Modelling the spread of influenza on long distance travel networks with real air traffic data

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1. Introduction

The global network of human transportation has been playing a paramount role in the spatial spread of infectious diseases. The high connectedness of distant territories by air travel makes it possible for a disease to invade regions far away from the source faster than ever. Some infectious diseases, such as tuberculosis, measles and seasonal influenza have been known to be transmissible during commercial flights. The purpose of this work is to formulate a model to describe the temporal evolution of influenza in regions connected by long distance travel, such as intercontinental flights.

2. The model

We consider two distant regions connected by air travel. We divide the population of the two regions and the population of traveling individuals into five groups: Susceptible (S), Exposed (E), symptomatically Infected (I), Asymptomatically infected (A), Recovered (R). Upper indeces ‚r' and ‚v' indicate that we distinguish local residents from temporary visitors. Classes marked by red are originated from region 1, blue represents classes of region 2. Arrows of the same colors indicate how the disease progresses. Green dot-dashed arrows represent that individuals are traveling. Green solid arrows show the dynamic of the pandemics during the travel.

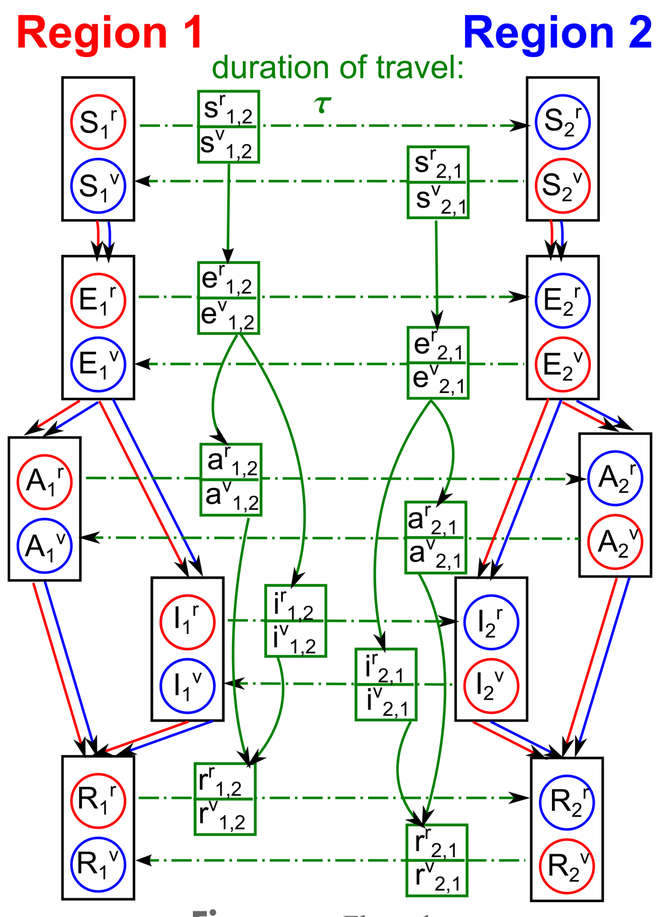


Figure 1: Flow chart

We present two equations of the differential equation system corresponding to visitors of region 2.

recruitment, natural death, new infections, traveling to region 1, inflow of travelers from region 1

$$\begin{cases} \dot{S}_2^v(t) = \Lambda_2 - d_2^v S_2^v(t) - S_2^v(t)\dfrac{\beta_2^{rv}(I_2^r(t)+\rho A_2^r(t)) + \beta_2^{vv}(I_2^v(t)+\rho A_2^v(t))}{N_2(t)} - \gamma_2 S_2^v(t) + s_{1,2}^r(\tau, t-\tau), \\ \quad \dots \\ \dot{R}_2^v(t) = -d_2^v R_2^v + \mu_I I_2^v(t) + \mu_A A_2^v(t) - \gamma_2 R_2^v(t) + r_{1,2}^r(\tau, t-\tau), \end{cases}$$

recovery from I and A; inflow of travelers from region 1

Solution at $\theta = \tau, t_* = t - \tau$

The following differential equation system decribes the transmission during travel from region 1 to region 2, which started at t_*. θ denotes the time elapsed since the beginning of travel. The solution determines the inflow terms of individuals completing travel.

$$\begin{cases} \dfrac{d}{d\theta} s_{1,2}^r(\theta, t_*) = -s_{1,2}^r(\theta, t_*)\beta^T \dfrac{(i_{1,2}^r(\theta, t_*) + i_{1,2}^v(\theta, t_*) + \rho(a_{1,2}^r(\theta, t_*) + a_{1,2}^v(\theta, t_*)))}{n_{1,2}(\theta, t_*)}, \\ \quad \dots \\ \dfrac{d}{d\theta} r_{1,2}^r(\theta, t_*) = \mu_A a_{1,2}^r(\theta, t_*) + \mu_I i_{1,2}^r(\theta, t_*), \end{cases}$$

3. The reproduction number

Travel and multiple regions make it very complicated to follow the new infections caused by an infected agent. We construct a 4x4 next generation matrix, the reproduction number is defined as the spectral radius of the NGM. $R_0 > 1$ indicates an epidemic outbreak. R_{12}^{rv} represents the number of secondary infections among visitors of region 2 generated by a single resident of region 1. The other elements of the NGM can be defined similarly.

