EL PAPEL DE LA MOVILIDAD GEOGRÁFICA EN LA EXPANSIÓN DE *AEDES ALBOPICTUS* Y EN LA TRANSMISIÓN DE ENFERMEDADES INFECCIOSAS

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Big Mosquito Bytes

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OUTLINE

1. *Aedes albopictus* dispersion

   Data-based analysis of the invasion of the province of Girona during 2009-2011.

2. Epidemic spread on networks

   Development of a theoretical framework for the modelling of the spread of infectious diseases.

Aedes albopictus dispersion

AEDES ALBOPICTUS PRESENCE IN SPAIN

Aedes albopictus was not an endemic species in Spain until recent years, when the rise of temperatures associated to the global warming made some regions of the Mediterranean coastline well-suited for the mosquito's proliferation. Its first presence was recorded in Sant Cugat del Vallès in 2004. As explained in [1]:

> "Interestingly, no used-tyre dumps or plant nurseries were found associated with the presence of *Aedes albopictus* in the area."

What could cause the appearance of the mosquito? As found in [2]:

> "We sampled 770 cars in north-eastern Spain, discovering 4 adult female tiger mosquitoes that had entered cars prior to sampling (...). Our Bayesian model suggests that of the 6.5 million daily car trips in the Barcelona metropolitan area, between 13,000 and 71,500 facilitate tiger mosquito movement."

Mobility patterns and the intricacy of human behaviour challenge our current understanding of the world. This calls for interdisciplinary approaches and advanced techniques in the study of the dynamics involved in complex processes.

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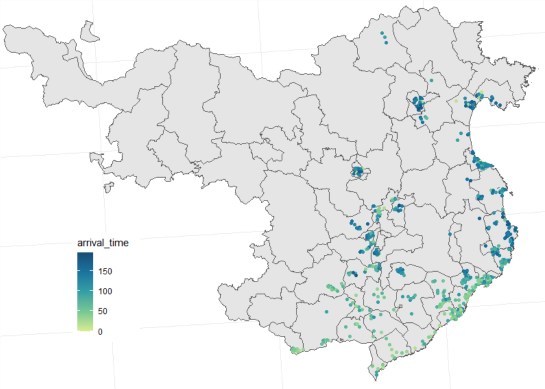
[1] Eritja *et al*: "First record and establishment of the mosquito *Aedes albopictus* in Spain", Medical and Veterinary Entomology (2006).

[2] Bartumeus *et al*: "Direct evidence of adult *Aedes albopictus* dispersal by car", Scientific Reports (2017).

SPREADING OF THE MOSQUITO

During the warmer months of 2009, 2010 and 2011, the establishment of *Aedes Albopictus* was observed in the province of Girona. Over 900 ovitraps were placed to record its spatiotemporal evolution.

The drivers of the mosquito's spread are unknown. Does it expand from a few imported source locations? Is there a mosquito "rain" over the whole region? Does it colonize from adjacent regions where it is already established?



Another relevant question for the control and well-preparedness for possible future outbreaks of mosquito-borne diseases arises: how important is the role played by human mobility in the spatial dispersal of the vectors?

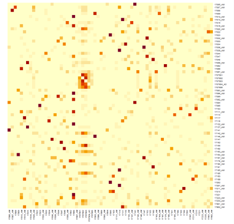
MEASURING HUMAN MOBILITY

Both MITMA and INE have made data on human mobility flows available between regions in the province. We use these to compute a sort of distance associated to human mobility, following [3].

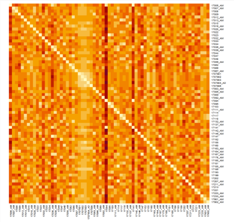
This *effective distance* is computed as a logarithmic transformation of the proportion of outbound flow from a given location to another

$$\text{distance from } A \text{ to } B = 1 - \log \frac{\text{flow from } A \text{ to } B}{\text{total flow leaving } A}.$$

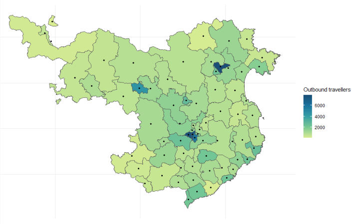
Therefore, the largest the proportion of outbound flow from A goes to B, the closest point A is to point B. The underlying network structure of the province allows us to find the shortest paths between regions as well.



