Discrete-valued spatio-temporal data are ubiquitous across an ever-increasing number of scientific disciplines, including areas as diverse as abundance estimation of various species in ecological monitoring studies, small-area samples from national surveys, epidemiological and transportation data, and environmental applications, among others. We propose general methodology for modeling spatio-temporal count data as well as capture-recapture data. Although the models are of independent interest and can be applied in many settings, we illustrate the methods through applications to estimating (relative) abundance.

In the context of measuring population abundance two types of sampling designs often arise. In the first sampling design, preselected spatial locations are sampled during scheduled visits, resulting in spatially referenced count-data collected over certain temporal periods. In this arena, depending on the availability of information to inform detectability, we develop two general models that can be used. For the case where no information is available to inform detectability, we develop Hierarchical Bayesian spatio-temporal Conway-Maxwell Poisson (CMP) models with dynamic dispersion that take advantage of nonlinear dimension reduction. This model is illustrated through simulated examples and through out-of-sample one-year-ahead prediction of waterfowl migratory patterns. In the presence of information for detectability, we develop a class of Binomial-CMP models. The Binomial-CMP mixture models we propose explicitly account for spatial dependence through low-rank basis functions and allow for automated variable selection and grouping of dispersion parameters. The effectiveness this models is illustrated through simulated examples and through application to a long-term ecological monitoring study.

In the context of capture-recapture sampling designs, individuals are distinctly tagged during each scheduled visit in addition to recording the number of species observed. For this type of data, we introduce a Jolly-Seber model with time-varying continuous individual covariates. The effectiveness of this model is demonstrated using data on meadow voles (Microtus pennsylvanicus). Next, we develop a Bayesian hierarchical multi-population multistate Jolly-Seber (MP-MSJS) model with covariates. The MP-MSJS model we propose allows a borrowing of strength across multiple synchronous populations and is useful for analyzing sparse data, e.g., for endangered species. We illustrate the effectiveness of this MP-MSJS model through a simulated example.