Lecture 6: Species distributions and 2D spatial models

May 3, 2016

Why might we care about 2D spatial models?

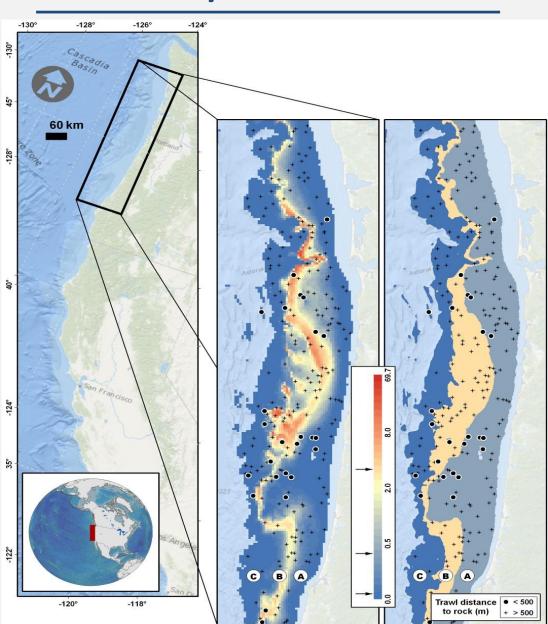
- 1. Experimental plots
 - Often uses grid
- 2. Observational analysis
 - Fish surveys

Species distribution models

- Widely used tool in zoology, conservation-planning, and invasion biology
- Synonyms:
 - Climate envelop model Fit model to species observations, and then identify other areas with suitable conditions
 - Species density model Sometimes used when fitting to density rather than presence/absence data
- Often used to infer "Grinnellian niche"
 - Distribution is a product of niche, dispersal ability, and species interactions

Spatial models are useful for estimating species distribution

- Capture fine-scale variation
- Decrease residual variation -> Decrease standard errors
- Shelton Thorson Ward
 Feist (2014) CJFAS



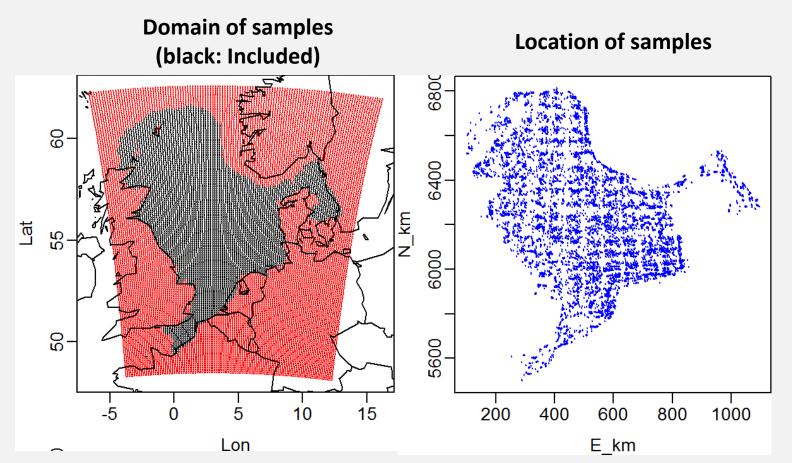
Two potential treatments

- 1. Equally spaced grid
- 2. Unequal or sporadic spacing

Two potential treatments

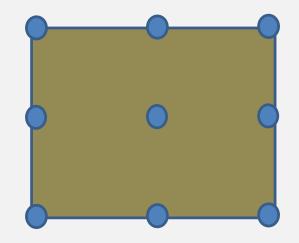
1. Equally spaced grid

Example #1: Divide north sea into grid



Imagine a 3x3 grid

- Equal spacing among sample locations
- ε_{ij} is the value for row *i* and column *j*
- ε_i is the value for row i and all columns
- E is the value for all rows and columns



Review

• Let's assume first-order autoregression:

$$\varepsilon_{s+1} \sim Normal(\rho \varepsilon_s, \sigma_{\varepsilon}^2)$$

Then the joint distribution is multivariate normal

$$\varepsilon \sim MVN(0, \Sigma)$$

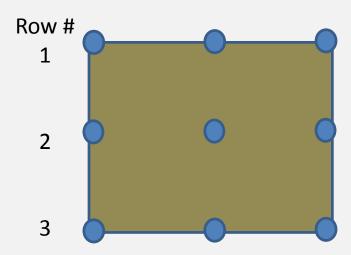
where

$$\Sigma = \frac{\sigma_{\varepsilon}^{2}}{1 - \rho^{2}} \begin{bmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{bmatrix}$$

$$\Sigma^{-1} = \frac{1}{\sigma_{\varepsilon}^{2}} \begin{bmatrix} 1+\rho^{2} & -\rho & 0\\ -\rho & 1+\rho^{2} & -\rho\\ 0 & -\rho & 1+\rho^{2} \end{bmatrix}$$

