Analysis using large–scale ringing data

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Birds are highly mobile organisms and there is increasing evidence that studies at large spatial scales are needed if we are to properly understand their population dynamics. While classical metapopulation models have rarely proved useful for birds, more general metapopulation ideas involving collections of populations interacting within spatially structured landscapes are highly relevant (Harrison, 1994). There is increasing interest in understanding patterns of synchrony, or lack of synchrony, between populations and the environmental and dispersal mechanisms that bring about these patterns (Paradis et al., 2000). To investigate these processes we need to measure abundance, demographic rates and dispersal at large spatial scales, in addition to gathering data on relevant environmental variables.

There is an increasing realisation that conservation needs to address rapid declines of common and widespread species (they will not remain so if such trends continue) as well as the management of small populations that are at risk of extinction. While the knowledge needed to support the management of small populations can often be obtained from intensive studies in a few restricted areas, conservation of widespread species often requires information on population trends and processes measured at regional, national and continental scales (Baillie, 2001). While management prescriptions for widespread populations may initially be developed from a small number of local studies or experiments, there is an increasing need to understand how such results will scale up when applied across wider areas. There is also a vital role for monitoring at large spatial scales both in identifying such population declines and in assessing population recovery.

Gathering data on avian abundance and demography at large spatial scales usually relies on the efforts of large numbers of skilled volunteers. Volunteer studies based on ringing (for example Constant Effort Sites [CES]; Peach et al., 1998; DeSante et al., 2001) are generally co–ordinated by ringing centres such as those that make up the membership of EURING. In some countries volunteer census work (often called Breeding Bird Surveys) is undertaken by the same organizations while in others different bodies may co–ordinate this aspect of the work.

This session was concerned with the analysis of such extensive data sets and the approaches that are being developed to address the key theoretical and applied issues outlined above. The papers reflect the development of more spatially explicit approaches to analyses of data gathered at large spatial scales. They show that while the statistical tools that have been developed in recent years can be used to derive useful biological conclusions from such data, there is additional need for further developments. Future work should also consider how to best implement such analytical developments within future study designs. In his plenary paper Andy Royle (Royle, 2004) addresses this theme directly by describing a general framework for modelling spatially replicated abundance data. The approach is based on the idea that a set of spatially referenced local populations constitutes a metapopulation, within which local abundance is determined as a random process. This provides an elegant and general approach in which the metapopulation model as

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described above is combined with a data–generating model specific to the type of data being analysed to define a simple hierarchical model that can be analysed using conventional methods. It should be noted, however, that further software development will be needed if the approach is to be made readily available to biologists. The approach is well suited to dealing with sparse data and avoids the need for data aggregation prior to analysis.

Spatial synchrony has received most attention in studies of species whose populations show cyclic fluctuations, particularly certain game birds and small mammals. However, synchrony is in fact a much more widespread process, with bird populations across wide areas showing similar trends and fluctuations as a result of common climatic and environmental factors (Paradis et al., 2000). Dispersal may also play an important role in such synchrony but its role is less well understood. Nigel Yoccoz and Rolf Ims (Yoccoz & Ims, 2004) show how synchrony can be investigated using data at three spatial scales taken from their field studies of the population dynamics of small mammals in North Norway. Small mammal abundance was estimated from trapping data using closed population models and also from total numbers of individuals captured. They use simulated data to show that synchrony, measured by the correlation coefficients between time series, was biased low by up to 30% when sampling variation was ignored. Appropriate analysis of such data will require simultaneous modelling of process and sampling variation, for example through the use of state–space models (Buckland et al., 2004). This view links back nicely to the approaches proposed by Andy Royle (Royle, 2004).

Cycles in the abundance of small mammals have major affects on the demography of their predators, as is shown in the paper by Pertti Saurola and Charles Francis (Saurola & Francis, 2004). They report on the design and results of large–scale, long–term studies of owl populations by a network of amateur bird ringers in Finland. They show that breeding success varies with the stage of the microtine cycle. They also show how their data can be used to estimate dispersal over large spatial scales and illustrate the importance of correcting for uneven spatial variation in sampling effort. Further results from this study are reported in a companion paper within the population dynamics session (Francis & Saurola, 2004).

Multi–species analyses of population dynamics are developed further in the paper by Romain Julliard (Julliard, 2004). He combines counts from the French Breeding Bird Survey with survival and recruitment estimates from the French CES scheme to assess the relative contributions of survival and recruitment to overall population changes. He develops a novel approach to modelling survival rates from such multi–site data by using within–year recaptures to provide a covariate of between–year recapture rates. This provided parsimonious models of variation in recapture probabilities between sites and years. The approach provides promising results for the four species investigated and can potentially be extended to similar data from other CES/MAPS schemes.

The final paper by Blandine Doligez, David Thomson and Arie van Noordwijk (Doligez et al., 2004) illustrates how large-scale studies of population dynamics can be important for evaluating the effects of conservation measures. Their study is concerned with the reintroduction of White Stork populations to the Netherlands where a re–introduction programme started in 1969 had resulted in a breeding population of 396 pairs by 2000. They demonstrate the need to consider a wide range of models in order to account for potential age, time, cohort and "trap–happiness" effects. As the data are based on resightings such trap–happiness must reflect some form of heterogeneity in resighting probabilities. Perhaps surprisingly, the provision of supplementary food did not influence survival, but it may have had an indirect effect via the alteration of migratory behaviour.

Spatially explicit modelling of data gathered at many sites inevitably results in starting models with very large numbers of parameters. The problem is often complicated further by having relatively sparse data at each site, even where the total amount of data gathered is very large. Both Julliard (2004) and Doligez et al. (2004) give explicit examples of problems caused by needing to handle very large numbers of parameters and show how they overcame them for their particular data sets. Such problems involve both the choice of appropriate starting models for sparse data and the speed with which convergence is achieved. Further analytical and software developments are needed in order to make it easier to analyse such data sets.

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