

# Using R for the Analysis of Bird Demography on a Europe-wide Scale

Christian Kampichler<sup>1,2</sup>, Henk van der Jeugd<sup>1</sup>, Alison Johnston<sup>3</sup>, Rob Robinson<sup>3</sup>, Stephen Baillie<sup>3</sup>

<sup>1</sup> Vogeltrekstation – Dutch Centre for Avian Migration and Demography, Netherlands Institute of Ecology, Wageningen, Netherlands;

<sup>2</sup> División de Ciencias Biológicas, Universidad Juárez Autónoma de Tabasco, Villahermosa, Mexico;

<sup>3</sup> British Trust for Ornithology, Thetford, U.K.

Contact: c.kampichler@nioo.knaw.nl

Bird populations are not constant in time but experience variation due to internal dynamics or to the action of external forces such as climatic change or habitat destruction. They are often used as indicators for the trends of wider biodiversity because our knowledge on them is generally good [1]. Beginning in the early 1980s, a Europe-wide network of more than 400 constant effort sites operating in 12 countries has been established, where birds are captured and ringed with a unique mark, according to a standardised protocol [2]. This scheme allows the monitoring of demographic parameters (abundance, reproduction rate, survival rate) of a large number of songbird species. The European database currently holds records of more than five million captures and recaptures.

Annual and site-specific reproduction rates are calculated by GLM based on the ratio of occurrences of adult and juvenile birds per site and year. The estimation of survival rates is somewhat more sophisticated and requires GLM with multinomial response variables for the application of specific capture-recapture models [3]. Basically, input data consist of a capture history for each ringed specimen of a given species where years are coded as 1 (specimen captured) and 0 (specimen not captured). Each possible capture history—for example, 111, 110, 101 or 100 for a three-years mark-recapture study—has a corresponding probability which is composed of the probability that a bird has survived from the preceding year ( $\Phi$ ) and the probability it is captured conditional on having survived ( $p$ ). For the four capture histories above, the probabilities are  $\Phi_1 p_2 \Phi_2 p_3$ ,  $\Phi_1 p_2 (1 - \Phi_2 p_3)$ ,  $\Phi_1 (1 - p_2) \Phi_2 p_3$  and  $1 - \Phi_1 p_2 - \Phi_1 (1 - p_2) \Phi_2 p_3$ . The capture history probabilities are weighed by their frequency in the dataset and the parameters are estimated using maximum likelihood or Markov chain Monte Carlo methods.

The most widely used application currently available for survival analysis using data from marked individuals is Program MARK [4] (URL <http://www.phidot.org/software/mark/>). On the one hand, it is extremely comprehensive, offering a wide range of different models. On the other hand, its data and model manipulation facilities are rather restricted—they are based on a conventional GUI with numerous pull-down menus and check-box options—making the repeated analyses of many species (or for many locations) a cumbersome and extremely error-prone task. We thus use RMark [5] (URL <http://www.phidot.org/software/mark/rmark/>) as an interface, allowing for the use of the powerful formula and design matrix functions in R. A key advantage of R for monitoring is that one does not need to recreate the analyses each year with extra data. Having a set of automated scripts makes producing trends easy when resources are often tight. Furthermore, the possibility of using and exchanging scripts facilitates the communication among the various institutions running national constant effort site programmes and assures a unified analytical approach.

## References

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