SPATIAL MODEL FOR DICE – VERSION 2

Countries/counties/regions will be mapped to a spatial grid. Each grid point will represent a country/county/region (whatever is the level we are working on).

Density of each grid point is known – we will use our high resolution 1 km2 population density data to get an average for the country/county/region. Since density is known and the area it represents is also known we can get the number of individuals in each pixel.

Note – we are aggregating physical regions of different sizes to the same pixel size in the spatial model – is this a problem?

We will distinguish between events- infection/recovery and states: S, I, R.

Each pixel has its three states: S, I, R as well as population, N.

We are following the Mills/Riley logic and equations.

The total number of pixels is *D*.

At each point in time and for each pixel we update the three states as follows:

We need to provide the prescription for calculating where *event=inf, rec* and =S, I.

**Step 1:**

At each time step and for each pixel, *i*, the probability that any event will happen is:

where *He* are the rates of events that may occur in that compartment. To calculate the rate of infection (*Hinf*) we use the force of infection (or average rate that susceptible individuals in pixel *i* became infected) per time-step:

Where *D* is the total number of pixels, *N*j is the number of individuals in pixel *j* , *Ij* is the number of infected individuals (in pixel *j*) and infectious contacts are made with other individuals present in the pixel at a rate **.

The mixing matrix, *mij*, denotes the mixing within and between pixels. Mills & Riley use a mobility model for it (using a modified gravity model).

Question – After testing with the same mixing model are we moving to use our own version based on flight information?

**Step 2:**

For each pixel, *i*, and state  (=*S, I, R*), the total number of people experiencing any event (event=inf, rec) is chosen from a binomial distribution:

(We calculated the probability in step 1 and we now the total number of individuals in state  in pixel *i*. So we have all what we need.)

**Step 3:**

The number of individuals experiencing each event, , are drawn from a multi-nomial distribution with trials and the normalized selection probabilities where

For each pixel, and each event we can use the inf/rec rate to calculate the probability of that event for that pixel .

It is step 3 that will give us the and that we need to update the number of individuals in each state in each pixel.

After writing all of this down I am not sure that I see how these equations really take into account infection via the here different mechanisms:

  (a) People in state "S" in pixel 'i' being infected by interacting with people in the same pixel from state "I"

  (b) People in state "S" in pixel 'i' being infected by interacting with people from pixel 'j' who traveled to pixel 'i' are and are in state 'I'

  (c) People from state "S" in pixel 'i' travel to pixel 'j' and interact there with people who are in state 'I"