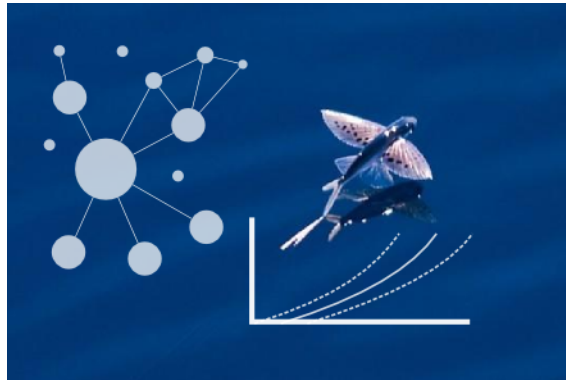


# A spatial Poisson transmission model for Ebola (and other diseases)

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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. Optionally, it can include infection from an unsampled reservoir. Unlike *outbreaker*, we are not trying to model individual ancestries, but merely dynamics within and between patches. In its simplest form, the model has only two parameters and its likelihood can be computed very fast. More complex extensions can allow for time-varying reproduction number, and/or time/spatially varying infection from the reservoir.

## 1 Notations

- $T$ : number of time steps in the data
- $P$ : number of patches
- $I_t^i$ : observed incidence in patch  $i$  at time  $t$  (data)
- $N_t^i$ : true, unobserved incidence in patch  $i$  at time  $t$  (augmented data)
- $I_t, N_t$ : vectors of (observed, true) incidence of all patches ( $I_t = (I_t^1, \dots, I_t^P)$ ;  $N_t = (N_t^1, \dots, N_t^P)$ )
- $I, N$ : matrix of observed / true incidence of all patches at all time steps ( $I = (I_1, \dots, I_T)$ ;  $N = (N_1, \dots, N_T)$ )
- $I_{1 \rightarrow t}, N_{1 \rightarrow t}$ : matrices of observed / true incidence from time 1 to time  $t$  ( $I_{1 \rightarrow t} = (I_1, \dots, I_t)$ ;  $N_{1 \rightarrow t} = (N_1, \dots, N_t)$ )
- $D_{ij}$ : distance between  $i$  and  $j$
- $w(\cdot)$ : the known probability mass distribution of the generation time / serial interval
- $d_{j \rightarrow i}$ : intensity of dispersion from  $j$  to  $i$
- $\delta$ : general dispersal parameter
- $\pi$ : proportion of cases reported
- $R$ : the effective reproduction number
- $k(a, b)$ : a spatial kernel for a distance  $a$  and a parameter  $b$
- $\theta_\delta$ : (fixed) parameter for the prior of  $\delta$
- $\theta_\pi$ : (fixed) parameter for the prior of  $\pi$

## 2 Model

We want to sample from the posterior distribution proportional to:

$$p(I, N, R, \delta, \pi) = p(I, N | R, \delta, \pi) p(R, \delta, \pi) \quad (1)$$

which can be rewritten

$$\underbrace{p(I | N, \pi) p(N | R, \delta)}_{\text{likelihood}} \underbrace{p(R) p(\delta) p(\pi)}_{\text{priors}} \quad (2)$$

The term  $p(I|N, \pi)$  is the probability of the observed incidence given the true incidence  $N$  and the reporting probability  $\pi$ . It is computed as:

$$p(I|N, \pi) = \prod_i \prod_t p(I_t^i | N_t^i, \pi) \quad (3)$$

with:

$$p(I_t^i | N_t^i, \pi) = f_{\mathcal{B}}(I_t^i, N_t^i, \pi) \quad (4)$$

where  $f_{\mathcal{B}}(x, a, b)$  is the Binomial p.m.f. for  $x$  successes,  $a$  draws and a probability  $b$ .

The term  $p(N|R, \delta)$  is the probability of the true incidence given the infectivity in the system and the spatial processes at play. It is computed as:

$$p(N|R, \delta) = p(N_1, \dots, N_t | R, \delta) \quad (5)$$

$$= \underbrace{(N_1 | R, \delta)}_{\text{constant}} p(N_2 | N_1, R, \delta) \dots p(N_t | N_1, \dots, N_{t-1}, R, \delta) \quad (6)$$

$$\propto \prod_{t=2}^T p(N_t | N_{1 \rightarrow t-1}, R, \delta) \quad (7)$$

$$= \prod_{t=2}^T \prod_{i=1}^P p(N_t^i | N_{1 \rightarrow t-1}, R, \delta) \quad (8)$$

$$(9)$$

with:

$$p(N_t^i | N_{1 \rightarrow t-1}, R, \delta) = f_{\mathcal{P}}(N_t^i, \lambda_t^i) \quad (10)$$

where  $f_{\mathcal{P}}$  is the p.m.f of a Poisson distribution and  $\lambda_t^i$  the force of infection towards patch  $i$  and time  $t$ .  $\lambda_t^i$  is a sum over of the forces of infection of all patches towards  $i$  (including  $i \rightarrow i$ ). We note  $\beta_t^j$  the global infectiousness coming from infected individuals in patch  $j$  at time  $t$ , defined by the renewal equation:

