Information and Communication Technologies

EPIWORK

Developing the Framework for an Epidemic Forecast Infrastructure

http://www.epiwork.eu

Project no. 231807

D1.1 Analysis of Epidemic Dynamics on Clustered Networks

Period covered: months 1st – 12th
Start date of project: February 1st, 2009
Due date of deliverable: **January 31st, 2010**
Distribution: public

Date of preparation:
Duration: 1-year
Actual submission date: February, 8th 201
Status:

Project Coordinator: Alessandro Vespignani
Project Coordinator Organization Name: ISI Foundation
Lead contractor for this deliverable: Tel Aviv University

Work package participants

The following partners have taken active part in the work leading to the elaboration of this document, even if they might not have directly contributed writing parts of this document:

- **London School of Hygiene and Tropical Medicine**
- **Faculty of Sciences, University of Lisbon. Portugal**
- **Bar Ilan University**
- **Tel Aviv University**

Change log

Version	Date	Amended by	Changes

Executive Summary

WP1 Deliverable 1 "Epidemic Dynamics on Clustered Networks"

One of the key aims of the EPIWORK project is to provide general tools for the realistic modeling of the spread of epidemics in structured populations. The first theme of Work Package 1 concerns population contact networks that characterize the non-random and often clustered manner in which individuals in large populations come into contact. These contacts are usually represented in the form of a connectivity matrix or a graph. The work outlined in this Deliverable explores how heterogeneities due to population aggregation and spatial structuring control epidemic size and extinction thresholds. Classical theory has largely been concerned with random contact network structure, while our research aims to push this to more realistic scenarios.

The Deliverable outlined here discusses the results of four research groups. The group of the London School of Tropical Health deals extensively with the impact of clustered contact networks on sexually transmitted diseases, taking HIV as a case study.

Using theoretical models, the group of the University of Lisbon, Portugal, examines how spatially restricted contact networks, namely those with power law distributed connectivity, yield super-diffusive spreading, and thus influence epidemic threshold behavior especially for models with re-infection.

The Bar Ilan University group provide an unique mathematical analysis of how vaccination strategies need to be modified when contact networks are clustered, if they are to be effective.

The Tel Aviv University group discusses extensively the contact network structure of the Israeli population and the manner in which it affected the spread of the H1N1 influenza pandemic in 2009. In addition, they provide a theoretical analysis of clustered contact networks that gives clear predictions of how clustering (as measured by the relative number of triangles in a network) controls the epidemic size and the epidemic threshold.

Contents

We present the Deliverables for each of the four research groups in turn:
A) London School of Tropical Health,
B) Faculty of Sciences, University of Lisbon, Portugal,
C) Bar Ilan University**,**
D) Tel Aviv University.

A) London School of Hygiene and Tropical Medicine

Santhakumaran, S., O'Brien; K., Bakker, R., Ealden, T., Shafer, LA., Daniel, RM., Chapman, R., Hayes, RJ., White, RG1. *The potential impact of polygyny on long-duration STI prevalence using simulated sexual networks* (Submitted to the journal STI)

Our paper discusses models for sexually transmitted infectious diseases (STI's) focusing in particular on the effects of concurrent sexual partnerships (partnerships with an overlapping partner). Such partnerships have been proposed as an explanation for the high prevalence of HIV infection in some countries. While modeling suggests that the presence of concurrent sexual partnerships can increase the rate of invasion of sexually transmitted infections (STIs). We have designed a model of HIV, which describes the dynamics of infection on a clustered contact network. Differences in how concurrent partnerships occur in polygynous versus non-polygynous populations can lead to rather diverse clustering in the contact networks. In contrast to conventional wisdom, our study supports the hypothesis that polygyny, a specific form of institutionalized concurrency, may be protective against HIV at the population level.

B) Faculty of Sciences, University of Lisbon, Portugal

Martins, J., Pinto, A., Stollenwerk, N. (2009), *A scaling analysis in the SIRI epidemiological model*, Journal of Biological Dynamics, 479--496.

Martins, J., Aguiar, M., Pinto, A., Stollenwerk, N. (2009), *On the series expansion of the spatial SIS evolution operator*, accepted for publication in Journal of Difference Equations and Applications.

J.P. Boto and N. Stollenwerk (2009). *Fractional calculus and Levy flights:*

modelling spatial epidemic spreading, Proceedings of 9th Conference on Computational and Mathematical Methods in Science and Engineering, CMMSE 2009, edited by Jesus Vigo Aguiar et al., Salamanca, pp. 177—188.

Nico Stollenwerk, J.P. Boto, (2009), *Reaction-superdiffusion systems in epidemiology, an application of fractional calculus*, Proceedings of the International Conference on Numerical Analysis and Applied Mathematics, ICNAAM, Simos, Theodore E.; Psihoyios, George; Tsitouras, Ch., (eds.)

