Explicit integrated population modeling: Escaping the conventional assumption of independence

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Abstract: Integrated population modeling is a relatively new development in statistical ecology that permits the joint analysis of different sources of data. Typically, the joint likelihood is obtained using an independence assumption so that it can be conveniently expressed as a product of the likelihoods of the respective datasets (Schaub and Abadi, 2011). In this talk, I present a new Bayesian model that can be used when the independence assumption is not suitable. A key aspect of the model is that it makes use of latent variables that keep track of the states of the marked and unmarked individuals separately while allowing unmarked individuals to become marked when so. I describe the situations in which this explicit model is preferable (e.g. large capture probabilities) over the usual model (based on an independence assumption). I also present the results of a simulation study that compare, under various scenarios, the explicit and independent models in terms of mean and standard error of the Bayes estimator. Finally, I apply the methods to capture-recapture and count data from a colony of Greater horseshoe bats (*Rhinolophus ferrumequinum*) in the Valais, Switzerland.

References

Schaub M. and Abadi F. (2011). Integrated population models: A novel analysis framework for deeper insights into population dynamics. *Journal of Ornithology*. 152 (Suppl. 1): 227-237.