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Spatial Generalized Linear Models in R Using spmodel

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Abstract

Non-Gaussian data are common in practice and include binary, count, skewed, and proprtion data types. Often, non-Gaussian data are modeled using a generalized linear model (GLM). GLMs typically assume that observations are independent of one another. This is an impractical assumption for spatial data, as nearby observations tend to be more similar than distant ones. The **spmodel** package in R provides a suite of tools for fitting spatial generalized linear models (SPGLMs) to non-Gaussian data and making spatial predictions (i.e., Kriging). SPGLMs for point-referenced data (x- and y-coordinates) are fit using the `spglm()` function, while SPGLMs for areal (lattice, polygon) data are fit using the `spgautor()` function. Both `spglm()` and `spgautor()` maximize a novel Laplace likelihood which marginalizes over the model's fixed effects and latent mean while formally incorporating spatial covariance. The inputs and outputs of `spglm()` and `spgautor()` closely resemble the `glm()` function from base R, easing the transition from GLMs to SPGLMs. **spmodel** provides and builds upon several commonly used helper functions for model building like `summary()`, `plot()`, `fitted()`, and `tidy()`, among others. Spatial predictions of the latent mean at unobserved locations are obtained using `predict()` or `augment()`. **spmodel** accommodates myriad advanced modeling features like geometric anisotrpoy, nonspatial random effects, analysis of variance, and more. Throughout, we use **spmodel** to fit SPGLMs to moose presence and counts in Alaska, United States (US), skewed conductivity data in the Southwestern US, harbor seal abundance trends in Alaska, US, and voter turnout rates in Texas, US.

Keywords: autoregressive model, geostatistical model, inverse link function, Poisson regression, link function, logistic regression, spatial covariance, spatial correlation.

1. Introduction

In practice, non-Gaussian data (e.g., binary, count, skewed, and proportion data) are ubiquitous. Non-Gaussian data that belong to an exponential family can be naturally modeled using a generalized linear model (GLM) regression framework (Nelder and Wedderburn 1972; McCullagh and Nelder 1989). In a GLM, an $n \times 1$ response variable $\mathbf{y}$ belongs to a statistical distribution (e.g., Binomial, Poisson) with some mean and variance. Often, the analysis goal is to study the impact of a linear function of several explanatory variables on the mean of $\mathbf{y}$ through a GLM. In this context, the latent (i.e., unobserved) mean of $\mathbf{y}$, $\boldsymbol{\mu}$, is linked to these explanatory variables via a link function:

$$f(\boldsymbol{\mu}|\mathbf{X}, \boldsymbol{\beta}) \equiv \mathbf{w} = \mathbf{X}\boldsymbol{\beta}, \tag{1}$$

where for a sample size n, $f(\cdot)$ is a link function that connects $\boldsymbol{\mu}$ to $\mathbf{w}$, $\mathbf{X}$ is the $n \times p$ design matrix of explanatory variables, and $\boldsymbol{\beta}$ is the $p \times 1$ vector of fixed effects. While the mean is typically constrained in some way (e.g., if a probability, between zero and one), the link function generally makes $\mathbf{w}$ unconstrained. Common link functions include the log odds (i.e., logit) link for binary and proportion data and the log link for count and skewed data. Equation 1 can also be written in terms of the inverse link function, $f^{-1}(\cdot)$:

$$\boldsymbol{\mu}|\mathbf{X}, \boldsymbol{\beta} \equiv f^{-1}(\mathbf{w}) = f^{-1}(\mathbf{X}\boldsymbol{\beta}).$$

The GLM fixed effects ($\boldsymbol{\beta}$) are typically estimated via maximum likelihood (Chambers and Hastie 1992). It is often convenient to compute the maximum likelihood estimates using the iteratively reweighted least squares (IRWLS) algorithm (Wood 2017), which is the approach used by the `glm()` function in the R programming language (R Core Team 2024). GLMs add an additional layer of complexity compared to linear regression models, as the left-hand side of Equation 1 is a function of the mean of $\mathbf{y}$ rather than $\mathbf{y}$ itself (as in linear regression models).

The standard GLM assumes the elements of $\mathbf{y}$ are independent. This independence assumption is typically impractical for spatial data. For spatial data, nearby observations tend to be more similar than distant observations (Tobler 1970), which leads to positive spatial covariance. The consequences of ignoring spatial covariance in statistical models for spatial data can be severe and include imprecise parameter estimates as well as misleading standard errors that inflate Type-I error rates and decrease power (Zimmerman and Ver Hoef 2024).

An approach for handling spatial data using a GLM is to assume the elements of $\mathbf{w}$ exhibit covariance that varies spatially and nonspatially. This is achieved by adding to Equation 1 two random effects, $\boldsymbol{\tau}$ and $\boldsymbol{\epsilon}$. The random effect $\boldsymbol{\tau}$ is an $n \times 1$ column vector of spatially dependent random errors. We assume that $\mathrm{E}(\boldsymbol{\tau}) = \mathbf{0}$ and $\mathrm{Cov}(\boldsymbol{\tau}) = \sigma^2_\tau \mathbf{R}$, where $\mathrm{E}(\cdot)$ and $\mathrm{Cov}(\cdot)$ denote expectation and covariance, respectively. The variance parameter σ^2_τ controls the magnitude of spatial covariance and is often called a partial sill. The matrix $\mathbf{R}$ is an $n \times n$ spatial correlation matrix that depends on a range parameter controlling the distance-decay rate of the spatial correlation. One example of a spatial covariance matrix is the "exponential," which is given by

$$\mathrm{Cov}(\boldsymbol{\tau}) = \sigma^2_\tau \mathbf{R}_{exp} = \sigma^2_\tau \exp(-\mathbf{H}/\phi), \tag{2}$$

where $\mathbf{H}$ is a matrix of pairwise distances among the elements of $\mathbf{y}$ and ϕ is the range parameter. From Equation 2, as the distance between two elements of $\mathbf{y}$ increases, the spatial

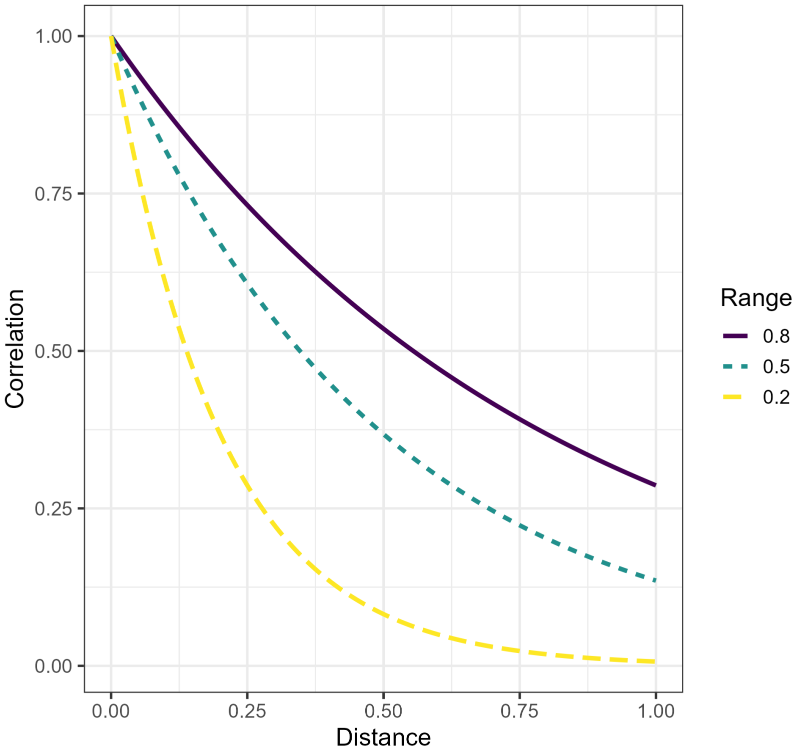

Figure 1: An exponential spatial correlation function with varying range parameters.

covariance decreases, which reflects intuition. Moreover, as the range parameter, ϕ, increases, the strength of spatial dependence increases (Figure 1). The random effect $\boldsymbol{\epsilon}$ is an $n \times 1$ column vector of independent random errors. We assume that $\mathrm{E}(\boldsymbol{\epsilon}) = \mathbf{0}$ and $\mathrm{Cov}(\boldsymbol{\tau}) = \sigma^2_\epsilon \mathbf{I}$, where $\mathbf{I}$ is an $n \times n$ identity matrix. The variance parameter σ^2_ϵ controls the magnitude of nonspatial variability (i.e., fine-scale variation) and is often called a nugget. Often in spatial statistics, quantities are explicitly referenced with respect to $\mathbf{s}$, a vector of spatial coordinates indexing the observation (Cressie 1993). For example, $\mathbf{y}$ and $\mathbf{X}$ may instead be written $\mathbf{y}(\mathbf{s})$ and $\mathbf{X}(\mathbf{s})$, respectively. We acknowledge the utility of this nomenclature but drop the explicit dependence on $\mathbf{s}$ for simplicity of notation moving forward.

Through inclusion of $\boldsymbol{\tau}$ and $\boldsymbol{\epsilon}$, the spatial GLM (SPGLM) can be written as

$$f(\boldsymbol{\mu}|\mathbf{X}, \boldsymbol{\beta}, \boldsymbol{\tau}, \boldsymbol{\epsilon}) \equiv \mathbf{w} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\tau} + \boldsymbol{\epsilon}. \tag{3}$$

Assuming independence among $\boldsymbol{\tau}$ and $\boldsymbol{\epsilon}$, it follows that

$$\mathrm{Cov}(\boldsymbol{\tau} + \boldsymbol{\epsilon}) = \mathrm{Cov}(\boldsymbol{\tau}) + \mathrm{Cov}(\boldsymbol{\epsilon}) = \sigma^2_\tau \mathbf{R} + \sigma^2_\epsilon \mathbf{I}.$$

Henceforth, we refer to σ^2_τ as σ^2_{de} (for spatially dependent error variance) and σ^2_ϵ as σ^2_{ie} (for independent error variance). The parameters σ^2_{de}, σ^2_{ie}, and ϕ, in addition to any other parameters in $\mathbf{R}$, compose $\boldsymbol{\theta}$, the covariance parameter vector.

Fitting and using SPGLMs is challenging both conceptually and computationally (Bolker, Brooks, Clark, Geange, Poulsen, Stevens, and White 2009). Recently, however, there have been numerous, significant advances in R software that have made these models more accessible to practitioners. The **brms** (Bürkner 2017), **carBayes** (Lee 2013), **ngspatial** (Hughes and

Cui 2020), **R-INLA** (Lindgren and Rue 2015) and **inlabru** (Bachl, Lindgren, Borchers, and Illian 2019), **spBayes** (Finley, Banerjee, and Carlin 2007), **spOccupancy** (Doser, Finley, Kéry, and Zipkin 2022), **spAbundance** (Doser, Finley, Kéry, and Zipkin 2024), and **spNNGP** (Finley, Datta, and Banerjee 2022) packages take a Bayesian approach, either directly sampling from posterior distributions of parameters (e.g., using MCMC) or approximating them. A benefit of Bayesian approaches is that prior information can be incorporated and uncertainty quantification of parameter estimates is straightforward. However, Bayesian approaches, especially those using MCMC, can be computationally expensive. In order to reduce computation time, many of these packages work with the precision matrix instead of the covariance matrix so that computationally expensive matrix inversion is not required. For example, **R-INLA** uses the precision matrix and tends to be very fast. Working with precision matrices, however, can be more restrictive and less intuitive than working directly with the covariance matrix. The **FRK** (Sainsbury-Dale, Zammit-Mangion, and Cressie 2024), **glmmTMB** (Brooks, Kristensen, van Benthem, Magnusson, Berg, Nielsen, Skaug, Maechler, and Bolker 2017), **hglm** (Ronnegard, Shen, and Alam 2010), **mgcv** (Wood 2017), and **spaMM** (Rousset and Ferdy 2014) packages directly use Laplace, quasi-likelihood, or reduced-rank approaches to estimate parameters. These direct approaches tend to be computationally efficient, as they don't rely on MCMC sampling. In contrast to the Bayesian approach, a drawback of these direct approaches is that prior information cannot be formally incorporated and covariance parameter uncertainty is more challenging to quantify. The **sdmTMB** (Anderson, Ward, English, Barnett, and Thorson 2024) package combines elements of **R-INLA**, **glmmTMB**, and Gaussian Markov random fields to fit a wide variety of SPGLMs, while **tinyVAST** (Thorson, Anderson, Goddard, and Rooper 2025) extends some of these models to multivariate or (dynamic) structural equation models.

