be independent across individuals and along time. Moreover, the population is assumed to be *open*, meaning that individuals can either enter (e.g. birth or immigration) or exit (e.g. death or emigration) the population during the study. Notably, we assume that individuals leaving the population cannot come back in it. Here, we adopt the Bayesian framework illustrated by Royle & Dorazio (2012), where the super-population size (N_{super}) is provided with a discrete uniform distribution in the interval $\{0, \dots, M\}$, with M sufficiently large. The hyperparameter M can be seen as an upper bound for the super-population size and it implies the use of an augmented dataset of M individuals. Moreover, we consider a sampling scheme divided in T periods and, for each time $t = 1, \dots, T$, a number J_t of capture sessions. Thus, the augmented data matrix $\mathbf{Y} = [y_{it}]$ has M rows and T columns and contains the capture frequency of each individual in each period. If D is the number of individuals that have been observed at least once, the matrix contains $M - D$ rows of zeros: among them, $N_{\text{super}} - D$ rows correspond to individuals which belong to the super-population but have never been captured, while $M - N_{\text{super}}$ correspond to *pseudo*-individuals which do not belong to the super-population.

Recruitment and survival process Population dynamics consisting in recruitment and survival can be expressed through the following latent binary variables:

- r_{it} which is equal to 1 iff individual i is recruitable at time t ;

• z_{it} which is equal to 1 iff individual i belongs to the population at time t . Let ϕ_t be the probability of remaining in the population at time t , being in the population at time $t - 1$, and let ρ_t be the probability of belonging to the super-population *and* being recruited into the population at time t . Without loss of generality, in this context we assume these two parameters to be constant over time, i.e. $\phi_t = \phi$ and $\rho_t = \rho$. Following Royle & Dorazio (2012), it can be proved that, for $i = 1, \dots, M$, $r_{i1} = 1$ and $z_{i1} \sim \text{Bern}(\rho)$, and

$$r_{it} = \min\{r_{i,t-1}, 1 - z_{i,t-1}\}, \quad t > 1$$

$$z_{it} | z_{i,t-1}, r_{it} \sim \text{Bern}(\phi \cdot z_{i,t-1} + \rho \cdot r_{it}), \quad t > 1.$$

Notice that when an individual becomes part of the population, it cannot be recruitable any more: for $t > 1$, r_{it} and z_{it} cannot simultaneously be equal to 1.

Detection process In this work, we consider a finite mixture model in order to model the different propensity to the capture among different groups of individuals. The generic element of the augmented data matrix is such that

$$y_{it} | z_{it}, c_i = g \sim \text{Binom}(J_t, p_g \cdot z_{it}), \quad g = 1, \dots, G,$$

with p_g being the capture probability of individuals in group g and $P(c_i = g) = w_g$ being the probability that the i -th individual belongs to the g -th mixture component. Notice that $y_{it} = 0$ almost surely when $z_{it} = 0$, so that the previous model corresponds to a finite mixture of zero-inflated binomial distributions.

Abundance estimation The population size at time t and the super-population size can be estimated through the latent variables z 's, namely, $N_t = \sum_{i=1}^M z_{it}$ and $N_{\text{super}} = \sum_{i=1}^M \mathbb{1}_{\{\sum_{t=1}^T z_{it} > 0\}}$.

3 Illustration

A graphical visualization of the main components of the model is provided by the DAG in *Figure 1*. The model is used to estimate the abundance of bottlenose dolphins between 2017 and 2020 at the Tiber Estuary (Mediterranean Sea, Rome, Italy) and identifying groups of animals with different propensities to the capture: individuals with a low detection probability are considered *non-resident*, while the others are considered *resident*. The model is implemented using JAGS (Plummer, 2003) and the results will be shown in details during the conference.

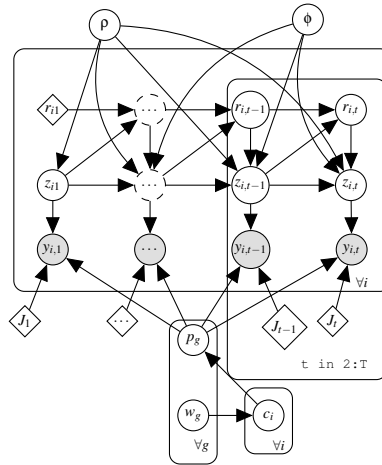



Figure 1. Bayesian DAG with the main components of the model. White rhombi represent deterministic variables. White circles represent latent variables and parameters. Grey circles represents observable variables.

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