In the above publications, we have investigated spatially restricted contact networks, namely those with power law distributed connectivity to study super-diffusive spreading. This type of contact networks is relevant for practical applications as shown by empirical data of human contact proxies as travel networks or money bills mobility notifications. The influence of these contact networks on epidemic thresholds is studied, and turns out to be especially important for models with re-infection. These models, besides the typical local spreading epidemic threshold, also present other important properties such as a crossover between SIR and SIS type behavior, which is related to the re-infection threshold.

C) Bar Ilan University:

Manuscript in preparation.

In this study, we construct networks with a variable clustering coefficient. The clustering coefficient accounts for the probability that two neighbors of an individual are neighbors of each other. By varying the clustering coefficient, we study its effect on various quantities of interest for the description of epidemics. In particular, how the clustering affects the different immunization strategies. As the clustering coefficient of the network increases, we find that the acquaintance immunization becomes far more effective than random immunization.

D1) Tel Aviv University (TAU)

Roll U.[1], Katriel G.[1], Yaari R.[1], Stone L.[1*], Barnea O.[1], Mendelson E.[2], Mendelboim M.[2] and Huppert A.[3] Onset of a pandemic: characterizing and modeling the initial phase of the swine flu (H1N1) epidemic in Israel

The **TAU** team has been working on the emergence and size of the giant component in clustered random graphs with a given degree distribution. The paper published in Physical Review Letters provides a new generating function approach to clustered networks. The group was also active on the study of the early stage swine flu contact networks in Israel based on surveillance of the 2009 pandemic in Israel. Most individuals tested for swine flu were asked by their doctor to identify who they believed they were infected by, thereby providing important information concerning the contact structure of the Israeli population. Of the 713 cases, 183 (or 25.6%) were able to provide information establishing contact links. The data was used to assemble contact networks which map the connections between an infected person (infector) and the different individuals he/she infected (infectees). The networks are visualized by portraying individuals as nodes in a graph and placing a directed edge from any infector to the individuals he/she infects. The networks thus reveal who infected who. Altogether there were 66 separate infection networks totaling 183 nodes, with 123 links between them. The significant mismatch between number of nodes and links is due to the fact that the networks were largely disconnected with many isolated links. The mean number of outgoing links per network was 0.67. Most nodes, i.e. 55.2%, had no outgoing links, 33.3% had one outgoing link, 7.1% had two out going links and 2.7 % had three outgoing links. In addition, there were three patients having the status of what might be considered "superinfectors" with four, seven and ten outgoing links respectively.

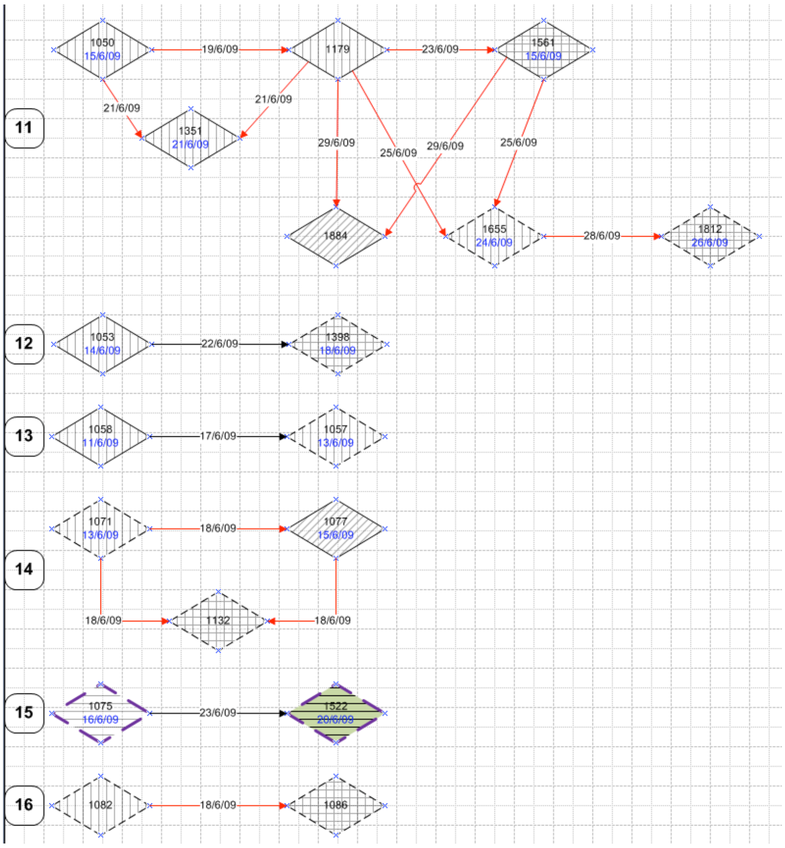


Fig.1 Contact networks between selected individuals with swine flu in Israel

Based on the contact networks, it was possible to determine the generation-time interval distribution for swine flu. The mean generation-time was found to be m=2.92 and its standard deviation s=1.79, based on a generation time distribution of up to seven days. The contact networks also provided revealing information concerning who infected who in terms of the age-class structure of the patients.