Building from Evangelou, Zhu, and Smith (2011) and Bonat and Ribeiro Jr (2016), Ver Hoef, Blagg, Dumelle, Dixon, Zimmerman, and Conn (2024) proposed a novel approach for fitting SPGLMs that leverages the Laplace approximation while marginalizing over both the latent $\mathbf{w}$ and the fixed effects ($\boldsymbol{\beta}$) and accommodating general covariance structures, including spatial ones. This approach performed efficiently in a variety of simulation settings, generally having appropriate confidence interval coverage for the fixed effects and prediction interval coverage for $\mathbf{w}$ at new locations. The approach performed similarly to the Bayesian SPGLM approach in **spBayes** and the automatic differentiation SPGLM approach in **glmmTMB** but was much faster. At small sample sizes, the approach outperformed the approximate Bayesian SPGLM approach in **R-INLA** and had similar computational times. For moderate sample sizes, it performed similarly to **R-INLA**, though **R-INLA** was faster. The novel Laplace approach is particularly attractive for two reasons. First, it is general enough that it can be applied to any covariance structure (not just spatial). Second, after estimating the covariance parameters, analytical solutions exist for the fixed effects (and their standard errors) as well as predictions of the latent $\mathbf{w}$ at new locations (and their standard errors).

The **spmodel** R package (Dumelle, Higham, and Ver Hoef 2023) recently made public a full set of modeling tools for SPGLMs fit using the novel Laplace approach described by Ver Hoef *et al.* (2024). These modeling tools are approachable and mirror the familiar `glm()` syntax from base-R, making the transition from GLMs to SPGLMs relatively seamless. The `spglm()` function fits SPGLMs for point-referenced data (e.g., x- and y-coordinates representing point locations in a field; these models are sometimes called "geostatistical" models), while the `spgautor()` function fits SPGLMs for areal data (e.g., polygon boundaries representing geo-

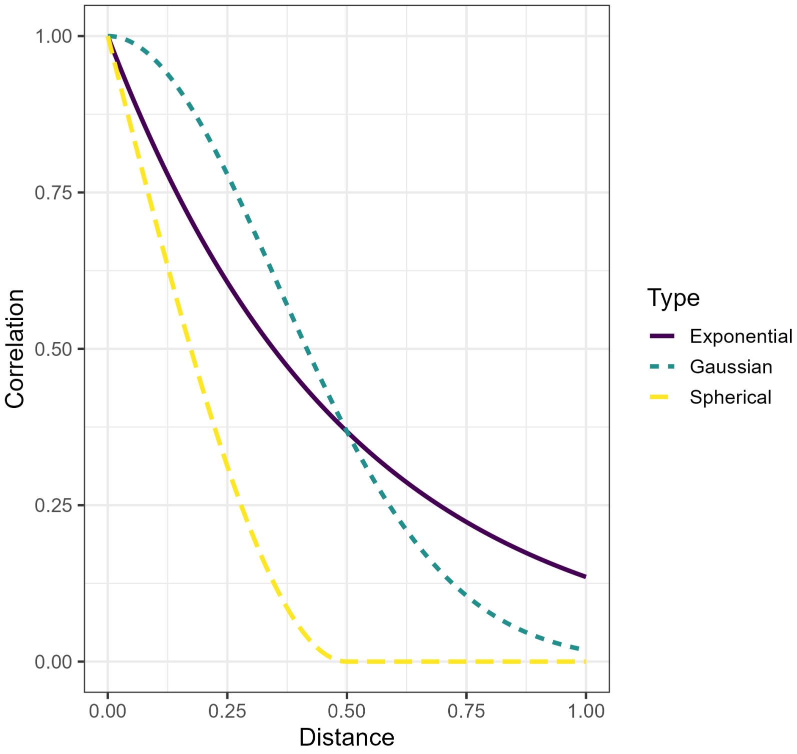

Figure 2: Exponential, Gaussian, and spherical spatial correlation functions all with range parameters equal to 0.5.

graphic subsets of a region; these models are sometimes called "autoregressive" models). For both point-referenced data and areal supports, **spmodel** supports the binomial distribution for binary data, Poisson and negative binomial distributions for count data, Gamma and inverse Gaussian distributions for skewed data, and the beta distribution for proportion data. There are 20 different spatial covariance structures available including the exponential, Gaussian, and spherical for point-referenced data (Figure 2) and the conditional autoregressive, and simultaneous autoregressive structures for areal data. **spmodel** provides tools for commonly used model summaries, visualizations, and diagnostics (e.g., Cook's distance) using standard R helper functions like `summary()`, `plot()`, `fitted()`, and `tidy()`, among others. **spmodel** also provides tools to predict $\mathbf{w}$ at new locations and quantify uncertainty in those prediction using `predict()` and `augment()`. This core functionality, combined with several advanced features we describe throughout the manuscript, enables **spmodel** to introduce novel, important SPGLM modeling tools previously missing from the existing R ecosystem.

Of the existing R packages for SPGLMs, **spmodel** (version 0.11.0) is arguably most similar to **sdmTMB** (version 0.7.4) in terms of scope and feel. Both packages use similar syntax as `glm()`, accommodate flexible `formula` arguments (e.g., offsets, splines), handle spatial covariance that decays at different rates in different directions (i.e., geometric anisotropy), incorporate nonspatial random effects, support other R packages for modeling like **broom** (Robinson, Hayes, and Couch 2021; Kuhn and Silge 2022), **emmeans** (Lenth 2024), and **car** (Fox and Weisberg 2019), and have tools for model summaries, prediction, and simulating data. There are some notable differences between the two packages, however. **sdmTMB** supports several additional GLM distributions like the Tweedie, supports Hurdle models, and can incorporate prior information through Bayesian applications. **sdmTMB** also provides tools for working with temporal data and spatiotemporal data and provides enhanced visualizations of the model's marginal effects. **sdmTMB** does require a preprocessing step of constructing a mesh prior to model fitting (using the stochastic partial differential equation approach), and the density of the mesh can affect model results and computational complexity. On the other hand, **spmodel** does not require the construction of a mesh prior to model fitting. **spmodel** supports 20 different spatial covariances and models them directly, rather than using a precision matrix approximation to the Matérn spatial covariance as in **sdmTMB**. **spmodel** can model data directly using neighborhood distance and autoregressive models, rather than relying on the polygon centroid (as in **sdmTMB**), which may not be within the polygon's boundaries. **spmodel** provides experimental design tools (e.g., analysis of variance, contrasts), supports **sf** objects in modeling and prediction functions (Pebesma 2018), has several specialized model diagnostics like leverage values and Cook's distances, and has analytic solutions for fixed effect and prediction standard errors. Other similarities and differences do exist between **sdmTMB** and **spmodel**, and both packages continue to evolve. Overall, we believe that these packages are complementary and enhance the suite of SPGLM tools accessible to practitioners.

The rest of this article is organized as follows. In Section 2, we provide some background for the SPGLM fitting and prediction routines in **spmodel**. In Section 3, we provide an overview of core SPGLM functionality in **spmodel** by modeling moose presence in Alaska, United States (US). In Section 4, we model moose counts in Alaska, US; skewed lake conductivity in the Southwestern US; harbor seal abundance trend behavior in Alaska, US; and voter turnout rates in Texas, US. And in Section 5, we end with a discussion synthesizing **spmodel**'s contributions to the analysis of SPGLMs in R.

2. The spatial generalized linear model and marginalization

The novel Laplace approach implemented in **spmodel** formally maximizes a hierarchical GLM likelihood (Lee and Nelder 1996; Wood 2017), making likelihood-based statistics for model comparison like AIC (Akaike 1974), AICc (Hoeting, Davis, Merton, and Thompson 2006), BIC (Schwarz 1978), deviance (McCullagh and Nelder 1989), and likelihood ratio tests available. These types of statistics are not available for quasi-likelihood (Wedderburn 1974; Breslow and Clayton 1993) or pseudo-likelihood approaches (Wolfinger and O'connell 1993), which only specify the first two moments of a distribution. Next, we describe a brief overview of the approach and how it can be used for several primary data analysis tasks (Tredennick, Hooker, Ellner, and Adler 2021) like model comparison, parameter estimation, inference, model diagnostics, and prediction. Then in Section 3 and Section 4, we show how to use **spmodel** to carry out these primary data analysis tasks with various data sets.

2.1. Formulating the hierarchical likelihood

We can write the SPGLM likelihood hierarchically as

$$[\mathbf{y}|\mathbf{X}, \varphi, \boldsymbol{\theta}] = \int_{\mathbf{w}} \int_{\boldsymbol{\beta}} [\mathbf{y}|f^{-1}(\mathbf{w}), \varphi][\mathbf{w}|\mathbf{X}, \boldsymbol{\beta}, \boldsymbol{\theta}] d\boldsymbol{\beta} d\mathbf{w}, \tag{4}$$

where $[\mathbf{y}|f^{-1}(\mathbf{w}), \varphi]$ is the density for the appropriate response distribution of $\mathbf{y}$ (e.g., binomial, Poisson) given the latent $\mathbf{w}$ and dispersion parameter (φ), and $[\mathbf{w}|\mathbf{X}, \boldsymbol{\beta}, \boldsymbol{\theta}]$ is the multivariate Gaussian density for $\mathbf{w}$ given the explanatory variables ($\mathbf{X}$), fixed effects ($\boldsymbol{\beta}$), and spatial covariance parameters ($\boldsymbol{\theta}$). The elements of $[\mathbf{y}|f^{-1}(\mathbf{w}), \varphi]$ are conditionally independent (given $\mathbf{w}$), but the elements of $[\mathbf{w}|\mathbf{X}, \boldsymbol{\beta}, \boldsymbol{\theta}]$ share spatial covariance. Following Harville (1977), we can integrate $\boldsymbol{\beta}$ out of Equation 4, which yields

$$[\mathbf{y}|\mathbf{X}, \varphi, \boldsymbol{\theta}] = \int_{\mathbf{w}} [\mathbf{y}|f^{-1}(\mathbf{w}), \varphi][\mathbf{w}|\mathbf{X}, \boldsymbol{\theta}] d\mathbf{w}, \tag{5}$$

where $[\mathbf{w}|\mathbf{X}, \boldsymbol{\theta}]$ is the restricted (i.e., residual) multivariate Gaussian density (Patterson and Thompson 1971) for $\mathbf{w}$ given the explanatory variables and covariance parameters. The restricted multivariate Gaussian density is given by

$$[\mathbf{w}|\mathbf{X}, \boldsymbol{\theta}] = \frac{\exp(-\frac{1}{2}(\mathbf{y} - \mathbf{X}\tilde{\boldsymbol{\beta}})\boldsymbol{\Sigma}^{-1}(\mathbf{y} - \mathbf{X}\tilde{\boldsymbol{\beta}})^\top)}{(2\pi)^{(n-p)/2}|\boldsymbol{\Sigma}|^{1/2}|\mathbf{X}^\top\boldsymbol{\Sigma}^{-1}\mathbf{X}|^{1/2}},$$

where $\tilde{\boldsymbol{\beta}} = (\mathbf{X}^\top\boldsymbol{\Sigma}^{-1}\mathbf{X})^{-1}\mathbf{X}^\top\boldsymbol{\Sigma}^{-1}\mathbf{w}$, $\boldsymbol{\Sigma}$ denotes the covariance matrix (of $\mathbf{w}$), and $|\cdot|$ denotes the determinant. Equation 5 can synonymously be written after profiling the overall variance out of $\boldsymbol{\Sigma}$, which reduces the dimension of $\boldsymbol{\theta}$ by one for optimization (Wolfinger, Tobias, and Sall 1994). Next, let

$$\ell_{\mathbf{w}} = \log([\mathbf{y}|f^{-1}(\mathbf{w}), \varphi][\mathbf{w}|\mathbf{X}, \boldsymbol{\theta}])$$

and rewrite Equation 5 as

$$[\mathbf{y}|\mathbf{X}, \varphi, \boldsymbol{\theta}] = \int_{\mathbf{w}} \exp(\ell_{\mathbf{w}}) d\mathbf{w}.$$

