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

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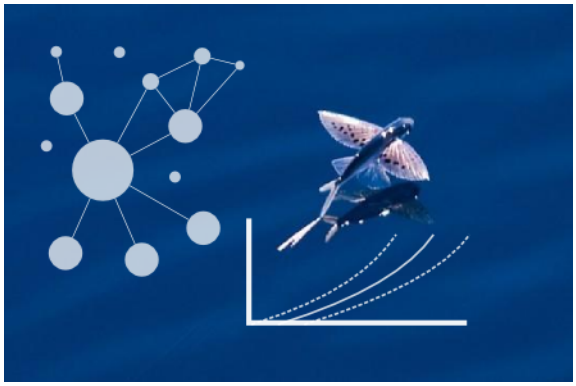

Abstract

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

2 Model

We want to sample from the posterior distribution proportional to:

$$p(I, N, R, \delta, \pi) = p(I, N|R, \delta, \pi)p(R, \delta, \pi) \tag{1}$$

which can be rewritten

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

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

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

with:

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

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:

$$\begin{aligned}
p(N|R,\delta) &= p(N_1,\ldots,N_t|R,\delta) && (5)\\
&= \underbrace{(N_1|R,\delta)}_{constant} p(N_2|N_1,R,\delta)\ldots p(N_t|N_1,\ldots,N_{t-1},R,\delta) && (6)\\
&\propto \prod_{t=2}^{T} p(N_t|N_{1\to t-1},R,\delta) && (7)\\
&= \prod_{t=2}^{T}\prod_{i=1}^{P} p(N_t^i|N_{1\to t-1},R,\delta) && (8)\\
& && (9)
\end{aligned}$$

with:

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

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

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

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

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

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

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

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 δ is an exponential distribution of parameter θ_δ:

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

The prior of π is a beta distribution of parameter θ_π:

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

3 Data augmentation

3.1 Proposal distribution

We seek a clever proposal for the augmented incidence N, based on the approximation of the distribution of N conditional on everything else. We have:

$$\begin{aligned} p(N|I,R,\delta,\pi) &= p(N_1|I,R,\delta,\pi)\prod_{t=2}^{T} p(N_t|N_1,...,N_{t-1},I,R,\delta,\pi) && (16)\\ &\propto \prod_{t=2}^{T} p(N_t|N_1,...,N_{t-1},I,R,\delta,\pi) && (17)\end{aligned}$$

where:

$$\begin{aligned} p(N_t|N_{1\to t-1},I,R,\delta,\pi) &\propto p(N_{1\to t},I,R,\delta,\pi) && (18)\\ \propto p(I_{1\to t}|N_{1\to t},\pi)p(I_{t+1\to T}|N_{1\to t},\pi)p(N_t|N_{1\to t-1},R,\delta) && (19)\end{aligned}$$

Unfortunately, we cannot compute $p(I_{t+1\to T}|N_{1\to t},\pi)$ as the force of infection generated after t are not known. We approximate this distributon by:

$$\begin{aligned} & p(I_{1\to t}|N_{1\to t},\pi)p(N_t|N_{1\to t-1},R,\delta) && (20)\\ =& (\prod_{s=1}^{t} p(I_s|N_s,\pi))\ p(N_t|N_{1\to t-1},R,\delta)) && (21)\\ \propto& \ p(I_t|N_t,\pi)\ p(N_t|N_{1\to t-1},R,\delta) && (22)\\ =& (\prod_{j=1}^{P} f_{\mathcal{B}}(I_t^j,N_t^j,\pi))(\prod_{j=1}^{P} f_{\mathcal{P}}(N_t^j,\lambda_t^j)) && (23)\end{aligned}$$

$$= \prod_{j=1}^{P} [\binom{N_t^j}{I_t^j} \pi^{I_t^j} (1-\pi)^{N_t^j - I_t^j} \ \frac{{\lambda_t^j}^{N_t^j} e^{-\lambda_t^j}}{N_t^j!}] \tag{24}$$

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

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

$$\propto \prod_{j=1}^{P} \frac{1}{(N_t^j - I_t^j)!} [(1-\pi)\lambda_t^j]^{N_t^j - I_t^j} \tag{27}$$

$$\propto \prod_{j=1}^{P} f_{\mathcal{P}}(N_t^j - I_t^j, (1-\pi)\lambda_t^j) \tag{28}$$

In other words, our approximation of the conditional distribution of N_t is 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 (π) and higher forces of infection (λ_t^j).

3.2 MH algorithm

We use the result derived above in a Metropolis-Hasting algorithm:

1. propose $N_t^{j*} \sim I_t^j + \mathcal{P}((1-\pi)\lambda_t^j)$ where $\mathcal{P}(.)$ refers to a Poisson distribution

2. accept N_t^{j*} with probability:

$$min(1, \frac{post(N_t^{j*})}{post(N_t^j)} \times \frac{p(N_t^{j*} \to N_t^j)}{p(N_t^j \to N_t^{j*})})$$

   where $post(.)$ is the posterior density and $p(a \to b)$ is the probability of proposing b while being in state a.

We have:

$$p(N_t^{j*} \to N_t^j) = f_{\mathcal{P}}(N_t^j, (1-\pi)\lambda_t^{j*}) \tag{29}$$

where λ_t^{j*} is the force of infection experienced by patch j at time t with a true incidence N_t^{j*}. However, as the force of infection at time t only depends on previous time steps, we have $\lambda_t^{j*} = \lambda_t^j$.

Therefore, the acceptance ratio is:

$$min(1, \frac{post(N_t^{j*})}{post(N_t^j)} \times \frac{f_{\mathcal{P}}(N_t^j, (1-\pi)\lambda_t^j)}{f_{\mathcal{P}}(N_t^{j*}, (1-\pi)\lambda_t^j)}) \tag{30}$$