Parallel Session

Epidemiology VIII

AN EDGE-BASED SEIR MODEL ON A STATIC RANDOM NETWORK

Carlene P. C. Pilar-Arceo

cparceo@up.edu.ph

Institute of Mathematics, University of the Philippines Diliman

Joint work with Cherrylyn P. Alota (Department of Mathematics, University of the Philippines Cebu) and Aurelio A. delos Reyes V (Institute of Mathematics, University of the Philippines Diliman).

Keywords: Stochastic, Network, Epidemic, SEIR.

Mathematical models and methods of epidemics have been developed since Bernoulli's 1760 smallpox model. The most well-known model so far is the 1927 classical epidemic model of Kermack and McKendrick, which assumes a homogeneously mixed population divided into susceptible, infectious and recovered (SIR) compartments of individuals.

In reality, however, disease transmission between individuals is usually a random occurrence. Moreover, the heterogeneity of a population with respect to contact rates, and therefore each individual's susceptibility and infectiousness, should affect the dynamics of epidemics. This realization has led to models which veer away from the homogeneous-mix assumption and instead take to network methods of describing and analyzing disease transmission. It is indeed more realistic to picture the spread of a disease from one individual to another as if it were going from one node in a graph to another via a connecting edge. In this study, the authors extend the 2008 SIR model of Volz, which makes use of network- or edge-based methods.

The Volz model, as mentioned, utilizes only the three compartments, S, I and R. For many infectious diseases, it is often the case that a latent or incubation period elapses first. That is, an individual, after being infected, is not immediately infectious but first remains in an asymptomatic and un-infectious state. Over this time span, the individual is said to be in the exposed (E) state. In this state, an individual cannot transmit infection to susceptible individuals yet. It is in consideration of this additional compartment that the authors seek to extend Volz's model to include the exposed state and construct an SEIR model.

In this study, individuals are represented as nodes, and the relationship between two individuals is represented by an edge connecting them to each other through a random network. We assume a closed population and full immunity upon recovery. At the end of the epidemic, we determine its final size. The model is verified by comparing its predictions to the stochastic simulations of the SEIR dynamics in large networks. Numerical simulations are performed through random network generation and "next event" determination. The Molloy-Reed algorithm as well as the Poisson and scale-free networks are employed.

Parallel Session

Epidemiology VIII

MAXIMUM EPIDEMIC SIZE FOR A NONLINEAR SEIR MODEL WITH LIMITED RESOURCES

Mariajesus Lopez-Herrero

lherrero@ucm.es

Complutense University of Madrid

Keyword: Stochastic epidemic model.

This communication deals with a stochastic SEIR model with nonlinear incidence rate and limited resources for a treatment. We focus on a long term study of the maximum of individuals simultaneously infected during an outbreak of the communicable disease.

The maximum number of infective in the course of the epidemic is the *peak size* of the epidemic curve and it gives an idea of how large treatment resources should be with the purpose of keeping demand for facilities around the available amount. As we are dealing with a model having a limited number of resources, the interest in characterizing the maximum of simultaneous infective individuals involved during an outbreak is well justified. In fact control strategies should include the objective of lowering the peak size in the way that demand for facilities stand below the available resources.

Acknowledgements: This work is supported by the Spanish Ministry of Economy, Industry and Competitiveness, Project MTM2014-58091-P.

Parallel Session

Epidemiology VIII

THE SHAR MODEL AND ITS EFFECTIVE INFECTION RATE: ANALYTICAL RESULTS ON SEVERE *VS* ASYMPTOMATIC INFECTION

Raquel Filipe

rmfilipe@fc.ul.pt

Centro de Matemática, Aplicações Fundamentais e Investigação Operacional, Faculdade de Ciências, Universidade de Lisboa, Portugal

Joint work with Nico Stollenwerk, Luís Mateus, Scott Halstead and Maíra Aguiar.

Keyword: Epidemiology.