A second-order Taylor series expansion of $\ell_{\mathbf{w}}$ around a point $\hat{\mathbf{w}}$ yields

$$[\mathbf{y}|\mathbf{X}, \varphi, \boldsymbol{\theta}] \approx \int_{\mathbf{w}} \exp(\ell_{\hat{\mathbf{w}}} + \mathbf{g}^\top(\mathbf{w} - \hat{\mathbf{w}}) + \frac{1}{2}(\mathbf{w} - \hat{\mathbf{w}})^\top\mathbf{G}(\mathbf{w} - \hat{\mathbf{w}})) d\mathbf{w},$$

where $\mathbf{g}$ and $\mathbf{G}$ are the gradient and Hessian, respectively, of $\ell_{\mathbf{w}}$ with respect to $\mathbf{w}$. If $\hat{\mathbf{w}}$ is a value for which $\mathbf{g} = \mathbf{0}$,

$$[\mathbf{y}|\mathbf{X}, \varphi, \boldsymbol{\theta}] \approx \exp(\ell_{\hat{\mathbf{w}}}) \int_{\mathbf{w}} \exp(-\frac{1}{2}(\mathbf{w} - \hat{\mathbf{w}})^\top(-\mathbf{G})(\mathbf{w} - \hat{\mathbf{w}})) d\mathbf{w}. \tag{6}$$

The integral in Equation 6 can be solved by leveraging properties of the normalizing constant of a multivariate Gaussian distribution. Thus, rewriting $\exp(\ell_{\hat{\mathbf{w}}})$ yields

$$[\mathbf{y}|\mathbf{X}, \varphi, \boldsymbol{\theta}] \approx [\mathbf{y}|f^{-1}(\hat{\mathbf{w}}), \varphi][\hat{\mathbf{w}}|\mathbf{X}, \boldsymbol{\theta}](2\pi)^{n/2}| - \mathbf{G}_{\hat{\mathbf{w}}}|^{-1/2}. \tag{7}$$

Maximizing the natural logarithm of Equation 7 requires a doubly iterative process over $\boldsymbol{\theta}$ and φ as well as $\mathbf{w}$, eventually yielding the the marginal restricted maximum likelihood estimators $\hat{\varphi}$ and $\hat{\boldsymbol{\theta}}$ and their corresponding values of $\hat{\mathbf{w}}$. Maximizing this log likelihood requires repeatedly evaluating $\boldsymbol{\Sigma}^{-1}$, $\mathbf{g}$, and $\mathbf{G}$; see Ver Hoef *et al.* (2024) for more details and comparisons to other approaches as well as forms of $\mathbf{g}$ and $\mathbf{G}$ for various response distributions.

2.2. Estimating fixed effects

Though the fixed effects are integrated out of the likelihood, we can still estimate them using generalized least squares (GLS) principles, a common practice for linear models estimated using restricted maximum likelihood methods. Had we observed $\mathbf{w}$, a GLS estimator for $\boldsymbol{\beta}$ is given by

$$\hat{\boldsymbol{\beta}} = (\mathbf{X}^\top \boldsymbol{\Sigma}^{-1} \mathbf{X})^{-1} \mathbf{X}^\top \boldsymbol{\Sigma}^{-1} \mathbf{w} = \mathbf{B}\mathbf{w},$$

where $\mathbf{B} = (\mathbf{X}^\top \boldsymbol{\Sigma}^{-1} \mathbf{X})^{-1} \mathbf{X}^\top \boldsymbol{\Sigma}^{-1}$. However, we only observe $\hat{\mathbf{w}}$, so it is reasonable to define $\hat{\boldsymbol{\beta}} = \mathbf{B}\hat{\mathbf{w}}$. Thus, to derive properties of $\hat{\boldsymbol{\beta}}$ like expectation and variance, we must derive these properties for $\hat{\mathbf{w}}$. To do so, we must condition on $\mathbf{w}$ as if it were observed and invoke properties of the laws of total expectation and variance. Because $\hat{\mathbf{w}}$ was obtained by maximizing the likelihood, we may assume that given $\mathbf{w}$, $\hat{\mathbf{w}}$ has mean $\mathbf{w}$ and variance approximately equal to $-\mathbf{H}^{-1}$ (the inverse Hessian). It follows that $\mathrm{E}(\hat{\mathbf{w}})$ is given by

$$\mathrm{E}(\hat{\mathbf{w}}) = \mathrm{E}(\mathrm{E}(\hat{\mathbf{w}}|\mathbf{w})) = \mathrm{E}(\mathbf{w}) = \mathbf{X}\boldsymbol{\beta}$$

and $\mathrm{Var}(\hat{\mathbf{w}})$ is given by

$$\begin{aligned}\mathrm{Var}(\hat{\mathbf{w}}) &= \mathrm{E}(\mathrm{Var}(\hat{\mathbf{w}}|\mathbf{w})) + \mathrm{Var}(\mathrm{E}(\hat{\mathbf{w}}|\mathbf{w})) \\ &= \mathrm{E}(-\mathbf{H}^{-1}) + \mathrm{Var}(\mathbf{w}) \\ &= -\mathbf{H}^{-1} + \boldsymbol{\Sigma}\end{aligned}$$

Putting this all together, it follows that $\hat{\boldsymbol{\beta}}$ is unbiased for $\boldsymbol{\beta}$:

$$\mathrm{E}(\hat{\boldsymbol{\beta}}) = \mathrm{E}(\mathbf{B}\hat{\mathbf{w}}) = \mathbf{B}\mathrm{E}(\hat{\mathbf{w}}) = (\mathbf{X}^\top \boldsymbol{\Sigma}^{-1} \mathbf{X})^{-1} (\mathbf{X}^\top \boldsymbol{\Sigma}^{-1} \mathbf{X})\boldsymbol{\beta} = \boldsymbol{\beta}.$$

Moreover, it follows that

$$\begin{aligned}\mathrm{Var}(\hat{\boldsymbol{\beta}}) &= \mathrm{Var}(\mathbf{B}\hat{\mathbf{w}}) \\ &= \mathbf{B}\mathrm{Var}(\hat{\mathbf{w}})\mathbf{B}^\top \\ &= \mathbf{B}(-\mathbf{H}^{-1} + \boldsymbol{\Sigma})\mathbf{B}^\top \\ &= \mathbf{B}(-\mathbf{H})^{-1}\mathbf{B}^\top + \mathbf{B}\boldsymbol{\Sigma}\mathbf{B}^\top \\ &= \mathbf{B}(-\mathbf{H})^{-1}\mathbf{B}^\top + (\mathbf{X}^\top \boldsymbol{\Sigma}^{-1} \mathbf{X})^{-1}.\end{aligned}$$

In practice, $\mathrm{Var}(\hat{\boldsymbol{\beta}})$ is estimated by evaluating $\boldsymbol{\Sigma}$ at $\hat{\boldsymbol{\theta}}$, the estimated covariance parameter vector.

These results are important because they justify closed-form solutions for $\hat{\boldsymbol{\beta}}$ and its associated variance. Closed-form solutions are useful because they bypass the need for sampling-based strategies to evaluate the mean and variance of $\hat{\boldsymbol{\beta}}$, a common technique for other approaches to SPGLMs like Bayesian MCMC.

2.3. Inspecting model diagnostics

Inspecting model diagnostics is an important step of the modeling process that can yield valuable insights into model behavior and unusual observations. Montgomery, Peck, and Vining (2021) contextualize three components of unusual observations: outliers, leverage, and influence. An observation is an outlier if it has an extreme response value relative to expectation. The response GLM residuals simply compare the observation to its fitted latent mean:

$$\mathbf{r}_r = \mathbf{y} - f^{-1}(\hat{\mathbf{w}})$$

Because observations often have a unique support in a GLM (e.g., only two possible response values for binary data) and the variance of an observation generally depends on its mean, response residuals lack some utility. Deviance residuals are a function of response residuals that are appropriately scaled to behave more like response residuals in a standard linear model. Deviance residuals are given by

$$\mathbf{r}_d = sign(\mathbf{r}_r)\sqrt{\mathbf{d}},$$

where $\mathbf{d}$ is a vector of individual deviances. The sum of the squared deviance residuals equals the sum of $\mathbf{d}$. The sum of $\mathbf{d}$ is the deviance of the model fit, which quantifies twice the difference in log likelihoods between the a saturated model that fits every observation perfectly (i.e., $\mathbf{y} = f^{-1}(\hat{\mathbf{w}}_i)$ for all i) and the fitted model (Myers, Montgomery, Vining, and Robinson 2012). Deviance is often used as a fit statistic; lower values of deviance imply a better model fit (compared to the observed data). Pearson and standardized residuals are other types of GLM residuals that involve a scaling of the response residuals; the Pearson residuals scale $\mathbf{r}_r$ by the square root of $\mathbf{V}$, while the standardized residuals scale the deviance residuals by $\frac{1}{\sqrt{(1-\mathbf{L}_{ii})}}$, where $\mathbf{L}_{ii}$ is the ith diagonal element of the leverage matrix, which we discuss next.

An observation has high leverage if its combination of explanatory variables is far away from other observations. In a linear model, the leverage (i.e., hat) values are the diagonal of the leverage (i.e., projection, hat) matrix, $\mathbf{L} = \mathbf{X}(\mathbf{X}^\top\mathbf{X})^{-1}\mathbf{X}^\top$. In a GLM, the leverage matrix is given by

$$\mathbf{L} = \mathbf{V}^{1/2}\mathbf{X}(\mathbf{X}^\top\mathbf{V}\mathbf{X})\mathbf{X}^\top\mathbf{V}^{1/2},$$

where $\mathbf{V}$ is a diagonal matrix with ith diagonal element equal to the variance of the response distribution evaluated at $f^{-1}(\mathbf{w}_i)$ (Faraway 2016); $\mathbf{V}$ is sometimes called the GLM weight matrix. The larger the value of $\mathbf{L}_{ii}$, the more severe the leverage from the ith observation.

