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Data-driven modeling of contagion processes

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08.45-09.00	opening
09.00-09.40	*Invited talk – Estimating infectious disease parameters based on serological and social contact data* Niel Hens (Hasselt University and University of Antwerp, Belgium)
09.40-10.00	*The impact of current demographic trends on the dynamics and control of vaccine preventable childhood infections* Alessia Melegaro, Piero Poletti, Stefano Merler, Marco Ajelli, Piero Manfredi (Pisa University, Italy)
10.00-10.20	*Studying Disease Dynamics under Diverse Population Structures and Contagion Scenarios* Iris Gomez-Lopez (University of North Texas, United States), Olivia Loza, Armin R Mikler
10.20-10.40	*Measles in Italy: strategies for control and elimination* Marco Ajelli, Caterina Rizzo, Stefano Merler (Bruno Kessler Foundation, Italy)
10.40-11.10	break
11.10-11.30	*Optimizing vaccine allocation for pandemic influenza* Laura Matrajt (University of Washington, United States), M. Elizabeth Halloran, Ira M. Longini Jr.
11.30-11.50	*Modelling Respondent Driven Sampling (a novel approach)* Jo Moir (University of Warwick, United Kingdom), Leon Danon, Matt J. Keeling
11.50-12.10	*Malaria epidemic spreading and risk perception in community networks in South East Asia Region* Shiv Sankar, Sarita Azad, Ankit Bansal, Pietro Lio (University of Cambridge, United Kingdom)
12.10-12.30	*Stochastic Computational, Thermal, and Vertical Transmission Models to Simulate Dengue Persistence in Vector and Human Populations* Angel Bravo-Salgado, Thiraphat Meesumrarn, Armin Mikler (University of North Texas, United States)
12.30-14.00	Lunch
14.00-14.40	*Invited talk – The Dynamics of Health Behavior Sentiments on a Large Online Social Network* Marcel Salathé (Penn State University, United States)
14.40-15.00	*An infectious disease model on empirical networks of human contact: bridging the gap between dynamic network data and contact matrices* Anna Machens (Centre de Physique Théorique, Aix-Marseille University, France), Caterina Rizzo, Alberto Tozzi, Alain Barrat, Ciro Cattuto
15.00-15.20	*Exploring spatio-temporal diffusion patterns from the London riots to investigate contagion in civil unrest* Peter Baudains (UCL, United Kingdom), Alex Braithwaite, Shane Johnson
15.20-15.40	*Optimizing surveillance for livestock disease spreading through animal movements* Paolo Bajardi (Computational Epidemiology Laboratory, ISI Foundation, Italy), Alain Barrat, Lara Savini, Vittoria Colizza
15.40-16.00	*Activity driven modeling of dynamic networks* Nicola Perra (Northeastern University, United States), Bruno Goncalves, Romualdo Pastor-Satorras, Alessandro Vespignani
16.00-16.40	break
16.40-17.00	*Building an Agent-based Model for assessing Default Contagion in Financial Networks* Tarik Roukny (IRIDIA, Université Libre de Bruxelles, Belgium), Stefano Battiston, Hugues Bersini and Hugues Pirotte
17.00-17.20	*DebtRank: Too Central to Fail? Financial Networks, the FED and Systemic Risk* Stefano Battiston (ETH Zurich, Switzerland), Michelangelo Puliga, Rahul Kaushik, Paolo Tasca, Guido Caldarelli
17.20-17.40	*Relevance of SIR Model for Real-world Spreading Phenomena: Experiments on a Large-scale P2P System* Daniel Bernardes (France Laboratoire d'informatique de Paris 6 - CNRS/UPMC), Matthieu Latapy, Fabien Tarissan
17.40-18.00	*Effect of bursty communication patterns on contagion in a threshold-based epidemic dynamics* Taro Takaguchi (The University of Tokyo, Japan), Naoki Masuda, Petter Holme

INVITED TALKS

Estimating infectious disease parameters based on serological and social contact data

Niel Hens
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Centre for Health Economic Research and Modelling Infectious Diseases, Vaccine and Infectious Disease Institute, University of Antwerp, Belgium

Mathematical models of infectious diseases rely on knowledge about how people in the population mix. Whereas in the past mixing patterns were mainly based on indirect observations, social contact surveys, where applied, have proven to provide an invaluable source of information to better parameterize mathematical models of infectious diseases spread from person to person through the respiratory or close contact route.