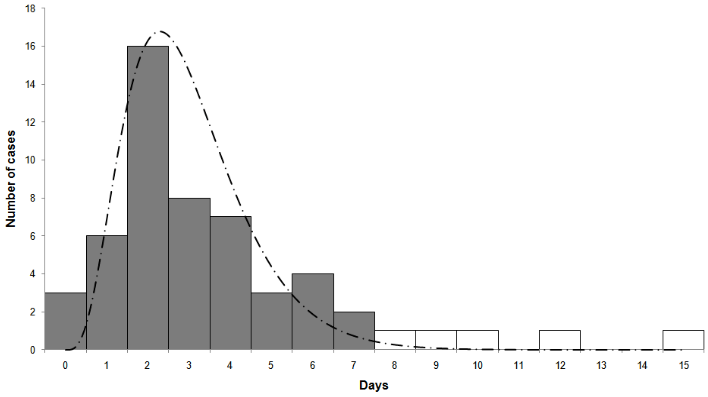


Figure 2: frequency distribution of the swine flu generation time. This is based on differences in reported disease initiation dates that were calculated from our infection networks. Also displayed is a Gamma distribution curve (dashed line) based on data only up to seven days – dark bars (see text for details).

D2) Tel Aviv University (TAU) - theory

Berchenko Y., Artzy-Randrop Y., Teicher M., Stone L. (2009) Emergence and size of the giant component in clustered random graphs with a given degree distribution. *Physical Review Letters.* Vol. 102 (13) 138701

This paper is the basis for the TAU work on clustered networks, as illustrated in the task 5, theme I of WP1.

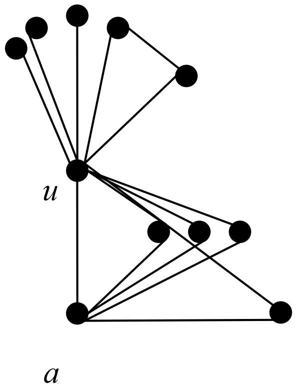
The great majority of efforts to model infectious diseases as they spread in populations invariably make use of the assumption of "random mixing". That is, each member of the population has an equal chance of meeting any other member. The same is true for most ecological models (e.g. predator-prey) of the Lotka-Volterra type. The great convenience of this so called "Mass Action" assumption is that it allows to solve "mean field" differential equation model of an infection as it propagates through the population. The great disadvantage of the approach is that it fails to take into account crucial spatial heterogeneities that may have great impact on the propagation dynamics.

If each individual of the population is considered a node in a graph, and the edges as connections between individuals (i.e., vehicles for disease transmission), then a good metaphor for the random mixing model may be the well known Erdos-Renyi random graph. We have moved beyond this standard model by examining the effects of clustering in the spreading dynamics on a network. Clustering is proportional to the number of "triangles" in the graph (i.e., where "a friend of a friend is also your friend), or loops of order 3: A→B→C→A. Triangles may be viewed as an alternative form of aggregation and perhaps a more accurate representation. Currently very little is known about how clustering affects network dynamics, although some recent important studies have appeared in the literature.

The main difficulty when studying clustered networks is that the branching processes, which are at the heart of the generating function formalism of Newman et al. (2001), are no longer applicable due to the formation of short loops, namely triangles. We have developed a more general theoretical approach that overcomes the aforementioned problems and yet it is still based on the generating function formalism.

<u>New Approach for Clustered Networks</u>: we developed a new approach that permits the analysis of clustered networks by adapting the generating function for un-clustered networks. We believe the mathematical infrastructure developed in our work will be able to contribute considerably in determining the effects of clustering in epidemiological models and population networks.

We then moved forward with respect to the results obtained in the above mentioned paper (Berchenko et al, PRL 102, 138701 (2009)) and considered running an SIR model of epidemic through a clustered network. In our paper, we propose a method for estimating an "R_0" which takes into account the redundancy in infection pathways, assuming the graph is almost treelike, and the only larger closed structures are disjoint triangles (see figure below).



In our work, we show that a stochastic process of the spread of a disease in a network is equivalent to the exploration of the network's giant component if the transmissibility is equal to 1 and the process is then completely deterministic. In this case, the resulting giant component will be identical to the giant component of the underlying network. We then obtain the same reproductive number as obtained in the Berchenko et al. paper.

The more interesting case transmissibility minor than 1 allows us to predict the threshold for the spread of an epidemic when the probability of infection is some value 0<T<1 rather than unity. We find a value for R0 under these conditions that can then be used to establish the epidemic threshold, occurring at R0=1. We have tested our prediction with simulated epidemics and found it highly accurate. This work is being prepared for publication.