(a) Mobility matrix



(b) Shortest paths



(c) Regions, coloured by outbound flows

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[3] Brockmann, Helbing: “The hidden geometry of complex, network-driven contagion phenomena”, Science (2013).

SOME RESULTS

We compute the correlation between:

1. the date the mosquito arrives at each ovitrap,
2. the distance from each ovitrap to the source location.

This is done for several possible sources of the spread process, and both for effective and geographical distances. We expect to find significantly higher correlations for sources and distances that are indeed related with the spread process of the mosquito.

Effective distance	Arrival times		
Origin of spread	2009	2010	2011
True source district	-0.26	-0.24	-0.38
Mean over all districts	0.12	0.06	-0.01
Barcelona city	0.31	0.31	0.28
Barcelona province	0.43	0.41	0.36
“Positive” municip. in BCN	0.5	0.46	0.39

Geographical distance	Arrival times		
Origin of spread	2009	2010	2011
True source district	-0.25	-0.42	-0.5
True source district (N)	0	-0.1	0.02
Latitude (all)	0.34	0.39	0.48
Latitude (S)	0.45	0.47	0.54
Longitude (all)	0.22	0.28	0.25

The correlation between these distances themselves is very low. Thus, it would seem that the mosquito followed a both geographical and human-driven expansion from the already colonized regions of Barcelona.

Epidemic spread on networks

COMPARTMENTAL MODELS

The classical SIR model describes the evolution of a disease in a population divided in three epidemiological status:

$$\begin{aligned}\frac{dS}{dt} &= -\beta\frac{S}{N}I,\\ \frac{dI}{dt} &= \quad\beta\frac{S}{N}I-\gamma I,\\ \frac{dR}{dt} &= \qquad\qquad\quad \gamma I,\end{aligned}$$

where S, I, R denote the number of susceptible, infected and recovered individuals respectively, and verify $S+I+R=N$.

Some thought may lead us to guess that the qualitative behaviour of the epidemic is controlled by a single parameter:

$$R_0 = \frac{\gamma}{\beta}.$$

This is confirmed by the mathematical properties of the system of differential equations.

METAPOPULATION MODELS

A possible generalization for this, comprising also geographical spread and interaction between a patch-structured population, is given by

$$\begin{aligned}
\frac{dS_k}{dt} &= -\beta \frac{S_k}{N_k} I_k && - \sum_{j=1}^{N} \beta c_{jk} \frac{S_k}{N_k} I_j, \\
\frac{dI_k}{dt} &= \beta \frac{S_k}{N_k} I_k - \gamma I_k && + \sum_{j=1}^{N} \beta c_{jk} \frac{S_k}{N_k} I_j, \\
\frac{dR_k}{dt} &= \gamma I_k.
\end{aligned}$$

The coefficients c_{jk} model the interaction between the infected individuals at patches j and k.

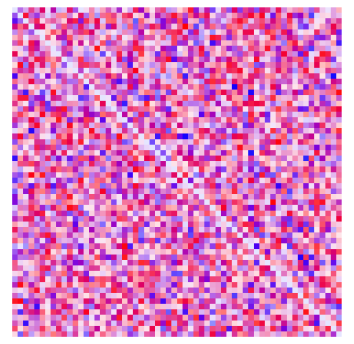
The mathematical properties of this system show that the corresponding epidemiological parameter is now given by the largest eigenvalue of the Jacobian of the model:

$$J = \begin{pmatrix}
\beta - \gamma & \beta c_{12} & \beta c_{13} & \dots & \beta c_{1N} \\
\beta c_{21} & \beta - \gamma & \beta c_{23} & \dots & \beta c_{2N} \\
\beta c_{31} & \beta c_{32} & \beta - \gamma & \dots & \beta c_{3N} \\
\vdots & \vdots & \vdots & & \vdots \\
\beta c_{N1} & \beta c_{N2} & \beta c_{N3} & \dots & \beta - \gamma
\end{pmatrix}.$$