An observation is influential if it has a sizable impact on model fit. Influence is measured using Cook's distance (Cook 1979; Cook and Weisberg 1982), which is given for a GLM by

$$\mathbf{c} = \frac{\mathbf{r}_s^2}{\mathrm{tr}(\mathbf{L})}\frac{diag(\mathbf{L})}{(\mathbf{1} - diag(\mathbf{L}))},$$

where $\mathbf{r}_s^2$ are the standardized residuals and $diag(\mathbf{L})$ indicates the diagonal elements of the leverage matrix. The larger the value of $\mathbf{c}_i$, the more severe the influence from the ith observation. Montgomery *et al.* (2021) provide guidance for interpreting these types of statistics, including cutoffs to consider when identifying extreme residual, leverage, or influence values.

In a linear model, the R^2 (R-squared) statistic quantifies the proportion of variability in the data captured by the explanatory variables. It is calculated as one minus the ratio of the error sum of squares to the total sum of squares (Rencher and Schaalje 2008). In a GLM, there are many ways to define a statistic that emulates the aforementioned meaning of R^2 from the linear model (Smith and McKenna 2013). This statistic is called a pseudo R-squared (PR^2).

One PR^2 for GLMs simply replaces the sums of squares ratio from the linear model with the deviance ratio:

$$PR^2 = 1 - \frac{deviance_{error}}{deviance_{total}},$$

where $deviance_{error}$ is the deviance of the fitted model (sometimes called the error or residual deviance) and $deviance_{total}$ is the deviance of the intercept-only model (sometimes called the total or null deviance). In practice, $deviance_{total}$ is derived by computing $\hat{\mathbf{w}}$ when $\mathbf{X} \equiv \mathbf{1}$ (a column of all ones), given $\hat{\boldsymbol{\theta}}$ and $\hat{\varphi}$ from the fitted model. Like R^2, PR^2 can be adjusted to account for the numbers of parameters estimated in a model. Like R^2, PR^2 can be adjusted to account for the numbers of parameters estimated in a model. Because the $deviance_{total}$ denominator changes across fitted models (as the values of $\hat{\boldsymbol{\theta}}$ and $\hat{\varphi}$ change), this statistic should not be used as a model comparison tool. Rather, it should be used as an informative diagnostic tool that is unique to each model fit and describes how much variability from that model is attributable to the explanatory variables.

2.4. Predicting at new locations

We may also predict values of the latent mean (on the link scale) at new locations by leveraging the spatial covariance between observed locations and new locations (spatial prediction is also called Kriging; see Cressie (1990)). Again suppose that we observed $\mathbf{w}$ and we want to make predictions at $\mathbf{u}$, a vector of latent means at the new locations that follows the same SPGLM from Equation 3 and has design matrix, $\mathbf{X_u}$. The vector $(\mathbf{w}, \mathbf{u})^\top$ has expectation $(\mathbf{X}\boldsymbol{\beta}, \mathbf{X_u}\boldsymbol{\beta})^\top$ and covariance matrix $\begin{bmatrix} \boldsymbol{\Sigma} & \boldsymbol{\Sigma}_{\mathbf{wu}} \\ \boldsymbol{\Sigma}_{\mathbf{uw}} & \boldsymbol{\Sigma}_{\mathbf{uu}} \end{bmatrix}$, where $\boldsymbol{\Sigma} = \mathrm{Var}(\mathbf{w}, \mathbf{w})$, $\boldsymbol{\Sigma}_{\mathbf{wu}} = \mathrm{Var}(\mathbf{w}, \mathbf{u})$, $\boldsymbol{\Sigma}_{\mathbf{uw}} = \boldsymbol{\Sigma}_{\mathbf{wu}}^\top$ and $\boldsymbol{\Sigma}_{\mathbf{u,u}} = \mathrm{Var}(\mathbf{u}, \mathbf{u})$. By assumption, we have observed $\mathbf{w}$, so we may derive the conditional distribution of $\mathbf{u}|\mathbf{w}$, which has the following properties:

$$\begin{aligned} \mathrm{E}(\mathbf{u}|\mathbf{w}) &= \mathbf{X_u}\boldsymbol{\beta} + \boldsymbol{\Sigma}_{\mathbf{u,w}}\boldsymbol{\Sigma}^{-1}(\mathbf{w} - \mathbf{X}\boldsymbol{\beta}) \\ \mathrm{Var}(\mathbf{u}|\mathbf{w}) &= \boldsymbol{\Sigma}_{\mathbf{u,u}} - \boldsymbol{\Sigma}_{\mathbf{u,w}}\boldsymbol{\Sigma}^{-1}\boldsymbol{\Sigma}_{\mathbf{w,u}} \end{aligned}$$

Ver Hoef *et al.* (2024) show how these equations are adjusted to reflect uncertainty in both $\hat{\boldsymbol{\beta}}$ and $\hat{\mathbf{w}}$ while leveraging the laws of total expectation and variance yet again. They derive the predictor of $\mathbf{u}$, $\hat{\mathbf{u}}$, and its associated variance, given by:

$$\begin{aligned} \hat{\mathbf{u}} &= \mathbf{X_u}\hat{\boldsymbol{\beta}} + \boldsymbol{\Sigma}_{\mathbf{u,w}}\boldsymbol{\Sigma}^{-1}(\hat{\mathbf{w}} - \mathbf{X}\hat{\boldsymbol{\beta}}) \\ \mathrm{Var}(\hat{\mathbf{u}}) &= \boldsymbol{\Sigma}_{\mathbf{u,u}} - \boldsymbol{\Sigma}_{\mathbf{u,w}}\boldsymbol{\Sigma}^{-1}\boldsymbol{\Sigma}_{\mathbf{w,u}} + \mathbf{K}(\mathbf{X}^\top\boldsymbol{\Sigma}^{-1}\mathbf{X})^{-1}\mathbf{K}^\top + \boldsymbol{\Lambda}(-\mathbf{H})^{-1}\boldsymbol{\Lambda}^\top, \end{aligned}$$

where $\mathbf{K} = \mathbf{X_u} - \boldsymbol{\Sigma}_{\mathbf{u,w}}\boldsymbol{\Sigma}^{-1}\mathbf{X}$ and $\boldsymbol{\Lambda} = \mathbf{X_u}\mathbf{B} + \boldsymbol{\Sigma}_{\mathbf{u,w}}\boldsymbol{\Sigma}^{-1}(\mathbf{1} - \mathbf{X}\mathbf{B})$ for a vector of ones, $\mathbf{1}$. As with $\hat{\boldsymbol{\beta}}$, in practice these covariance matrices are evaluated at $\hat{\boldsymbol{\theta}}$.

3. Modeling moose presence in Alaska, USA

The `moose` data in **spmodel** contain information on moose (Alces Alces) presence in the Togiak region of Alaska, USA. `moose` is an `sf` object, a special data frame that is supplemented with spatial information using the **sf** package in R (Pebesma 2018). After loading **spmodel**, the first few rows of `moose` look like:

```
R> library("spmodel")
```

```
R> head(moose)
```

```
Simple feature collection with 6 features and 4 fields
Geometry type: POINT
Dimension:     XY
Bounding box:  xmin: 281896.4 ymin: 1518398 xmax: 311325.3 ymax: 1541016
Projected CRS: NAD83 / Alaska Albers
# A tibble: 6 x 5
   elev strat count presence           geometry
  <dbl> <chr> <dbl> <fct>           <POINT [m]>
1  469. L         0 0        (293542.6 1541016)
2  362. L         0 0        (298313.1 1533972)
3  173. M         0 0        (281896.4 1532516)
4  280. L         0 0        (298651.3 1530264)
5  620. L         0 0        (311325.3 1527705)
6  164. M         0 0        (291421.5 1518398)
```

There are five columns: `elev`, the numeric site elevation (meters); `strat` a stratification variable for sampling with two levels, `"L"` and `"M"`, which are categorized by landscape metrics at each site; `count`, the number of moose at each site; `presence`, a factor that indicates whether at least one moose was observed at each site (`0` implies no moose; `1` implies at least one moose); and `geometry`, the NAD83/Alaska Albers (EPSG: 3338) projected coordinate of each site. These data are point-referenced because each observation occurs at point coordinates and are represented by a `POINT` geometry. Moose are most prevalent in the southwestern and eastern parts of the Togiak region (Figure 3).

The `moose_preds` data in **spmodel** is an `sf` object with point locations at which moose presence predictions are desired. Like `moose`, `moose_preds` contains `elev` and `strat` for each site:

```
R> head(moose_preds)
```

```
Simple feature collection with 6 features and 2 fields
Geometry type: POINT
Dimension:     XY
Bounding box:  xmin: 291839.8 ymin: 1436192 xmax: 401239.6 ymax: 1512103
Projected CRS: NAD83 / Alaska Albers
# A tibble: 6 x 3
   elev strat           geometry
  <dbl> <chr>        <POINT [m]>
1  143. L     (401239.6 1436192)
2  324. L     (352640.6 1490695)
3  158. L     (360954.9 1491590)
4  221. M     (291839.8 1466091)
5  209. M     (310991.9 1441630)
6  218. L     (304473.8 1512103)
```

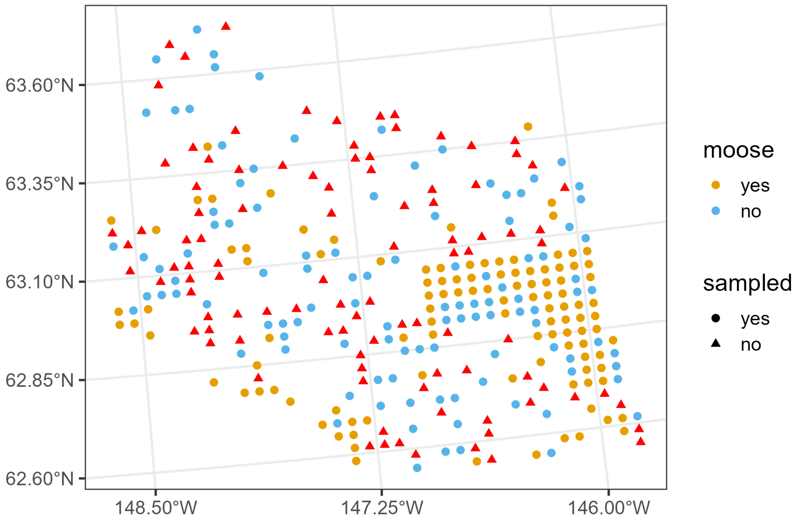

Figure 3: Moose presence in Alaska. Circles represent moose presence or absence (based on color) and triangles represent locations at which moose presence probability predictions are desired.

3.1. Model Fitting

SPGLMs in **spmodel** for point-referenced data are fit using the `spglm()` function. The `spglm()` function requires four arguments: `formula`, the relationship between the response and explanatory variables; `family`, the response distribution assumed for the response variable; `data`, the data frame that contains the variables in `formula`, and `spcov_type`, the type of spatial covariance. The `formula`, `family`, and `data` arguments are the three required arguments to `glm()` for nonspatial GLMs. So, the transition from `glm()` to `spglm()` simply requires one additional argument: `spcov_type`. When `data` is not an `sf` object, `spglm()` also requires the `xcoord` and `ycoord` arguments, which indicate the columns in `data` that represent the projected x- and y-coordinates, respectively.

