Our statistical model is similar to models that are frequently used for wildlife studies known as occupancy models. These occupancy models attempt to understand both the factors that determine which sites are occupied by the target species as well as which factors influence the detection of this species. In our case, we are interested in determining which factors influence the invasion probability of counties as well as which factors influence the detectability of new leishmaniases cases.

Let denote if cases were observed in county i at time t (0 and 1 represent the absence and presence of cases, respectively). We assume the following Bernoulli distribution for this variable:

where is the detection probability and is the true infection status of county i at time t. We assume that the detection probability depends on several covariates through the following relationship:

where is the design vector containing covariates and is a vector of regression coefficients. For the first time step, we assume that the latent invasion status is given by:

where is another design vector containing covariates and is a vector of regression coefficients. For subsequent years, we assume that:

In other words, once a location has been invaded, if remains invaded. We use a logistic regression framework to model the invasion process (i.e., the probability of invasion for counties that have not been invaded):

where is a vector of regression coefficients. Finally, we finish specifying this model by assuming that:

#-------------------------------------------------------------------

Full conditional distributions

We sample these parameters using an MH algorithm

where A is the set for which .

I will only sample this when