The POLYMOD study was the first study that surveyed contact patterns from representative samples of eight different European countries using a common paper-diary methodology (Mossong et al., 2008). Here, I review the results of POLYMOD and illustrate how these results have been used in mathematical and statistical models for infectious diseases (see e.g. Ogunjimi et al., 2009; Goeyvaerts et al., 2010, 2011; Hens et al., 2012).

I will further elaborate on more recently conducted large-scale social contact surveys in Flanders (Belgium), France, Peru, South-East Asia and Vietnam. These surveys, although largely based on POLYMOD, also focused on assessing the impact of behavioral factors, network characteristics, weather patterns and animal-human interaction patterns on contact patterns to better inform the contagion process. I will end with a discussion on the limitation of using social contacts data to inform the estimation of infectious disease parameters.

Goeyvaerts, N., Hens, N., Aerts, M., and Beutels, P. (2011). Model structure analysis to estimate basic immunological processes and maternal risk for parvovirus B19. Biostatistics, 12(2):283–302.

Goeyvaerts, N., Hens, N., Ogunjimi, B., Aerts, M., Shkedy, Z., Van Damme, P., and Beutels, P. (2010). Estimating infectious disease parameters from data on social contacts and serological status. Journal of the Royal Statistical Society Series C, 59:255–277.

Hens, N., Shkedy, Z., Aerts, M., Faes, C., Van Damme, P., and Beutels, P. (2012). Infectious Disease Parameters for Transmission Models: A Modern Statistical Perspective. Springer-Verlag.

Mossong, J., Hens, N., Jit, M., Beutels, P., Auranen, K., Mikolajczyk, R., Massari, M., Salmaso, S., Scalia Tomba, G., Wallinga, J., Heijne, J., Sadkowska-Todys, M., Rosinska, M., and Edmunds, J. (2008). Social contacts and mixing patterns relevant to the spread of infectious diseases. PLoS Medicine, 5(3):381–391.

Ogunjimi, B., Hens, N., Goeyvaerts, N., Aerts, M., Damme, P. V., and Beutels, P. (2009). Using empirical social contact data to model person to person infectious disease transmission: an illustration for varicella. Mathematical Biosciences, 218(2):80–87.

The Dynamics of Health Behavior Sentiments on a Large Online Social Network

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Modifiable health behaviors, a leading cause of illness and death in many countries, are often driven by individual beliefs and sentiments about health and disease. Individual behaviors affecting health outcomes are increasingly modulated by social networks, for example through the associations of like-minded individuals - homophily - or through peer influence effects. Using a statistical approach to measure the individual temporal effects of a large number of variables pertaining to social network statistics, we investigate the spread of a health sentiment towards a new vaccine on Twitter, a large online social network. We find that the effects of neighborhood size and exposure intensity are qualitatively very different depending on the type of sentiment. Generally, we find that larger numbers of opinionated neighbors inhibit the expression of sentiments. We also find that exposure to negative sentiment is contagious - by which we merely mean predictive of future negative sentiment expression - while exposure to positive sentiments is generally not. In fact, exposure to positive sentiments can even predict increased negative sentiment expression. Our results suggest that the effects of peer influence and social contagion on the dynamics of behavioral spread on social networks are strongly content-dependent.

CONTRIBUTED TALKS

The impact of current demographic trends on the dynamics and control of vaccine preventable childhood infections.