We use `spglm()` to fit a SPGLM (i.e., here, a spatial logistic regression model) quantifying the effect of elevation and strata on moose presence:

```
R> spbin <- spglm(
+   formula = presence ~ elev + strat,
+   family = binomial,
+   data = moose,
+   spcov_type = "exponential"
+ )
```

The `summary()` function returns a model summary with relevant information like the function call, deviance residuals, a coefficients table of fixed effects, the pseudo R-squared, spatial covariance parameters, and the GLM dispersion parameter (fixed at one in logistic regression):

```
R> summary(spbin)
```

```
Call:
spglm(formula = presence ~ elev + strat, family = binomial, data = moose,
    spcov_type = "exponential")

Deviance Residuals:
    Min      1Q  Median      3Q     Max
-1.7535 -0.8005  0.3484  0.7893  1.5797

Coefficients (fixed):
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.465713   1.486212  -1.659 0.097104 .
elev         0.006036   0.003525   1.712 0.086861 .
stratM       1.439273   0.420591   3.422 0.000622 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Pseudo R-squared: 0.06275

Coefficients (exponential spatial covariance):
       de        ie     range
5.145e+00 1.294e-03 4.199e+04

Coefficients (Dispersion for binomial family):
dispersion
         1
```

The model provides some evidence that elevation is positively associated with the log odds of moose presence (p value ≈ 0.087), after controlling for strata. The model also provides strong evidence that moose have a higher log odds of presence in the "M" strata compared to the "L" strata (p value < 0.001), after controlling for elevation.

The fixed effects coefficients table from `summary()` is often of primary scientific interest, but it is not immediately usable when printed directly to the R console. The `tidy()` function tidies this table, turning it into a data frame (i.e., a tibble) with standard column names:

```
R> tidy(spbin, conf.int = TRUE)
```

```
# A tibble: 3 x 7
  term        estimate std.error statistic  p.value conf.low conf.high
  <chr>          <dbl>     <dbl>     <dbl>    <dbl>    <dbl>     <dbl>
1 (Intercept) -2.47      1.49        -1.66 0.0971   -5.38e+0    0.447
2 elev         0.00604   0.00353      1.71 0.0869   -8.73e-4    0.0129
3 stratM       1.44      0.421        3.42 0.000622  6.15e-1    2.26
```

3.2. Model Comparison

The strength of spatial covariance in the data affects how beneficial an SPGLM is relative to a GLM. When the spatial covariance is strong, the SPGLM should notably outperform the GLM. When the spatial covariance is weak, the SPGLM and GLM should perform similarly. We can quantify the benefits of incorporating spatial covariance for a particular data set by comparing the fit of a SPGLM to a GLM. We can fit a GLM in `spmodel` by specifying `spcov_type = "none"`:

```
R> bin <- spglm(
+   formula = presence ~ elev + strat,
+   family = binomial,
+   data = moose,
+   spcov_type = "none"
+ )
```

While the `spglm()` approach evaluates the HGLMM likelihood with $\sigma^2_{de} = 0$ and $\sigma^2_{ie} \approx 0$ instead of just the GLM likelihood, the parameter estimates and their standard errors are the same:

```
R> bin_glm <- glm(
+   formula = presence ~ elev + strat,
+   family = binomial,
+   data = moose,
+ )
R> round(coef(bin), digits = 4)

(Intercept)        elev      stratM
    -0.4247     -0.0003      0.8070

R> round(coef(bin_glm), digits = 4)

(Intercept)        elev      stratM
    -0.4247     -0.0003      0.8070

R> round(sqrt(diag(vcov(bin))), digits = 4)

(Intercept)        elev      stratM
     0.4208      0.0019      0.2906

R> round(sqrt(diag(vcov(bin_glm))), digits = 4)

(Intercept)        elev      stratM
     0.4208      0.0019      0.2906
```

However, using `spglm()` instead of `glm()` ensures that **spmodel** helper functions are available and that each of the `spglm()` models uses the same likelihood:

```
R> glance(spbin)

# A tibble: 1 x 10
      n     p  npar value   AIC  AICc   BIC logLik deviance
  <int> <dbl> <int> <dbl> <dbl> <dbl> <dbl>  <dbl>    <dbl>
1   218     3     3  676.  682.  683.  693.  -338.     176.
# i 1 more variable: pseudo.r.squared <dbl>

R> glance(bin)

# A tibble: 1 x 10
      n     p  npar value   AIC  AICc   BIC logLik deviance
  <int> <dbl> <int> <dbl> <dbl> <dbl> <dbl>  <dbl>    <dbl>
1   218     3     0  708.  708.  708.  708.  -354.     294.
# i 1 more variable: pseudo.r.squared <dbl>
```

The likelihood-based statistics AIC, AICc, BIC, and deviance are much lower for the SPGLM, indicating a better fit relative to the GLM. We may also perform a likelihood ratio test (LRT) between the two models, as the GLM is a special case of the SPGLM (i.e., is nested within the SPGLM):

```
R> anova(spbin, bin)

Likelihood Ratio Test

Response: presence
             Df   Chi2 Pr(>Chi2)
spbin vs bin  3 31.546 6.525e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The LRT provides strong evidence that the SPGLM is preferred to the GLM (p value $<$ 0.001).

An alternative approach to model comparison is to use a cross-validation procedure (James, Witten, Hastie, and Tibshirani 2013). The `loocv()` function performs leave-one-out cross validation, comparing the predicted mean (on the response scale) to the observed response variable for each hold-out observation, recomputing estimates of $\boldsymbol{\beta}$ in each iteration. Performing leave-one-out cross validation tends to be more computationally efficient than fitting the model, as leave-one-out cross validation requires only one set of products involving the inverse covariance matrix (a primary computational burden), while fitting traditional models requires these products for each optimization iteration. After performing leave-one-out cross validation, statistics like bias, mean-squared-prediction error (MSPE), and the square root of MSPE (RMSPE) can be used to evaluate models:

```
R> loocv(spbin)
```

```
# A tibble: 1 x 3
       bias  MSPE RMSPE
      <dbl> <dbl> <dbl>
1 0.0000206 0.156 0.394
```

```
R> loocv(bin)
```

```
# A tibble: 1 x 3
      bias  MSPE RMSPE
     <dbl> <dbl> <dbl>
1 -1.23e-9 0.240 0.490
```

Both models have negligible bias, but the SPGLM has much lower MSPE and RMSPE than the GLM, indicating the SPGLM predictions are far more efficient. Three separate metrics (likelihood-based statistics, likelihood-ratio test, and leave-one-out cross validation) prefer the SPGLM to the GLM.

We can compare two SPGLMs with different spatial covariance functions using likelihood-based statistics and leave-one-out cross validation, but we can't use the LRT because generally, the spatial covariance functions are not nested:

```
R> spbin2 <- update(spbin, spcov_type = "gaussian")
R> glances(spbin, spbin2)
```

```
# A tibble: 2 x 11
  model      n     p  npar value   AIC  AICc   BIC logLik deviance
  <chr>  <int> <dbl> <int> <dbl> <dbl> <dbl> <dbl>  <dbl>    <dbl>
1 spbin2   218     3     3  674.  680.  680.  690.  -337.     198.
2 spbin    218     3     3  676.  682.  683.  693.  -338.     176.
# i 1 more variable: pseudo.r.squared <dbl>
```

```
R> loocv(spbin)
```

```
# A tibble: 1 x 3
       bias  MSPE RMSPE
      <dbl> <dbl> <dbl>
1 0.0000206 0.156 0.394
```

```
R> loocv(spbin2)
```

```
# A tibble: 1 x 3
       bias  MSPE RMSPE
      <dbl> <dbl> <dbl>
1 -0.000261 0.146 0.382
```

The "exponential" spatial covariance (spbin) has a slightly lower (better) deviance but slightly higher (worse) AIC, AICc, and BIC than the "gaussian" spatial covariance (spbin2).

Both spatial covariance functions have similar leave-one-out cross validation metrics, though the "gaussian" spatial covariance RMSPE is slightly lower (better). For practical purposes, these models fit similarly.

Frequently in spatial statistics, the difference in model fit between the best spatial model and worst spatial model is much smaller than the difference in model fit between the worst spatial model and the nonspatial model, implying that accounting for some form of spatial covariance is very beneficial. Two spatial covariance functions to consider starting with are the exponential and Gaussian, which have quite different origin behaviors (Figure 2), something Stein (1999) argues is important to characterize accurately.

3.3. Model Diagnostics

spmodel provides a suite of tools for model diagnostics. One is augment(), which augments the data used in the model with several model diagnostics (introduced in Section 2.3):

```
R> augment(spbin)
```

```
Simple feature collection with 218 features and 8 fields
Geometry type: POINT
Dimension:     XY
Bounding box:  xmin: 269085 ymin: 1416151 xmax: 419057.4 ymax: 1541016
Projected CRS: NAD83 / Alaska Albers
# A tibble: 218 x 9
   presence  elev strat .fitted .resid    .hat  .cooksd .std.resid
 * <fct>    <dbl> <chr>   <dbl>  <dbl>   <dbl>    <dbl>      <dbl>
 1 0         469. L       -1.95 -0.516 0.0476  0.00465      -0.528
 2 0         362. L       -2.70 -0.361 0.0123  0.000548     -0.363
 3 0         173. M       -1.96 -0.514 0.00455 0.000405     -0.516
 4 0         280. L       -3.15 -0.290 0.00413 0.000117     -0.291
 5 0         620. L       -1.19 -0.728 0.168   0.0427       -0.798
 6 0         164. M       -1.71 -0.576 0.00534 0.000598     -0.578
 7 0         164. M       -1.60 -0.606 0.00576 0.000714     -0.608
 8 0         186. L       -2.50 -0.397 0.00439 0.000233     -0.398
 9 0         362. L       -1.88 -0.532 0.0239  0.00237      -0.539
10 0         430. L       -1.54 -0.623 0.0497  0.00713      -0.639
# i 208 more rows
# i 1 more variable: geometry <POINT [m]>
```

The fitted values (.fitted) can be returned on either the link ($\hat{\mathbf{w}}$) or response ($f^{-1}(\hat{\mathbf{w}})$) scale and the residuals (.resid) can be deviance, Pearson, or response residuals. The default fitted values are on the link scale and the default residuals are deviance residuals. Also returned by augment() are the leverage (.hat), Cook's distance (.cooksd), and standardized residuals (.std.resid) described in Section 2.3. A benefit of using augment() when data is an sf object is that the output is also an sf object, which makes it straightforward to create spatial diagnostic plots (Figure 4). Standard R helpers (e.g., fitted(), residuals()) are also available to extract model diagnostics from the model object.

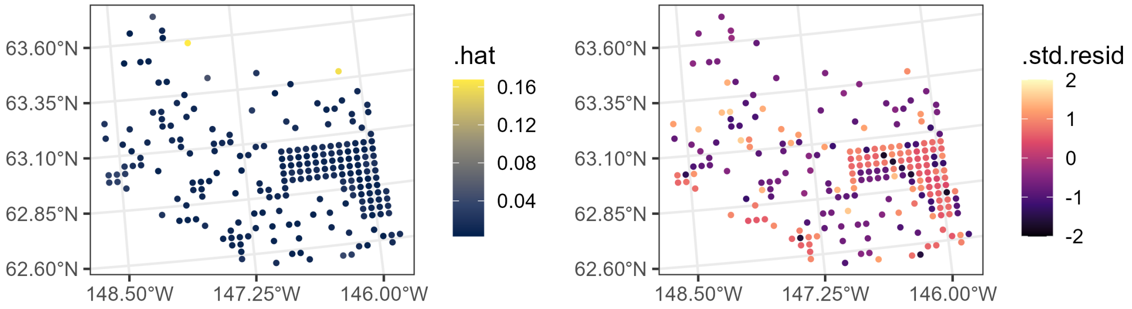

Figure 4: Moose presence model diagnostics, including leverage values (left) and standardized residuals (right).

The `plot()` function can also be used to return similar diagnostics as from `lm()` and `glm()`, with additional tools for diagnosing spatial covariance. For example, we can inspect Cook's distance values and the empirical spatial covariance as a function of distance with (Figure 5):

