Spatial networks of individuals, households and workplaces

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(Work from a smallpox project with Neil Ferguson)

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Post-meeting note:

This talk was about a network component of transmission used in (http://dx.doi.org/10.1073/pnas.0510873103) which is described in a supporting document (http://www.pnas.org/cgi/data/0510873103/DC1/3).

TRANSMISSION BETWEEN INDIVIDUALS CAN OCCUR IN ONE OF THREE WAYS



Why use a network?

- Contact tracing
- Degree of contact required
- Computationally efficient

WE KNOW WHERE PEOPLE LIVE, WORK AND HOW THEY TRAVEL





A REED-FROST TYPE MODEL IS USED FOR TRANSMISSION WITHIN EACH HOUSEHOLD



Each household member equally well connected

Probability of (1-p) of escaping each time step

Option for different risk of infection between fever and rash, h_r

WORKPLACES ARE USED TO CAPTURE COMMUTING BEHAVIOUR



Everybody has a household

Everybody has a workplace

Workplaces and households have spatial locations (census)

Colleagues have a probability $p_{\rm WP}\, of$ being contacts

Workplaces have size n

 $P_{\rm wp}$ and n allow us to select average degree and clustering

Final network is individual-individual, workplaces are only used during the setup procedure

THE MCMC UPDATES TEST MANY DIFFEERNT WORKER-WORKPLACE ASSIGNMENTS



PAIR-WISE CHOICE KERNEL

Defined by the relative probability of an individual choosing to work a specific distance away

Independent of household and workplace density

Intuitively, makes sense?

EXTRA UPDATE STEPS ARE REQUIRED FOR THE CHAIN TO MIX EFFICIENTLY (I)

- 1. Choose an individual *i* (of household located at \mathbf{r}_i) currently associated with peer-group *k* (located at \mathbf{r}_k) at random from the entire population
- 2. With probability p_{LOCAL} go to step 3, otherwise got to step 5.
- 3. If individual *i* has zero or one peer-groups in tiles adjacent to its own tile, i.e. if $s_G(i) < 2$, END.
- 4. Select an alternative peer-group l (located at \mathbf{r}_l), at random, only from the peer-groups in tiles adjacent to the tile containing individual i, then go to step 6.
- 5. Select an alternative peer-group l (located at \mathbf{r}_l), at random, from all peergroups.
- 6. If peer-group l is in a tile adjacent to the tile containing individual i, but peergroup k is not, go to step 9 with a probability equal to the minimum of 1 and

$$\frac{1}{1 + \frac{n_I p_{\text{LOCAL}}}{(1 - p_{\text{LOCAL}}) s_G(i)}} \frac{\kappa_{PW}(|\mathbf{r}_i - \mathbf{r}_l|)}{\kappa_{PW}(|\mathbf{r}_i - \mathbf{r}_k|)},$$

otherwise, END.

EXTRA UPDATE STEPS ARE REQUIRED FOR THE CHAIN TO MIX EFFICIENTLY (II)



EXTRA UPDATE STEPS ARE REQUIRED FOR THE CHAIN TO MIX EFFICIENTLY (III)

7. If peer-group k is in a tile adjacent to the tile containing individual i, but peer-group l is not, go to step 9 with a probability equal to the minimum of 1 and

$$\left(1 + \frac{n_I p_{\text{LOCAL}}}{(1 - p_{\text{LOCAL}}) s_G(i)}\right) \frac{\kappa_{PW}(|\mathbf{r}_i - \mathbf{r}_l|)}{\kappa_{PW}(|\mathbf{r}_i - \mathbf{r}_k|)},$$

otherwise, END.

8. If peer-group k and peer-group l are in tiles adjacent to that containing individual i, or if neither peer-group k nor peer-group l are in tiles adjacent to that containing individual i, go to step 9 with a probability equal to the minimum of 1 and

$$\frac{\kappa_{PW}(|\mathbf{r}_i-\mathbf{r}_l|)}{\kappa_{PW}(|\mathbf{r}_i-\mathbf{r}_k|)},$$

otherwise, END.

9. Accept the move: remove individual i from peer-group k and reallocate them to peer-group l. END.

LOCAL MOVES IMPROVE CONVERGENCE



MANY ITERATIONS OF THE MCMC ALGORITHM GIVES A "GOOD" FIT



MANY ITERATIONS OF THE MCMC ALGORITHM GIVES A "GOOD" FIT (I)



DISCUSSION

Resulting networks were useful for some smallpox containment questions

Generally, theory is way ahead of experimental/observational data

Combination of space and clustering... probably not much likelihood of useful analytical insight?

Inclusion of demography