Alessia Melegaro[1], Piero Poletti[1], Stefano Merler[2], Marco Ajelli[2], Piero Manfredi[3]
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European populations are currently undergoing a number of important transformations ranging from the generalized spread of low fertility, and related population ageing, the “postponement” of life events, and the increasing role of international immigration, even as a policy to counter population ageing. Even more massive transformations are occurring in the developing world as a consequence of the ongoing fertility transition and fast urbanization. We discuss the impact of demographic change on the dynamics and control of vaccine preventable childhood infectious disease from a modeling perspective. We first clarify the circumstances under which demographic change actually might have an impact on the dynamics of childhood infections. We suggest that to predict the impact of demographic change on infection dynamics we need to figure out the relation between population change and those demographic structures (by age, by household size, etc) which are key for the types of contact patterns relevant for infection transmission. To figure out such a relation we use an individual-based IBM model of infection where contacts occur in three “arenas”, i.e. the school (or work), the household, and “other” population contacts. By focusing on fertility decline we illustrate, under a variety of equilibrium or transient conditions, the effects of demographic change on arena-specific contact matrices, and through these on the general contact patterns of the population. By including available estimates of arena-specific transmission rates we are thus able to quantify the effects of demographic change on basic reproduction numbers, and therefore on infection control conditions. Our results might be useful from the standpoint of long term planning of immunization resources.

Studying Disease Dynamics under Diverse Population Structures and Contagion Scenarios

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Demographic and socio-economic factors are determinants for how contagion develops in human populations. The Center for Diseases Control (CDC) has reported that attributes such as age, gender, ethnicity, and race are associated to the emergence or prevalence of certain diseases[1]. In this regard, emerging infectious diseases have been a major concern for Public Health since the extent of strategies to anticipate or mitigate a contagion are limited[2]. Additionally, the increase in urbanization and modes of transportation in an ever changing world have also played a crucial factor for the transmission and persistence of pathogens. Several methodologies and theories have been utilized to implement insightful computational models to conduct public health and epidemiological investigations by studying epidemics and their associated factors[3]. By means of utilizing public information, we address and quantify the relevance of demographic and socio-economic factors in the contagion phenomena with a novel approach [4]. The proposed methodology, contributes to the understanding of contagion processes in communities of diverse characteristics. Taking into consideration community diversity and by constructing models to simulate epidemic scenarios, it is possible to study the dynamics of both populations and diseases. Also, strategies such as monitoring, vaccination, prophylaxis, and social distancing entirely rely on the understanding of the factors that steer the disease dynamics. In this context, experimentation allows to effectively analyze strategic approaches that lessen the effects of the spread of an infectious disease on a population. For instance, factors such as disease pathogenesis or social affinity of the population influence differently an infectious disease progression within the same community[5, 6]. Disease dynamics are strongly affected by the population characteristics. Demographic and geographic characteristics exert people to prefer individuals to interact with others of similar characteristics. Hence, the correlation among people characteristics and their preferences is expressed by distributing individuals into groups of similar characteristics [7]. In addition, a particular distribution of the population into groups depicts a community structure of groups with differentiated characteristics. It can be noticed that, within a set of groups also exists a preference of individuals to move from their group to another group of similar characteristics. In current work, both the dynamics of the disease and the structure of the population are modeled for experimentation and analysis of synthetic epidemic scenarios. In order to achieve this, the methodology is divided into four stages: a synthetic population is created; a structure of the population into groups is to be identified; a social network of groups is then constructed, and finally an infectious disease is initiated in the structured population to generate the contagion network. In the first stage, a synthetic population is constructed by disaggregating Census 2000 data. Demographic and geographic data are utilized to generate individuals with inherent attributes. Next, the attributes of the synthetic population are enhanced by linking their geographic attributes to the geographical boundaries of the US Independent School Districts. In the second stage, a clustering infrastructure is utilized to ascertain a distribution of the synthetic individuals into groups of people with similar attributes. For this, a hierarchy of the population attributes is established to assign differentiated weights to them and bias the identification of groups within the population. In the third stage, the generated groups are utilized to determine a structure of the population that depicts a social network of groups with nodes and edges representing groups and between-group affinity correspondingly. Finally in the last stage, an individual is randomly infected so that an infectious disease is spread throughout the structured population. Once the epidemic ceases progression, a contagion network is generated so that information about dynamics of both population structure and disease is extracted and analyzed. Observations about patterns of the spread are extracted. Routes of the disease spreading from group to group are identified and statistics of both local and global epidemic per group and across the network respectively are ascertained. In the current framework, it is possible to experiment with diverse and controlled epidemic scenarios by changing both the attribute-hierarchy and the assumptions that precede the construction of the population. As a result, diverse disease spread patterns can be extracted while experimenting with distinct epidemic scenarios with different population structures. Whereas experimentation on real populations is severely limited for both practical and ethical reasons, computer simulations and synthetic reconstruction of communities are useful tools to conduct public health and epidemiological investigations. Additionally in this project, statistics of the epidemic scenarios are computed to identify at-risk population groups and their underlying network. Hence, community-based models are constructed to provide a quantitative assessment of healthcare prophylaxis and intervention strategies. The contribution of incorporating demographics and geographic characteristics to social networks for analysis expands the scope of the social models to analyze epidemics and contributes to the analysis and investigation of possible scenarios.