```
R> plot(spbin, which = c(4, 7))
```

The `varcomp()` function partitions model variability into several different components, helping to elucidate the model's structure:

```
R> varcomp(spbin)

# A tibble: 3 x 2
  varcomp              proportion
  <chr>                     <dbl>
1 Covariates (PR-sq)     0.0627
2 de                     0.937
3 ie                     0.000236
```

The pseudo R-squared (PR^2) is reported in the first row. The remaining variability ($1-PR^2$) is allocated proportionally to `de` and `ie` according to σ^2_{de} and σ^2_{ie}. This variability partitioning is a useful tool that helps quantify how much the explanatory variables, residual spatial variance, and residual nonspatial variance contribute to model fit; as with PR^2, it should not be used for model comparison, but rather as a helpful model diagnostic.

3.4. Prediction

We can predict the probability of moose presence at the locations in `moose_preds` using `predict()`:

```
R> predict(spbin, newdata = moose_preds)[1:5]

          1           2           3           4           5
 0.06664165 -0.79069107 -1.60387940 -0.83159357  1.38183928
```

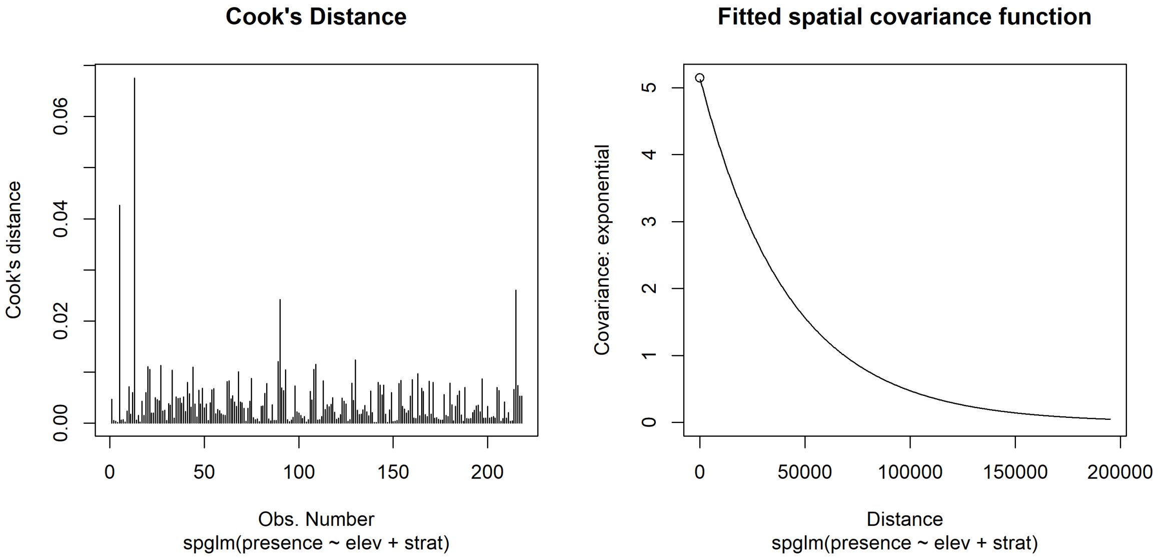

Figure 5: Moose presence model diagnostics, including Cook's distance (left) and the fitted spatial covariance as a function of distance (right).

By default, predictions are returned on the link scale, but this can be changed to the response scale via `type`:

```
R> predict(spbin, newdata = moose_preds, type = "response")[1:5]
```

```
        1         2         3         4         5 
0.5166542 0.3120203 0.1674401 0.3033082 0.7992862 
```

Predictions on the response scale are visualized alongside the fitted values ($f^{-1}(\hat{\mathbf{w}})$) in Figure 6. Prediction intervals for the probability of moose presence (on the link scale) are returned by supplying `interval`:

```
R> predict(spbin, newdata = moose_preds, interval = "prediction")[1:5, ]
```

```
          fit        lwr       upr
1  0.06664165 -2.0374370 2.1707203
2 -0.79069107 -3.4758514 1.8944692
3 -1.60387940 -4.0953329 0.8875741
4 -0.83159357 -3.0704818 1.4072947
5  1.38183928 -0.7692107 3.5328893
```

We can alternatively use `augment()` to augment the prediction data with predictions. Arguments to `predict()` can also be passed to `augment()`:

```
R> augment(spbin, newdata = moose_preds, interval = "prediction")
```

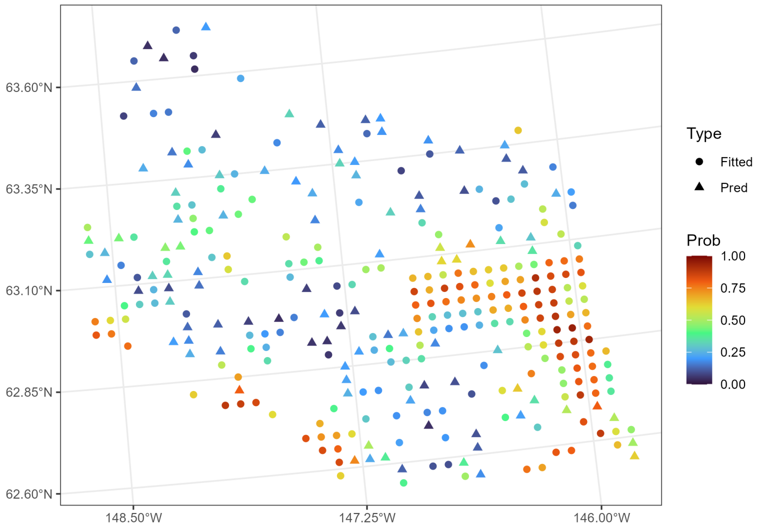

Figure 6: Moose presence probability fitted values and predictions. Fitted values are represented by circles and predictions by triangles.

```
Simple feature collection with 100 features and 5 fields
Geometry type: POINT
Dimension:     XY
Bounding box:  xmin: 269386.2 ymin: 1418453 xmax: 419976.2 ymax: 1541763
Projected CRS: NAD83 / Alaska Albers
# A tibble: 100 x 6
    elev strat .fitted .lower  .upper           geometry
 * <dbl> <chr>   <dbl>  <dbl>   <dbl>        <POINT [m]>
 1  143. L      0.0666 -2.04   2.17   (401239.6 1436192)
 2  324. L     -0.791  -3.48   1.89   (352640.6 1490695)
 3  158. L     -1.60   -4.10   0.888  (360954.9 1491590)
 4  221. M     -0.832  -3.07   1.41   (291839.8 1466091)
 5  209. M      1.38   -0.769  3.53   (310991.9 1441630)
 6  218. L     -2.59   -5.20   0.0177 (304473.8 1512103)
 7  127. L     -2.73   -5.24  -0.220  (339011.1 1459318)
 8  122. L     -2.32   -4.74   0.0920 (342827.3 1463452)
 9  191  L     -1.17   -4.01   1.66   (284453.8 1502837)
10  105. L     -0.905  -3.05   1.24   (391343.9 1483791)
# i 90 more rows
```

By using `augment()` when `newdata` is an `sf` object, predictions and their corresponding uncertainties are readily available for spatial mapping (Figure 7).

4. Additional applications

Throughout the remainder of this section, we briefly highlight some additional **spmodel** capabilities for SPGLMs. In Section 4.1, we fit Poisson and negative binomial models with

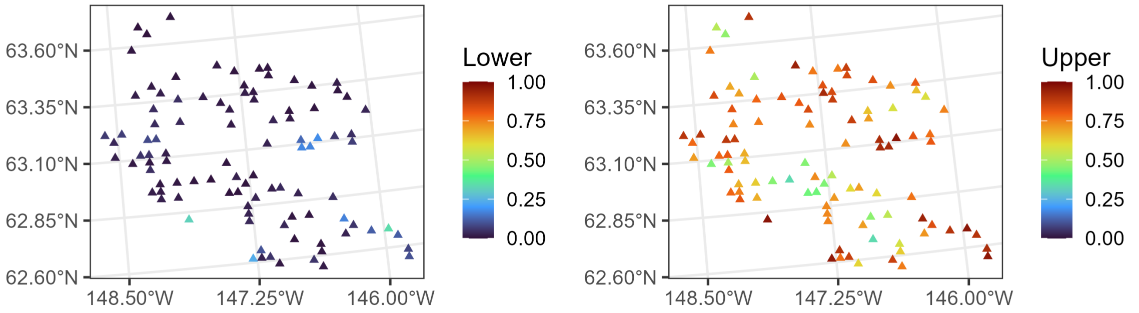

Figure 7: Moose presence 95% prediction interval lower bounds (left) and upper bounds (right).

Section	Data	Family	Geometry	Additional Features
4.1	Moose Counts	Poisson NBinomial	Point	Geometric Anisotropy
4.2	Lake Conductivity	Gamma	Point	Partition Factor ANOVA Contrasts
4.3	Harbor Seals	Binomial	Areal	Nonspatial Random Effects
4.4	Texas Voter Turnout	Beta	Point Areal	Likelihood-Ratio Test

Table 1: Section number, data set, family, geometry type, and additional features for each application.

and without geometric anisotropy for the point-referenced moose count data. In Section 4.2, we fit a Gamma model to the point-referenced lake conductivity data, showing how to fit a model with a partition factor, perform a spatial analysis of variance (ANOVA), and estimate contrasts for models with interactions. In Section 4.3, we fit a binomial model to the areal harbor seal trend data with a nonspatial random effect. Finally in Section 4.4, we fit beta models to Texas voter turnout data, which can be treated as point-referenced or areal, and use maximum likelihood to compare two models with different explanatory variables. Table 1 outlines, for each application, the section number, data set, family (i.e., response distribution), geometry type (point-referenced or areal), and additional **spmodel** features highlighted.

4.1. Modeling moose counts in Alaska, USA

In addition to moose presence, moose counts are also recorded in `moose` (Figure 8). The Poisson and negative binomial response distributions can be used to model SPGLMs for count data. The Poisson distribution mean is equal to its variance, while the negative binomial has an extra parameter to accommodate overdispersion (where the variance is larger than the mean). Using a spherical spatial covariance function, we may fit both a Poisson and negative binomial SPGLM changing the `family` argument:

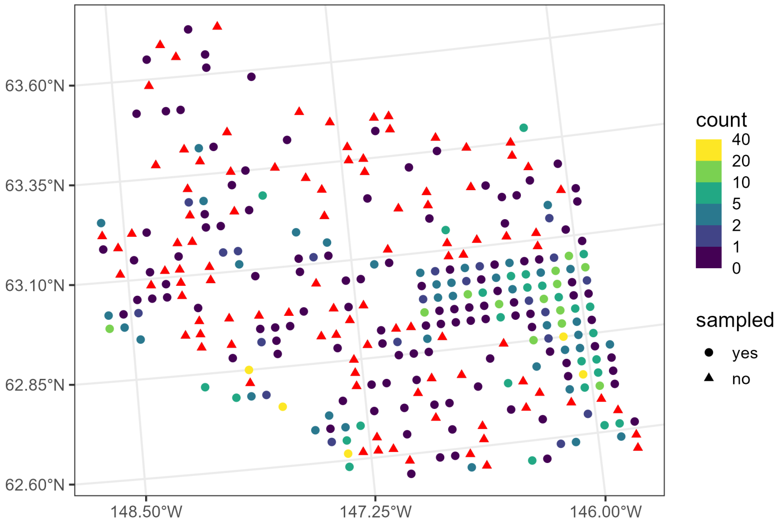

Figure 8: Moose counts in Alaska. Circles represent moose counts (based on color) and triangles represent locations at which mean count predictions are desired.

