SHIFT: A spatially explicit cellular model of species colonization

See: http://www.nrs.fs.fed.us/disturbance/climate_change/landscape_ecological_modeling/shift/

Details of the model:

SHIFT is a spatially explicit, cellular model where each iteration of the model represents one generation (~ 50 years) depending on the species. At each iteration, the probability of each unoccupied, forested cell becoming occupied is calculated using a dispersal and establishment function. The dispersal function specifies the probability that a propagule will successfully colonize an unoccupied cell from some occupied cell based on the distance between cells and the frequency/abundance of the migrating species within the occupied cells and the habitat quality of the cell (%forest).

$$P(i,t) = \Sigma\{ F(j,t) * H(i,t) (C / D(i,j)^k) \}$$

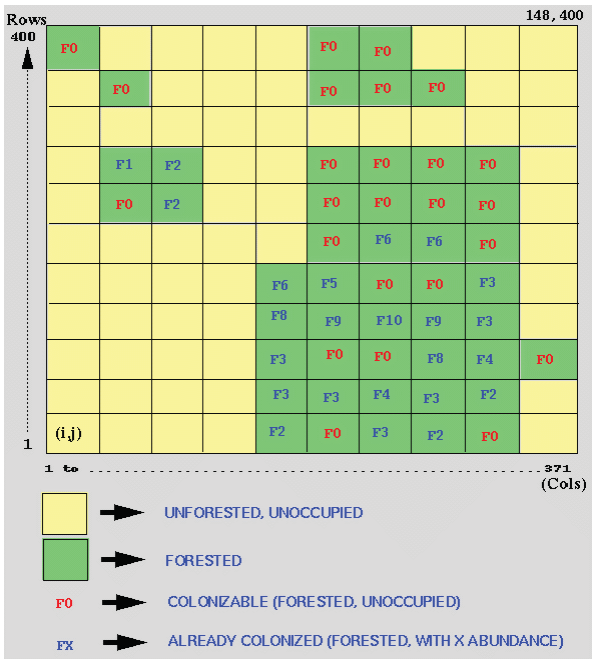
The probability of an unoccupied cell becoming colonized in each generation , P(i,t), is the cumulative probability of each occupied cell (j) sending a successful propagule to unoccupied cell (i).

In this model, the contribution of each occupied cell to the colonization probability, P(i,t) is an inverse function of the distance between the occupied and unoccupied cell D(i,j), such that colonization probability decreases with increasing distance between the cells. The distance exponent k controls the curve of the colonization probability.

Colonization probability is also a function of the relative frequency of the migrating species (abundance) within occupied cells in each generation F(j,t). This frequency scalar F(j,t) is low in newly colonized cells and increases between generations until reaching a predetermined carrying capacity F(max).

Colonization probability also depends on the habitat quality of the unoccupied cell - there is no colonization if it is unforested and increases with the %forest of the cell.

The calibration constant C is used to set the migration rate of the function under "pre-European settlement" conditions (defined as abundant available habitat (80% of cells forested) for a relatively abundant species (F(max) = 0.5).
To visualize the working of the model better, look at this grid-diagram.



For the model, the movement of the species range limit was calculated each iteration (50 yr generation). For each unoccupied cell, at each generation, a random number between 0 and 1 was selected to determine if the cell becomes colonized. If the cumulative probability of colonization, P(i,t) is > than the random number, the cell becomes colonized thus adding an element of stochasticity to the model. The position of the species front is determined at each generation.

This model was implemented in Fortran 95 language and various simulations were run.