$$\mathcal{NGM} = \begin{pmatrix} R_{11}^{rr} & R_{11}^{vr} & R_{21}^{rr} & R_{21}^{vr} \\ R_{11}^{rv} & R_{11}^{vv} & R_{21}^{rv} & R_{21}^{vv} \\ R_{12}^{rr} & R_{12}^{vr} & R_{22}^{rr} & R_{22}^{vr} \\ R_{12}^{rv} & R_{12}^{vv} & R_{22}^{rv} & R_{22}^{vv} \end{pmatrix}$$

4. Basic properties

Our model is equivalent to a large system of delay differential equations of the following form, where W represents the inflow terms of individuals after travel:

$$(1)\quad \begin{cases} x'(t) &= \mathcal{F}(x(t), x(t-\tau)) = f(x(t)) + W(x(t-\tau)), \\ x_0 &= \varphi, \end{cases}$$

where $t \in \mathbb{R}$, $x : \mathbb{R} \to \mathbb{R}^{20}$, $f, W : \mathbb{R}^{20} \to \mathbb{R}^{20}$, $\varphi \in \mathcal{C}([-\tau, 0], \mathbb{R}^{20})$

It is not a common DDE system, because the delay terms require the solution of the following differential equation system, which describes the transmission during travel:

$$(2)\quad \begin{cases} y'(s) &= g(y(s)), \\ y(0) &= y_*, \end{cases}$$

where $s \in [0, \tau]$, $y : [0, \tau] \to \mathbb{R}^{20}$, $g : \mathbb{R}^{20} \to \mathbb{R}^{20}$ and for $z \in \mathbb{R}^{20}$, $h : \mathbb{R}^{20} \to \mathbb{R}^{20}$,

$$W(z) := y(\tau, 0; h(z)).$$

We derive the following results for (1):

THEOREM

1. There exists a unique solution for system (1).
2. Nonnegative initial data give rise to nonnegative bounded solutions.
3. In the disease free subspace, there exists a unique positive equilibrium which is GAS.

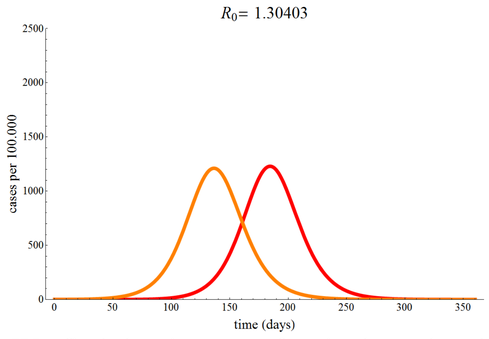
5. Simulations for influenza

In our simulations we ignore demography to model a single wave of influenza. We use real air traffic data (Biospora project), we summarize the key model parameter values in Table 1. We set up three scenarios for the origin-destination pairs to mimic relations.

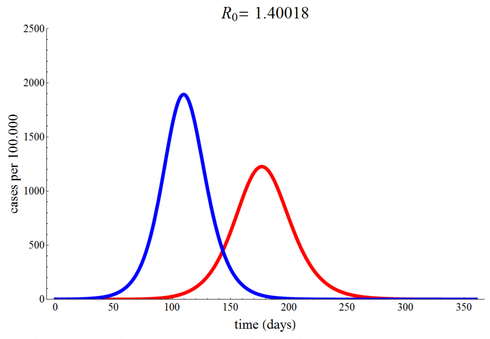
Description	Parameter	Value for influenza
Duration of travel	τ	0.5 days
Traveling rate of residents, visitors	$\alpha_j, \gamma_j, j \in \{1,2\}$	From air traffic data
Transmission rates in regions	β^T	15
Regional reproduction number in Canada, China, Mexiko	$R_{regional}$	1.3, 1.4, 1.4
Transmission rates in regions	$\beta_j^{m,n}, j \in \{1,2\}, m,n \in \{r,v\}$	From regional rep. number
Length of incubation period	$1/\mu_E$	1.25 days
Length of asymp., symp. infected periods	$1/\mu_A, 1/\mu_I$	4.1 days , 3 days
Probability of developing symptoms	p	0.7

Table 1: Key model parameters

Case 1: Canada - UK



Case 2: Canada - China



We find that in case of a single outbreak in the UK, the pandemic invades the disease-free Canada as well, altough the peak appears 50 days later. If there is an initial outbreak only in China, the Canadian peak follows the one in China after 65 days.

Case 3: Canada-Mexico

We fit the model to the first wave of H1N1 pandemic 2009. Day 0: Dec. 31, 2008.
Real peak Mexico: April 26, 2009 (Day 116),
Real peak Canada: June 21, 2009 (Day 172).

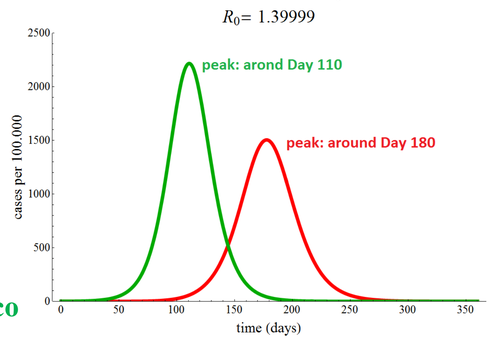


Figure 2, Figure 3, Figure 4:
Morbidity curves for **Canada**, **UK**, **China**, **Mexico**

6. Acknowledgements

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