```
R> sppois <- spglm(
+   formula = count ~ elev + strat,
+   family = poisson,
+   data = moose,
+   spcov_type = "spherical"
+ )
R> spnb <- update(sppois, family = nbinomial)
```

Because the Poisson and negative binomial distributions have the same response support (nonnegative integers), we can compare them using AIC, AICc, or BIC:

```
R> BIC(sppois, spnb)
```

```
       df      BIC
sppois  3 1344.574
spnb    4 1343.105
```

Implicit in our spatial covariance functions thus far has been an assumption of geometric isotropy. A spatial covariance function is geometrically isotropic if it decays with distance at the same rate in all directions (Figure 9; left). A spatial covariance is geometrically anisotropic if it decays with distance at different rates in different directions (Figure 9; right). Geometric anisotropy is formally incorporated by rotating and scaling original coordinates, yielding transformed coordinates that are geometrically isotropic:

$$\begin{bmatrix} x^* \\ y^* \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 0 & 1/\omega \end{bmatrix} \begin{bmatrix} \cos(\alpha) & \sin(\alpha) \\ -\sin(\alpha) & \cos(\alpha) \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}.$$

The parameters ω and α controls the scaling and rotation, respectively, of the major and minor axes of a level curve of equal spatial covariance (Figure 9). Using these transformed coordinates, the partial sill (σ^2_{de}), nugget (σ^2_{ie}), and range (ϕ) parameters are estimated. We accommodate geometric anisotropy by supplying `anisotropy`:

```
R> sppois_anis <- update(sppois, anisotropy = TRUE)
R> spnb_anis <- update(spnb, anisotropy = TRUE)
```

According to BIC, the spatial negative binomial model with geometric anisotropy performs best:

```
R> BIC(sppois, spnb, sppois_anis, spnb_anis)
```

```
            df      BIC
sppois       3 1344.574
spnb         4 1343.105
sppois_anis  5 1341.143
spnb_anis    6 1339.714
```

The `plot()` function can be used to visualize the anisotropy (Figure 9):

```
R> plot(spnb, which = 8)
R> plot(spnb_anis, which = 8)
```

The spatial covariance is strongest in a northwest-southeast direction and weakest in the northeast-southwest direction (Figure 9), which is intuitive given the similar patterns in moose counts from Figure 8.

4.2. Modeling lake conductivity in Southwest, USA

The `lake` data in `spmodel` contains climate and chemical data for several lakes in four southwestern states in the United States: Arizona, Colorado, Nevada, and Utah. We desire an SPGLM that characterizes the effect of temperature, state, and lake origin (whether the lake is naturally occurring or human made) on lake conductivity. Conductivity is a measure of dissolved ions (measured here in water), which is important for various physical, chemical, and biological processes. Chemical data are often heavily right-skewed, so we model them using an SPGLM assuming a Gamma distribution for the response. The `log_cond` variable in `lake` is the logarithm of conductivity, which we dynamically exponentiate within `formula` so that it is on the original scale:

```
R> spgam <- spglm(
+   formula = exp(log_cond) ~ temp * state + origin,
+   family = "Gamma",
+   data = lake,
+   spcov_type = "cauchy",
+   partition_factor = ~ year
+ )
```

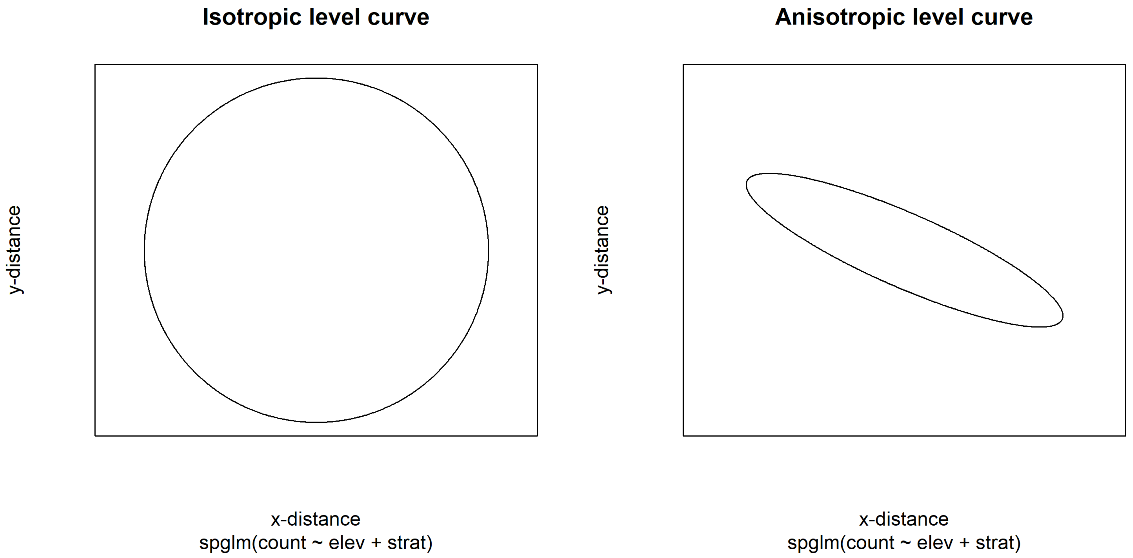

Figure 9: Level curves of equal spatial covariance for the negative binomial moose count models. The ellipse is centered at zero distance in the x-direction and y-direction, and points along the ellipse have equal levels of spatial covariance. In the isotropic level curve (left), spatial covariance decays equally in all directions. In the anistropic level curve (right), spatial covariance decays fastest in the northeast-southwest direction and slowest in the northwest-southeast direction (this pattern can be seen in the observed counts).

We model conductivity as a function of temperature, state, and lake origin, and we allow the effect of temperature to vary by state (`temp:state` interaction). The `year` partition factor (specified via `partition_factor`) restricts spatial covariance to be nonzero only for observations sampled during the same year. Data were collected in 2012 and 2017, so this partition factor assumes independence between observations in 2012 and 2017. While we used the partition factor here illustratively, more generally, the utility of partition factors can be highly context dependent.

When categorical variables have more than two levels, the default reference group contrasts are not well-suited to assess the variable's overall significance:

```
R> summary(spgam)


Call:
spglm(formula = exp(log_cond) ~ temp * state + origin, family = "Gamma",
    data = lake, spcov_type = "cauchy", partition_factor = ~year)

Deviance Residuals:
     Min       1Q   Median       3Q      Max
-1.35762 -0.20796 -0.03706  0.17869  1.10616

Coefficients (fixed):
```

```
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    3.59325    0.50058   7.178 7.06e-13 ***
temp           0.15182    0.03006   5.051 4.39e-07 ***
stateCO       -0.03214    0.56098  -0.057  0.95432
stateNV        0.75664    0.66851   1.132  0.25771
stateUT       -0.19696    0.55916  -0.352  0.72466
originNATURAL  0.08313    0.21988   0.378  0.70538
temp:stateCO   0.13679    0.04808   2.845  0.00444 **
temp:stateNV   0.01882    0.05820   0.323  0.74645
temp:stateUT   0.20015    0.04846   4.131 3.62e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Pseudo R-squared: 0.7061

Coefficients (cauchy spatial covariance):
       de        ie     range     extra
2.069e-02 2.952e-01 4.119e+06 5.645e-01

Coefficients (Dispersion for Gamma family):
dispersion
     3.761
```

A more effective approach is to use an analysis of variance (ANOVA), which is well-suited to assess the overall significance of each variable:

```
R> anova(spgam)

Analysis of Variance Table

Response: exp(log_cond)
            Df    Chi2 Pr(>Chi2)
(Intercept)  1 51.5270 7.062e-13 ***
temp         1 25.5146 4.390e-07 ***
state        3  3.0747 0.3802528
origin       1  0.1429 0.7053819
temp:state   3 19.7668 0.0001897 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The main effect for temperature and the temperature by state interaction are highly significant (p value < 0.001), while the main effects for state and lake origin are not significant.

Variance inflation factors assess the degree to which standard errors $\hat{\boldsymbol{\beta}}$ are inflated due to covariance among the columns of $\mathbf{X}$. Generalized variance inflation factors can capture the variance inflation for subsets of $\mathbf{X}$ that may include categorical variables with more than two levels (Fox and Monette 1992):

```
R> library("car")
```

```
R> vif(spgam)
```

```
                 GVIF Df GVIF^(1/(2*Df))
temp         4.691914  1        2.166083
state      127.082397  3        2.242234
origin       1.264940  1        1.124695
temp:state  76.387383  3        2.059856
```

The $\text{GVIF}^{1/2df}$ values for `temp`, `state`, and `temp:state` are just greater than two, which suggests moderate multicollinearity for these terms – unsurprising given the `temp:state` interaction in the model. The $\text{GVIF}^{1/2df}$ for `origin` is close to one, which suggests little to no multicollinearity for this term.

Because of the interaction between `temp` and `state`, contrasts that assess mean differences among states should condition upon a specific temperature value. By default, **emmeans** uses the mean temperature value (here, 7.63) to assess contrasts:

```
R> library("emmeans")
```

```
R> pairs(emmeans(spgam, ~ state | temp))
```

```
temp = 7.63:
 contrast estimate    SE  df z.ratio p.value
 AZ - CO    -1.012 0.337 Inf  -3.004  0.0142
 AZ - NV    -0.900 0.348 Inf  -2.584  0.0480
 AZ - UT    -1.331 0.326 Inf  -4.082  0.0003
 CO - NV     0.112 0.258 Inf   0.434  0.9727
 CO - UT    -0.319 0.223 Inf  -1.427  0.4822
 NV - UT    -0.431 0.244 Inf  -1.763  0.2915

Results are averaged over the levels of: origin
Degrees-of-freedom method: asymptotic
Results are given on the log (not the response) scale.
P value adjustment: tukey method for comparing a family of 4 estimates
```

Again, because of the interaction between `temp` and `state`, we should assess temperature trends separately for each state:

```
R> emtrends(spgam, ~ state, var = "temp")
```

```
 state temp.trend     SE  df asymp.LCL asymp.UCL
 AZ         0.152 0.0301 Inf    0.0929     0.211
 CO         0.289 0.0370 Inf    0.2161     0.361
 NV         0.171 0.0504 Inf    0.0718     0.270
 UT         0.352 0.0372 Inf    0.2791     0.425
```

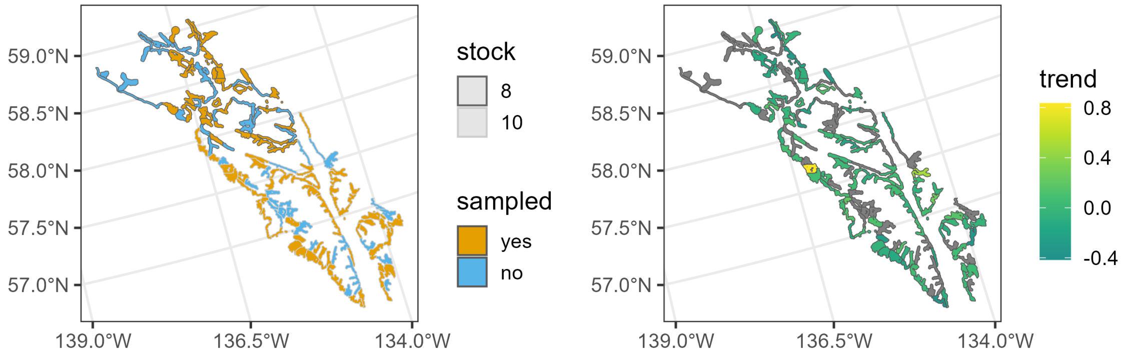

Figure 10: Seal trend distribution in Alaska. Observed and missing seal polygons by stock (left) and observed log seal trends (right).

```
Results are averaged over the levels of: origin
Degrees-of-freedom method: asymptotic
Results are given on the exp (not the response) scale.
Confidence level used: 0.95
```

4.3. Modeling harbor seal trends in Alaska, USA

The `seal` data in **spmodel** contains harbor seal abundance trends for two different harbor seal stocks (genetically distinct populations). While the `moose` and `lake` data were point-referenced, the `seal` data are areal. Each polygon in the `seal` data represents a distinct harbor seal haulout region (Figure 10). A haulout region is an area of coastal rocks that harbor seals go to rest, molt, and give birth.

