**Spatiotemporal Models for Ecologists**

**Spatial generalized linear mixed model**

Goal: Explore alternative options for specifying a two-dimensional spatial generalized linear mixed model for gridded point-count data

**Data generating process**

Envision a model for gridded densities using square grid cells in two dimensions. We have a vector of samples, with value for the th sample which occurs at location :

Where is a vector representing latent spatial variation with value at each location , is the intercept, and we specify a log-link function. We could specify the spatial variable in several ways:

1. Looping through rows, and using for joint AR1 process for columns within a row:

where is a matrix with the value for each row and column , with row , and creates a length matrix for each location . We then specify:

where is the correlation for a one-dimensional AR1 process:

1. Using the SPDE method, where:

Where:

And using package:fmesher to construct the matrices M-matrices.

Please load the point-count data from Barro Colorado data for Vismia baccifera (vismba.rds), and convert it to counts within 32 square grid cells (see Discretize\_samples.R). Fit the spatial GLMM using one or the other spatial method, and compute the deviance relative to a saturated model. For the Poisson distribution, this “relative deviance” for each sample is calculated as:

Where is the predicted value given estimated fixed and random effects.

For whichever model you choose, calculate the total relative deviance . Then refit a null model that has only a single intercept and no other fixed or random effects, and calculate the null deviance using that model. Calculate the percent-deviance explained as . How does the null deviance compare between the SPDE and two-dimensional AR1 specifications?