Intuitive to extend this

- What is the distribution for Row #2 conditional on Row #1
- [Work through on board]



Distribution for row *i+1* conditional on row *i*

$$\mathbf{\varepsilon}_{i+1} \sim MVN(\rho \mathbf{\varepsilon}_i, \mathbf{\Sigma})$$

Where

$$\Sigma = \frac{\sigma_{\varepsilon}^{2}}{1 - \rho^{2}} \begin{bmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{bmatrix}$$

 i.e., its identical to the 1D case, except replacing the normal distribution with a multivariate normal distribution

Joint distribution of all sites

- Then:

$$\text{vec}(\mathbf{E}) \sim MVN(0, \mathbf{\Sigma}_{\text{total}})$$

where

$$\Sigma_{\text{total}} = \frac{\sigma_{\varepsilon}^{2}}{1 - \rho^{2}} \begin{bmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{bmatrix} & \rho \begin{pmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{pmatrix} & \rho^{2} \begin{pmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{pmatrix} \\ \rho \begin{pmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{pmatrix} & \begin{pmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{pmatrix} & \rho \begin{pmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{pmatrix} \\ \rho^{2} \begin{pmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{pmatrix} & \rho \begin{pmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{pmatrix} & \begin{pmatrix} 1 & \rho & \rho^{2} \\ \rho & 1 & \rho \\ \rho^{2} & \rho & 1 \end{pmatrix} \end{bmatrix}$$

Joint distribution of all sites

– Then:

$$vec(\mathbf{E}) \sim MVN(0, \mathbf{\Sigma}_{\text{total}})$$

where

$$\Sigma_{\text{total}} = \Sigma \otimes \Sigma$$

Background:

─ ⊗ is the Kroenecker product

$$\mathbf{A} \otimes \mathbf{B} \equiv \begin{matrix} a_{11}\mathbf{B} & \dots & a_{1n}\mathbf{B} \\ \vdots & \ddots & \vdots \\ a_{n1}\mathbf{B} & \dots & a_{nn}\mathbf{B} \end{matrix}$$

Easy and compact way to explain spatio-temporal models

Kroenecker product inverse is easy

$$\Sigma_{\text{total}}^{-1} = (\Sigma \otimes \Sigma)^{-1} = \Sigma^{-1} \otimes \Sigma^{-1}$$

where we know how to calculate Σ^{-1}

$$\Sigma^{-1} = \frac{1}{\sigma_{\varepsilon}^{2}} \begin{vmatrix} 1+\rho^{2} & -\rho & 0\\ -\rho & 1+\rho^{2} & -\rho\\ 0 & -\rho & 1+\rho^{2} \end{vmatrix}$$

$$\Sigma_{total}^{-1} = \frac{1}{\sigma_{\varepsilon}^{-2}} \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix} - \rho \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix} = 0 \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix}$$

$$\Sigma_{total}^{-1} = \frac{1}{\sigma_{\varepsilon}^{-2}} \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix} + \rho \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix} - \rho \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix}$$

$$0 \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix} - \rho \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix}$$

$$0 \begin{bmatrix} 1+\rho^{2} & -\rho & 0 \\ -\rho & 1+\rho^{2} & -\rho \\ 0 & -\rho & 1+\rho^{2} \end{bmatrix}$$

- Kroenecker product conserves "sparseness"
 - If A ...
 - is n_A by n_A
 - It has n_A^2 elements
 - But has $m_A < n_A^2$ non-zero elements
 - It has "sparseness" = m_A/n_A^2
 - If **B** ...
 - has $m_B < n_B^2$ non-zero elements
 - Then $A \otimes B$...
 - Has "sparseness" $(m_B m_A)/(n_A n_B)^2$

Look at GitHub functions

- AR1
 - http://kaskr.github.io/adcomp/classdensity 1 1AR1 t.html
- SEPERABLE
 - http://kaskr.github.io/adcomp/classdensity 1 1SEPARABLE t.h
 tml

Modify code to avoid using Rmgauss

– How to do this?