For each polygon, a Poisson regression was used to quantify the mean trend in abundance over approximately 30 years (Ver Hoef, Peterson, Hooten, Hanks, and Fortin 2018). If the logarithm of mean abundance trends (`log_trend`) is negative (positive), it means abundance is decreasing (increasing). We use a binomial SPGLM to quantify the likelihood that mean abundance trends are decreasing:

```
R> is_decreasing <- seal$log_trend < 0
R> spbin <- spgautor(
+   formula = is_decreasing ~ 1,
+   family = binomial,
+   data = seal,
+   spcov_type = "car",
+   random = ~ stock
+ )
```

To model spatial dependence, we used a conditional autoregressive function. Conditional and simultaneous autoregressive functions characterize spatial distance through neighborhood relationships (rather than Euclidean distance) and have `spcov_type` values of `"car"` and "sar", respectively. By default, Queen's distance is used to determine whether two sites are neighbors, though custom neighborhood matrices can be passed via W. Row standardization is also assumed by default; this can be changed via row_st. Using random, we also specified a nonspatial random effect for seal stock, which implies seals belonging to the same stock share extra covariance. The random argument uses similar syntax as **lme4** (Bates, Mächler, Bolker, and Walker 2015) and **nlme** (Pinheiro and Bates 2006) to specify nonspatial random effects.

Tidying the model reveals the estimates and confidence intervals on the log odds scale:

```
R> tidy(spbin, conf.int = TRUE)

# A tibble: 1 x 7
  term        estimate std.error statistic p.value conf.low conf.high
  <chr>          <dbl>     <dbl>     <dbl>   <dbl>    <dbl>     <dbl>
1 (Intercept)    0.340     0.673     0.506   0.613   -0.979      1.66
```

Back-transforming the confidence interval to the probability scale yields:

```
R> emmeans(spbin, ~ 1, type = "response")

 1        prob    SE  df asymp.LCL asymp.UCL
 overall 0.584 0.164 Inf     0.273      0.84

Degrees-of-freedom method: asymptotic
Confidence level used: 0.95
Intervals are back-transformed from the logit scale
```

The SE column is the standard error on the response scale obtained from the delta method (Oehlert 1992; Ver Hoef 2012).

In contrast to point-referenced data, prediction locations for areal data must be specified at the time of model fitting, as they affect the spatial covariance function's neighborhood structure. Prediction locations whose response values have an NA (i.e., missing) value are converted into a newdata object that is stored in the model output. For example, rows one and nine are locations without seal trends, meaning they are not used in model fitting but are desired for prediction:

```
R> seal

Simple feature collection with 149 features and 2 fields
Geometry type: POLYGON
Dimension:     XY
Bounding box:  xmin: 913618.8 ymin: 855730.2 xmax: 1221859 ymax: 1145054
Projected CRS: NAD83 / Alaska Albers
# A tibble: 149 x 3
   log_trend stock                                                geometry
 *     <dbl> <fct>                                           <POLYGON [m]>
 1  NA       8     ((1035002 1054710, 1035002 1054542, 1035002 105354~
 2  -0.282   8     ((1037002 1039492, 1037006 1039490, 1037017 103949~
 3  -0.00121 8     ((1070158 1030216, 1070185 1030207, 1070187 103020~
 4   0.0354  8     ((1054906 1034826, 1054931 1034821, 1054936 103482~
 5  -0.0160  8     ((1025142 1056940, 1025184 1056889, 1025222 105683~
 6   0.0872  8     ((1026035 1044623, 1026037 1044605, 1026072 104461~
 7  -0.266   8     ((1100345 1060709, 1100287 1060706, 1100228 106070~
 8   0.0743  8     ((1030247 1029637, 1030248 1029637, 1030265 102964~
 9  NA       8     ((1043093 1020553, 1043097 1020550, 1043101 102055~
10  -0.00961 8     ((1116002 1024542, 1116002 1023542, 1116002 102254~
# i 139 more rows
```

Then, `predict()` can be called without having to specify `newdata`:

```
R> predict(spbin, type = "response", interval = "prediction")[1:5, ]
```

```
         fit       lwr       upr
1  0.6807677 0.3863736 0.8783808
9  0.5945680 0.2467634 0.8678078
13 0.6189055 0.2974432 0.8616799
15 0.6040102 0.2921802 0.8493132
18 0.6375700 0.3356282 0.8596641
```

We could have alternatively used a (geostatistical) SPGLM via `spglm()`. When areal data are used with `spglm()`, the centroids of each polygon are used as the point-referenced coordinates. We further explore comparisons between point-referenced and areal data in the next example.

4.4. Modeling voter turnout in Texas, USA

The `texas` data in **spmodel** contains voter turnout data for Texas counties in the 1980 United States Presidential Election (Bivand, Nowosad, and Lovelace 2024). The data are point-referenced, with polygon centroids representing the spatial location of each county (Figure 11). Beta regression is a GLM used to model rate and proportion data in the (0, 1) interval (Ferrari and Cribari-Neto 2004; Cribari-Neto and Zeileis 2010). We model voter turnout rates as a function of mean log income of county residents using an SPGLM assuming a beta distributed response variable:

```
R> spbeta_geo <- spglm(
+   formula = turnout ~ log_income,
+   family = "beta",
+   data = texas,
+   spcov_type = "matern"
+ )
```

Alternatively, we could use an autoregressive model to fit the model, constructing a neighborhood matrix by assuming centroids within `cutoff` of one another are neighbors:

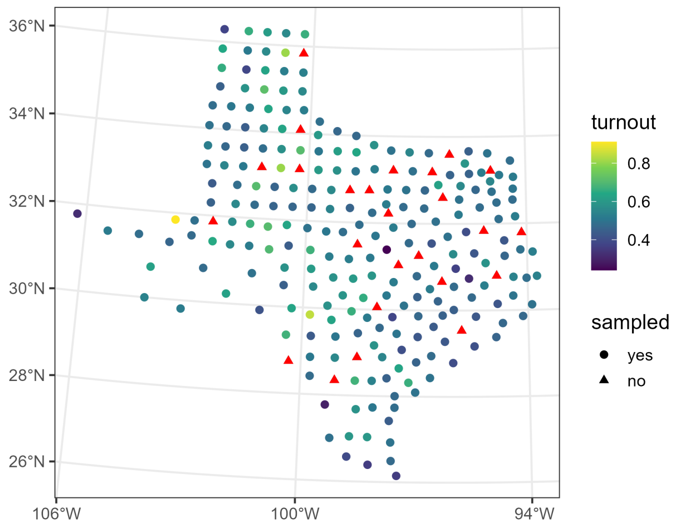

Figure 11: Proportion of voter turnout in Texas for the 1980 presidential election. Circles represent voter turnout (based on color) and triangles represent locations at which voter turnout predictions are desired.

```
R> spbeta_auto <- spgautor(
+   formula = turnout ~ log_income,
+   family = "beta",
+   data = texas,
+   spcov_type = "car",
+   cutoff = 1e5
+ )
```

According to AIC, the SPGLM for point-referenced data is preferred:

```
R> AIC(spbeta_geo, spbeta_auto)
```

```
            df       AIC
spbeta_geo   5 -44.53113
spbeta_auto  3 -22.46104
```

The default estimation method in **spmodel** for SPGLMs is restricted maximum likelihood (REML), while maximum likelihood (ML) can also be used. A benefit of benefit of REML is that it can yield unbiased estimates of covariance parameters (Cressie and Lahiri 1993), but a drawback is that likelihood-based statistics are only valid for model comparison when the models have the same explanatory variable and fixed effect structure (because the error contrasts used to construct the REML likelihood change based on $\mathbf{X}$ and $\boldsymbol{\beta}$). In contrast, ML estimators are generally biased for covariance parameters, though in practice this bias tends to be small. Moreover, when using ML, likelihood-based comparisons are valid for models having different explanatory variable and fixed effect structures. Using ML, we can evaluate the significance of log income on voter turnout using a likelihood ratio test:

```
R> spbeta_full_ml <- update(spbeta_geo, estmethod = "ml")
R> spbeta_red_ml <- update(spbeta_geo, estmethod = "ml", formula = turnout ~ 1)
R> anova(spbeta_full_ml, spbeta_red_ml)

Likelihood Ratio Test

Response: turnout
                                Df   Chi2 Pr(>Chi2)
spbeta_red_ml vs spbeta_full_ml  1 23.155 1.494e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The likelihood ratio test provides strong evidence that log income is significantly related to voter turnout (p value < 0.001). Alternatively, we could have instead used a different likelihood-based statistic like AIC:

```
R> AIC(spbeta_full_ml, spbeta_red_ml)

               df       AIC
spbeta_full_ml  7 -31.25900
spbeta_red_ml   6 -10.10354
```

The AIC also prefers the full model, suggesting that log income is important for predicting voter turnout.

5. Discussion

SPGLMs are fit in **spmodel** using a novel application of the Laplace approximation that simultaneously marginalizes over the latent (i.e., unobserved) random effects and the fixed effects. **spmodel**'s `spglm()` (for point-referenced data) and `spgautor()` (for areal data) fit SPGLMs that are similar in structure and syntax as base R's `glm()` function, easing the transition from GLMs to SPGLMs for practitioners. The `spglm()` and `spgautor()` functions support six response distributions for binary, count, and skewed data and 20 spatial covariance functions. **spmodel** has a suite of tools for data visualization, inference, model diagnostics, and prediction, providing a framework that can be used for all stages of a data analysis. There are many additional **spmodel** features that are not covered here, including fitting multiple models simultaneously, fixing spatial covariance and dispersion parameters at known values, fitting models to large non-Gaussian data having thousands of observations via spatial indexing (Ver Hoef, Dumelle, Higham, Peterson, and Isaak 2023), incorporating spatial dependence in machine learning (e.g., random forests; Breiman (2001)), simulating spatially dependent data (e.g., `spbinom()`, `sprpois()`, etc.), and more. Further details are provided by https://CRAN.R-project.org/package=spmodel and links therein.

Data and code availability

The results in this manuscript were obtained using R 4.4.0 with the **spmodel** 0.11.0 package. Figures were created using the ggplot2 3.5.1 package (Wickham 2016) and base R.

All writing and code associated with this manuscript is available for viewing and download on GitHub at `https://github.com/USEPA/spmodel.glm.manuscript`. All data used are part of the **spmodel** R package available for download from CRAN at `https://CRAN.R-project.org/package=spmodel`. Results were obtained using R 4.4.0 with the **spmodel** 0.11.0 package. Figures were created using the ggplot2 3.5.1 package (Wickham 2016) and base R.

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