One of the simplest epidemiological models is the famous SIR model in which we assume three types of individuals in our system: susceptible, infected and recovered. But what if, for example, we study an epidemic in which there are infected individuals who do not have symptoms? How can we model this? To get around this challenge we assume two types of infected individuals, symptomatic and asymptomatic, which then allows us to define the SHAR model. We then move on to study the infection rate of the SHAR model: the effective infection rate. [1]

References

[1] Raquel Filipe, *et al* (2016) *Effective infection rate in SIR-type models from models with symptomatic and asymptomatic infection*, Proceedings of the 16th International Conference on Computational and Mathematical Methods in Science and Engineering, ISBN 978-84-608-6082-2, 483-490.

Parallel Session

Epidemiology VIII

CORRELATIONS BETWEEN STOCHASTIC EPIDEMICS IN MULTIPLE INTERACTING SUBPOPULATIONS

Sophie R. Meakin

s.meakin@warwick.ac.uk

Centre for Complexity Science, University of Warwick, Coventry, CV4 7AL, England

Joint work with Matt J Keeling (Zeeman Institute: SBIDER, Mathematics Institute and School of Life Sciences, University of Warwick)

Keywords: Epidemiology, Metapopulation, Stochastic, Moment closure approximation.

Heterogeneity is commonly incorporated into epidemiological models by dividing the population into multiple interacting subpopulations. This partitioning captures a variety of characteristics of the whole population; the subpopulations may represent: geographically separated locations, high- and low-risk groups, age structure or multiple species. The strength of interaction, or 'coupling', between two populations is captured by a single phenomenological parameter; however, a limitation of this approach is how to infer this coupling parameter. Between-population interactions are complex and high quality data on relevant interactions are rarely available; how such data translates into a single coupling parameter is also unclear. We present a method that circumvents this problem by estimating the coupling using more widely-available data on disease incidence.

We begin with a stochastic SIR model in two identical interacting populations, where the force of infection in each population depends on a mixture of within-population and between-population transmission. By making a moment closure approximation we derive an approximation for the correlation between the number of infected individuals in each population as a function of the coupling. We show that our result holds for a range of parameter values and is supported by stochastic simulations – considering a measles-like disease as a specific example. Our result can also be generalised to three or more populations, to asymmetric transmission or to non-identical populations.

More importantly, we can reverse this process. The correlation between the number of infected individuals in two populations can be calculated from data on disease incidence and then used in conjunction with our result to estimate the coupling parameter. Crucially, this allows us to estimate the coupling between subpopulations even in the absence of data on human mobility. As heterogeneity is widely-acknowledged to promote to disease persistence, so accurate estimation of coupling parameters could be invaluable to disease eradication research.

Parallel Session

Epidemiology VIII

DYNAMICS OF EPIDEMIC MODELS WITH TWO STRAINS AND CROSS IMMUNITY

Antonio Gómez-Corral

antonio.gomez@icmat.es

Instituto de Ciencias Matemáticas CSIC-UAM-UC3M-UCM, Calle Nicolás Cabrera 13-15, 28049-Madrid, Spain

Joint work with E. Almaraz, J. Amador and D. Armesto (Universidad Complutense de Madrid, Spain)

Keywords: Epidemics, Extreme values, Final size, Multi-type SIS- and SIR-models.

The interest is in SIR and SIS epidemic models ([1, 2]) with two strains of a disease and cross immunity. We show how to derive the joint probability distribution of the maximum number of individuals simultaneously infected during an outbreak and the time to reach such a maximum number for the first time. This distribution is analyzed by distinguishing between a *global* outbreak and the *local* outbreaks, which are linked to the extinction of the disease and the extinction of particular strains of the disease, respectively. For illustrative purposes, the two-strain SIR- and SIS-models with cross immunity are applied to the study of the spread of antibiotic-sensitive and antibiotic-resistant bacterial strains within a hospital ward.

Acknowledgements: This work is supported by the Spanish Ministry of Economy, Industry and Competitiveness, Project MTM2014-58091-P.

References

[1] Amador J, Armesto D, Gómez-Corral A. (2018). *Extreme values in SIR epidemic models with two strains and cross immunity*, under review.