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Measles in Italy: strategies for control and elimination

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Since the introduction of measles vaccination in Italy at the beginning of the 80s, measles epidemiology has radically changed. The number of yearly cases dramatically decreased from a clearly endemic situation to the current figure characterized by the recurrence of localized outbreaks; at the same time, the average age at infection has increased from 5-6 years old to around 17. However, the disease is far from being eliminated. Here we propose a data-driven simulation model for assessing the effectiveness of the Italian immunization program, testing alternative strategies aimed at measles elimination and proposing new measures for the control of local epidemic outbreaks. Our results show that the ongoing 2-doses vaccination program, the first of which to 15 months-old infants (about 90% vaccination coverage) and the second one to 5-6 years-old children (about 75% vaccination coverage) is able to progressively reduce the number of measles infections, but is not sufficient to guarantee the elimination of localized epidemics even in 2025. On the other hand, we found that, by adding only in 2012 a vaccination campaign in schools for students aged 11-16 years, the probability of observing local outbreaks quickly decreases as well as the size of these outbreaks. An optimal strategy leading to the substantial elimination of the disease in the short term is to extend the campaign to individuals aged 11-30 years, in such a way to immunize the fraction of the population currently comprising the largest number of susceptibles. In addition, we found that the distribution of vaccines among students attending the same school of a notified case represents an effective option to control measles outbreaks: for instance, a vaccination coverage of about 40% leads to a reduction of 60%-70% of the outbreak size. In conclusion, this work shows that, in order to achieve the WHO goal of measles elimination in Europe by the end of 2015-2020, the current immunization program in Italy should be integrated with additional vaccination campaigns having as a target the susceptible individuals born soon after the introduction of measles immunization program in Italy, when low vaccination coverages were reached.

Optimizing vaccine allocation for pandemic influenza

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With new cases of avian influenza H5N1 (H5N1AV) arising frequently, the threat of a new influenza pandemic remains a challenge for public health. Because there is an important time lag between the emergence of a new pandemic strain and the development and distribution of a vaccine, shortage of vaccine is very likely at the beginning of a pandemic. We coupled a mathematical model with a genetic algorithm to optimally and dynamically distribute vaccine in a network of cities, connected by the airline transportation network. Because most of the human cases of H5N1AV have arisen in Southeast Asia, we used a network of 16 cities in this region that has been identified as a transmission cluster. We show that it is possible to significantly mitigate a more global epidemic with limited quantities of vaccine, provided that vaccination occurs within the first weeks of transmission.

Modelling Respondent Driven Sampling (a novel approach)

Jo Moir, Leon Danon, Matt J. Keeling
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Respondent-driven sampling (RDS) is a data collection and analysis method that has been used extensively in recent years to study hard to reach populations, such as drug users and sex workers. RDS data collection uses the underlying social network structure of the population by providing sampled individuals with small incentives to recruit their peers into the study. The data collection process spreads through a social contact network in a manner that has many analogies to infectious disease spread, and so the RDS methodology may be ideal for collecting epidemiological data. However it is important to understand the biases that arise from RDS. We model RDS data collection as a modified SIR (Susceptible-Infectious-Recovered) process. At time t, 'susceptible' (S) individuals are those who have not yet been recruited and 'infectious' (I) individuals are those that were recruited at the previous time step. 'Infectious' individuals can only 'infect' up to a fixed number of their 'susceptible' contacts (corresponding to the fixed number of vouchers that are given as part of the RDS recruitment methodology) and are then 'removed' (R) at the next time step. The S, I and R classes can be further stratified into different groups, for example by their number of contacts. We obtain good agreement between our analytical model and simulation results on synthetic networks. In addition we use data from a recent study of HIV in IDUs to validate our approach. This modelling work has the potential to deepen our understanding of RDS and its inherent biases, improve analysis of current RDS data and inform the design of future RDS studies.

