sdmTMB: Fast, flexible, and user-friendly spatial and spatiotemporal generalized linear mixed-effects models

Analyzing geostatistical data (spatially referenced observations) is becoming increasingly common in ecology for applications such as species distribution models (SDMs). These data often also include a discrete temporal dimension, such as yearly samples. Computational tools to model spatial and spatiotemporal processes have advanced considerably over the last decade. One major advancement has been the SPDE (Stochastic Partial Differential Equation) approach to enable rapid fitting to large spatial datasets. In this talk, we present a new R package, sdmTMB. The goal of sdmTMB is not to replace functionality in existing packages (e.g., inlabru, VAST, spaMM). Instead, the goal is to provide a user-friendly implementation of SPDE models, with an interface familiar to those who have used lme4 or glmmTMB, but focussing on spatial and spatiotemporal models. We extend generalized linear mixed-effect models (GLMMs) to include the following optional features:
- SPDE-based spatial random fields
- SPDE-based spatiotemporal random fields that may be independent by year or modeled as random walks or autoregressive processes
- penalized smooth terms for covariates, using the familiar s() notation from mgcv
- spatially varying coefficient models (SVCs)
- time-varying covariates (coefficients modeled as random walks)

Estimation is performed in sdmTMB via maximum marginal likelihood, implemented using Template Model Builder (TMB). The sdmTMB package also allows for models to be passed to Stan, allowing for Bayesian estimation. We provide a general overview of the package structure and demonstrate features using examples including Snowy Owl winter irruptions in North America and a dataset describing the distribution of Pacific Cod in British Columbia, Canada. We highlight advantages of using sdmTMB for these classes of models including (1) estimation in TMB is often faster than alternative estimation routines, (2) sdmTMB provides a user-friendly interface that is familiar to many R users, (3) sdmTMB allows for simple out-of-sample model validation, (4) non-stationary processes are easily constructed with a formula interface (time-varying coefficients, spatially varying coefficient models). For analysts fitting dynamic species distribution models to estimate standardized population abundance trends, sdmTMB provides specific functions for performing these calculations.