[2] Almaraz E, Gómez-Corral A. (2018). *Number of infections suffered by a focal individual in a two-strain SIS-model*, under review.

Parallel Session

Epidemiology VIII

CHAOS VIA TORUS DESTRUCTION IN POPULATION BIOLOGY: IMPLICATIONS FOR DATA ANALYSIS

Nico Stollenwerk

nico@ptmat.fc.ul.pt

CMAF-CIO, University of Lisbon, Portugal

Joint work with Maira Aguiar (Universidade Nova de Lisboa, Portugal) and Bob W. Kooi (Free University Amsterdam, The Netherlands).

Keywords: Dengue fever and ADE, Temporary cross-immunity, Rosenzweig-MacArthur model, Torus bifurcation, Arnold tongues.

In the analysis of relatively simple models for dengue fever epidemiology, describing antibody dependent enhancement ADE and temporary cross-immunity, we encountered Hopf and torus bifurcations and increasing parameters slightly further also the onset of deterministic chaos characterized by positive dominant Lyapunov exponents [1]. Such models describe well the large fluctuations observed in time series of dengue fever hospitalization cases. However the models are already high dimensional and any data analysis is difficult because of the chaotic behaviour and also the high number of initial conditions.

We therefore search for simpler models in population biology with similar dynamical behaviour, one of the simplest originating from ecological models of Rosenzweig-MacArthur (RMA) type. The classical RMA model shows a Hopf bifurcation which under seasonal forcing turns into a torus bifurcation. By increasing the forcing further the onset of deterministic chaos was observed and e.g. described in [2], but lacking a further analysis of the onset of chaos as the tori break off.

Via the analysis of two dimensional dominant Lyapunov exponent plots we revealed the chaotic regions to be inside Arnold tongues of the original tori [3]. This gives a first hint of further analysis of the original dengue fever models in which the interplay of different sub-systems can give rise to a similar scenario. Since the original dengue models are not seasonaly forced, the analysis of the autonomous systems place additional difficulties in identifying the interplaying frequencies. The full understanding of this dynamic scenario helps in the subsequent data analysis of empirical time series of dengue fever hospitalization cases, e.g. via iterated filtering, since it turns out that not a single model is describing the large fluctuations of the data but a dynamic scenario [4]. We will elaborate on this aspect of data analysis via quite new tools of model comparison as e.g. given by Bayes factor analysis. And again, the understanding of such models is vital for the understanding of any intervention measure, as e.g. the impact of the newly licensed dengue fever vaccine, which however turned out to be quite problematic exactly because of the subtle interplay between ADE and temporary cross-immunity [5, 6].

References

[1] M. Aguiar, N. Stollenwerk, B. Kooi (2009) *Torus bifurcations, isolas and chaotic attractors in a simple dengue fever model with ADE and temporary cross immunity*, Int. J. Comput. Math. 86, pp1867–1877.

[2] Y.A. Kuznetsov. *Elements of Applied Bifurcation Theory. No. 112, Applied Mathematical Sciences.* Springer-Verlag, 3rd edition, New York, 2004.

[3] N. Stollenwerk, P. Fuentes Sommer, B. Kooi, L. Mateus, P. Ghaffari, M. Aguiar (2017). *Hopf and torus bifurcations, torus destruction and chaos in population biology*, Ecological Complexity 30, pp91–99.

[4] N. Stollenwerk, M. Aguiar, S. Ballesteros, J. Boto, B. Kooi, L. Mateus (2012) *Dynamic noise, chaos and parameter estimation in population biology*, Interface Focus 2, pp156–169.

[5] M. Aguiar, N. Stollenwerk, S. Halstead (2016) *The Impact of the Newly Licensed Dengue Vaccine in Endemic Countries*, Plos Negl. Trop. Diseases 10(12), e0005179.

[6] M. Aguiar, N. Stollenwerk (2017) *Dengvaxia: age as surrogate for serostatus*, Lancet Infect. Dis., published online Dec 21., https://doi.org/10.1016/ S1473-3099(17)30752-1