Computing and software

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The reality is that the statistical methods used for analysis of data depend upon the availability of software. Analysis of marked animal data is no different than the rest of the statistical field. The methods used for analysis are those that are available in reliable software packages. Thus, the critical importance of having reliable, up–to–date software available to biologists is obvious. Statisticians have continued to develop more robust models, ever expanding the suite of potential analysis methods available. But without software to implement these newer methods, they will languish in the abstract, and not be applied to the problems deserving them.

In the Computers and Software Session, two new software packages are described, a comparison of implementation of methods for the estimation of nest survival is provided, and a more speculative paper about how the next generation of software might be structured is presented.

Rotella et al. (2004) compare nest survival estimation with different software packages: SAS logistic regression, SAS non–linear mixed models, and Program MARK. Nests are assumed to be visited at various, possibly infrequent, intervals. All of the approaches described compute nest survival with the same likelihood, and require that the age of the nest is known to account for nests that eventually hatch. However, each approach offers advantages and disadvantages, explored by Rotella et al. (2004).

Efford et al. (2004) present a new software package called DENSITY. The package computes population abundance and density from trapping arrays and other detection methods with a new and unique approach. DENSITY represents the first major addition to the analysis of trapping arrays in 20 years.

Barker & White (2004) discuss how existing software such as Program MARK require that each new model's likelihood must be programmed specifically for that model. They wishfully think that future software might allow the user to combine pieces of likelihood functions together to generate estimates. The idea is interesting, and maybe some bright young statistician can work out the specifics to implement the procedure.

Choquet et al. (2004) describe MSURGE, a software package that implements the multistate capture–recapture models. The unique feature of MSURGE is that the design matrix is constructed with an interpreted language called GEMACO. Because MSURGE is limited to just multistate models, the special requirements of these likelihoods can be provided.

The software and methods presented in these papers gives biologists and wildlife managers an expanding range of possibilities for data analysis. Although ease–of–use is generally getting better, it does not replace the need for understanding of the requirements and structure of the models being computed. The internet provides access to many free software packages as well as user–discussion groups to share knowledge and ideas. (A starting point for wildlife–related applications is http://www.phidot.org)

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