Homework 4: A generative model for species distribution

Step 1: Chose a study organism

Step 2: Decide on an environmental predictor variable that determines abundance of your organism

Step 3: Following the R code, "simulating a landscape.R," generate a map of your environmental variable using the Raster function.

Output:

   a) *Explain why your predictor variable is likely to represent the distribution of your organism.*
   b) *What is your phi value and why? (why is your environmental variable more or less spatially-autocorrelated)*

Step 4: Chose a number of points to sample for your study organism

   c) *What constrains the number of points you can sample?*
   d) *Include a map of your environmental variable + sampling points as output*

Step 5: We will be modeling organism abundance as a hurdle model, or zero-inflated negative binomial. This type of stochastic model has two components: a presence/absence component that represents dispersal and a count component that represents abundance. For each of these components, decide on an intercept and a slope (for your environmental covariate).

   e) *For your organism, what is a biological reason you might observe a hurdle model?*
   f) *By multiplying the binomial and negative binomial variable to get a total abundance, what are we assuming about these distributions?*
   g) *Create a plot of your abundance vs. your environmental covariate*

Step 6: Give a dataframe with your environmental covariate and abundance to your neighbor.

   h) *Analyze your neighbor's data. Can you recapture the true slope and intercept parameters they used to simulate the data?*
   i) *Given the multivariate normal we used to generate spatial patterns in our covariate, how might you analyze spatial autocorrelation for your response variable? (organism counts)*