RANDOM COEFFICIENTS

A further generalization of this approach is to model the parameters of the system with random variables, rather than assuming fixed values for them. For instance, we may assume that the mobility coefficients are drawn uniformly at random from the interval $[0, 1]$, or follow a Beta distribution, or a truncated normal...

$$c_{jk} \sim U(0,1),\ B(\alpha,\beta),\ \mathcal{N}(\mu,\sigma)\ldots$$

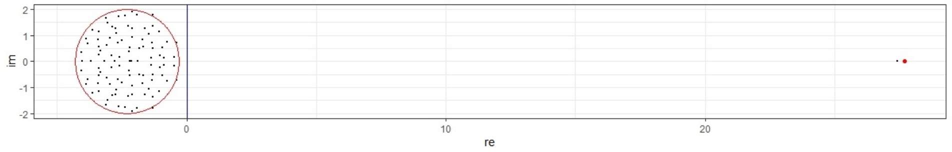


This provides two advantages from the theoretical point of view: first, it provides a more realistic approach to the modelling of intrinsically random rates; second, the estimations provided by the model are robust to stochastic variations in the corresponding quantities.

We thus arrive at the following question: can we determine the eigenvalues of a matrix which entries are random variables?

CIRCULAR LAW

As the size of the system (number of patches) grows big, the limiting distribution of the eigenvalues of the Jacobian of the system converges to the uniform distribution in a disk and a single outlier.



Let us assume the coefficients c_{jk} follow a distribution with mean μ and standard deviation σ. Then, the disk is centered at $(\beta(1-\mu)-\gamma, 0)$ and has radius $\beta\sigma\sqrt{N}$, and the outlier is located at $\beta(\mu(N-1)+1)-\gamma$. This provides the following "stability condition":

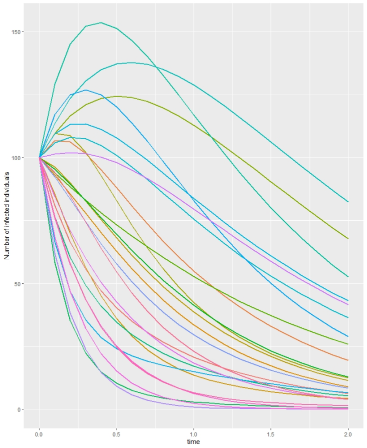
$$max\left\{\mu(N-1), \sigma\sqrt{N}-\mu\right\} < \frac{\gamma}{\beta} - 1.$$

This result is universal! That is, it only depends on the mean μ and standard deviation σ of the mobility coefficients, and not on the particular choice of distribution.

GENERALIZATIONS

The random matrix theory machinery is rich and well-developed: a wide range of generalizations of this problem can be analyzed. For instance, we consider in our work:

- Randomness in the epidemiological parameters as well, allowing for random transmission rates and increased/decreased contagion at specific nodes.
- More general mobility networks, with simulated scenarios. These include correlated flows, sparse connectivities, decreased/increased mobility at specific nodes (restrictions/events)...
- Two scales of mobility: a “short-term” one, as shown here, which may represent contagions due to everyday mobility (commuting), and a “long-term” one, which may represent migration flows.
- Numerical exploration and quantitative assessment of such models, to investigate further properties of the system (besides the predicted R_0).



SUMMARY

- We are working towards a more complete understanding of the colonization process of *Aedes albopictus*.

- We have developed a novel and flexible modelling framework for the spread of infectious diseases.

- These can be understood as part of a larger program. We are learning, using and developing several tools for the study of complex systems. These involve spreading processes over the nodes of a network.

- The spread process may either be the colonization of a region by a vector, the evolution of an epidemic over a population, or many other examples. In any case, the underlying network models the spatial distribution of the host of the process, and the temporal evolution in embedded in the underlying dynamical systems.

- Versatile tools and a complete perspective allow for comprehensive and accurate analysis of future problems. Combining techniques with an interdisciplinary approach is mandatory in the current complex real-word setting.

Gracias!