

A spatial Poisson transmission model for Ebola (and other diseases)

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Abstract

The model is a meta-population model using a known (spatial) connectivity matrix between patches and a simple kernel to model dispersal. The model is based on incidence data, with only infected individuals being known.

1 Notations

- I_t^i : incidence in patch i at time t (data)
- I_t : vector of incidence of all patches (I_t^1, \dots, I_t^N)
- T : the last date of the data
- D_{ij} : distance between i and j
- $w(\cdot)$: the known probability mass distribution of the generation time / serial interval
- N : number of patches in the model
- n_t^i : the number of infected individuals in patch i at time t
- $d_{j \rightarrow i}$: intensity of dispersion from j to i
- δ : general dispersal parameter
- R : the effective reproduction number
- t_k : the date of infection of individual k
- $f_{\mathcal{P}}(a, b)$: the Poisson density for a observations and a rate b
- $k(c, d)$: a spatial kernel for a distance c and a parameter d

2 Model

I_t^i is assumed to follow a Poisson distribution of parameter λ_t^i . λ_t^i is a sum over of the forces of infection of all patches towards i (including $i \rightarrow i$). We note β_t^i the force of infection coming from infected individuals in patch i at time t , defined as:

$$\beta_t^i = R \sum_{k=1}^{n_t^i} w(t - t_k) \quad (1)$$

The force of infection experienced by patch i at time t is then:

$$\lambda_t^i = \sum_{j=1}^N d_{j \rightarrow i} \beta_t^j \quad (2)$$

with:

$$d_{j \rightarrow i} = k(D_{ij}, \delta) \quad (3)$$

The likelihood of I_t is defined as:

$$p(I_t|R, \delta) = \prod_{i=1}^N f_{\mathcal{P}}(I_t^i, \lambda_t^i) \quad (4)$$

By extension, the likelihood for the entire data:

$$p(I_1, \dots, I_t|R, \delta) = \prod_{t=1}^T \prod_{i=1}^N f_{\mathcal{P}}(I_t^i, \lambda_t^i) \quad (5)$$