$$\beta_t^j = \sum_{s=1}^{t-1} N_s^j w(t-s) \quad (11)$$

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

$$\lambda_t^i = R \sum_{j=1}^P \beta_t^j k(d_{j \rightarrow i}, \delta) \quad (12)$$

where  $R$  is the reproduction number. The likelihood of the augmented data is thus given by:

$$p(N|R, \delta) \propto \prod_{t=2}^T \prod_{i=1}^P f_{\mathcal{P}}(N_t^i, R \sum_{j=1}^P \sum_{s=1}^{t-1} N_s^j w(t-s) k(d_{j \rightarrow i}, \delta)) \quad (13)$$

Note that we can easily turn it into a time-dependent term  $R_t$ , in which case we will have to assume i) a functional form or ii)  $R_t$  constant between break-points. Similarly, it can be turned into a patch-specific  $R_i$ , in which case heterogeneity between patches can be modeled using a given distribution.

The prior of  $\delta$  is an exponential distribution of parameter  $\theta_\delta$ :

$$p(\delta) = f_{exp}(\delta, \theta_\delta) \quad (14)$$

The prior of  $\pi$  is a beta distribution of parameter  $\theta_\pi$ :

$$p(\pi) = f_{beta}(\delta, \theta_\pi) \quad (15)$$

### 3 Data augmentation: Gibbs sampler

We seek a Gibbs sampler for the augmented incidence  $N$ . For this, we need to know (up to an additive or multiplicative constant) the distribution of  $N$  conditional on everything else. We have:

$$p(N|I, R, \delta, \pi) = p(N_1|I, R, \delta, \pi) \prod_{t=2}^T p(N_t|N_1, \dots, N_{t-1}, I, R, \delta, \pi) \quad (16)$$

$$\propto \prod_{t=2}^T p(N_t|N_1, \dots, N_{t-1}, I, R, \delta, \pi) \quad (17)$$

where:

$$p(N_t|N_{1 \rightarrow t-1}, I_{1 \rightarrow t-1}, R, \delta, \pi) \propto p(N_{1 \rightarrow t}, I_{1 \rightarrow t}, R, \delta, \pi) \quad (18)$$

$$\propto p(I_{1 \rightarrow t}|N_{1 \rightarrow t}, \pi) p(N_t|N_{1 \rightarrow t-1}, R, \delta) \quad (19)$$

$$= \left( \prod_{s=1}^t p(I_s|N_s, \pi) \right) p(N_t|N_{1 \rightarrow t-1}, R, \delta) \quad (20)$$

$$\propto p(I_t|N_t, \pi) p(N_t|N_{1 \rightarrow t-1}, R, \delta) \quad (21)$$

$$= \left( \prod_{j=1}^P f_B(I_t^j, N_t^j, \pi) \right) \left( \prod_{j=1}^P f_P(N_t^j, \lambda_t^j) \right) \quad (22)$$

$$= \prod_{j=1}^P \left[ \binom{N_t^j}{I_t^j} \pi^{I_t^j} (1 - \pi)^{N_t^j - I_t^j} \frac{\lambda_t^{j N_t^j} e^{-\lambda_t^j}}{N_t^{j!}} \right] \quad (23)$$

$$\propto \prod_{j=1}^P \left[ \frac{N_t^{j!}}{I_t^{j!} (N_t^j - I_t^j)!} (1 - \pi)^{N_t^j - I_t^j} \frac{\lambda_t^{j N_t^j}}{N_t^{j!}} \right] \quad (24)$$

$$\propto \prod_{j=1}^P \left[ \frac{1}{(N_t^j - I_t^j)!} (1 - \pi)^{N_t^j - I_t^j} \lambda_t^{j N_t^j - I_t^j} \lambda_t^{j I_t^j} \right] \quad (25)$$

$$\propto \prod_{j=1}^P \frac{1}{(N_t^j - I_t^j)!} [(1 - \pi)\lambda_t^j]^{N_t^j - I_t^j} \quad (26)$$

$$\propto \prod_{j=1}^P f_{\mathcal{P}}(N_t^j - I_t^j, (1 - \pi)\lambda_t^j) \quad (27)$$

The conditional distribution of  $N_t$  is therefore proportional to the probability of the number of unobserved cases  $N_t^j - I_t^j$ , given by a Poisson distribution of rate  $(1 - \pi)\lambda_t^j$ . This is an intuitive result: the actual incidence is larger for smaller reporting rates ( $\pi$ ) and higher forces of infection ( $\lambda_t^j$ ). In practice, we can derive  $N_t$  by sampling directly the number of unobserved cases  $N_t^j - I_t^j$  from a Poisson distribution of parameter  $(1 - \pi)\lambda_t^j$ .