Malaria epidemic spreading and risk perception in community networks in South East Asia Region

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Human communities are often organized in form of complex networks that are constantly reshaped by social and economic dynamics and also influenced by the information individuals have about the highly infective diseases. Epidemic spreading is certainly affected by (and affect) the local information of the availability of preventive and control measures. So far social network models have oversimplified cognitive behavior on disease risk perception.

Malaria determinants in the South East-Asia (SEA) Region are embedded in its climate, terrain, sociocultural milieu, vectors and persistent neglect. In this work we study the dynamics of the spread of malaria and different vulnerability of population in countries of SEAR region. Despite that the dynamics of the disease in different regions and communities may be similar from a microclimatic perspectives, the risk perception may be very different from community to community. This may depend on available health care facilities, awareness of people in the community, religion beliefs and many other factors. It is expected that social networks among health professionals and their interaction with people will have strong effect on risk perception. We aim at studying malaria socio- biology in SEAR countries through collection of data on health care systems, policy and anti-malarial program run by the Government. Based on this information and on gender, economic situation, education level, occupation we find that we can split a population into interacting communities with varying levels of awareness of the disease which helps in identifying which communities suffer most of the burden of the disease. Since malaria is transmitted by mosquitoes and not necessary through human interaction, the spreading of the vector will inform on interaction in different countries; most of this study will focus on communities within individual countries. The complexity of biology and of the infection is matched by the complexities of the human psychology and heuristics, health systems, migrants and economic crisis duress when facing a pandemic disease. In spite of very less interaction however we can learn from the results of one region and recommend appropriate measures for a different region. And with a better understanding of the effects that community structured networks and variations in awareness, or risk perception, have on the disease dynamics we identify the major factors that have a profound effect on risk perception of population of SEAR countries and mark these differences that change the perception of people in these countries.

Stochastic Computational, Thermal, and Vertical Transmission Models to Simulate Dengue Persistence in Vector and Human Populations

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University of North Texas, United States

Our research is motivated by the fact that emerging vector-borne diseases have triggered concerns among public health expert world wide as the number of cases increases in tropical and subtropical regions. For example, the World Health Organization (WHO) and Pediatric Dengue Vaccine Initiative (PDVI) have estimated that approximately 2.5 billion to 3.6 billion people are at risk to contract Dengue. Coping with yearly outbreaks requires public health intervention. Available health resources are used in all possible directions to embrace interventions that prevent, promote, cure, or rehabilitate. The total expenditure for dengue has been estimated for eight countries, in Asia and the Americas, to be I\$587 millions in a study conducted from 2004 to 2007. Hand in hand, mathematical and computational models provide a scale to predict the yearly outbreaks of vector-borne diseases. The use of analytic tools permit both quantitative and qualitative analysis to facilitate rapid intervention and optimal utilization of public health resources, anticipating the next epidemic season. Vector-borne models commonly consider solely horizontal transmission that is the transmission of the pathogen from one infectious human to a vector or one infectious vector to a human. It has been suggested that dengue vertical transmission, the infection of the vectors' offsprings during development, causes the persistence of the virus in the wild vector population. Studies have shown that virus infected offsprings can pass on the virus to future generations but at the same time, virus imposes a natural birth control over the vector population increasing the proportion of vector fatality. It is known that temperature affects multiple facets of the biology of the vector including development and survival of eggs, larvae, and pupae. Above all, it affects the life span of the vector. It is also known that the speed of development of arthropods' pathogens are largely determined by the changes in temperature. In our research, a stochastic computational model (GSCM) is combined with thermal(TM) and vertical transmission(VT) models to simulate the reemergence of dengue virus in a vector population during seasonal cycles and periods of unfavorable weather. The resulting model, referred to as GSCM-DEN, allows experts in the public health field to simulate and observed the unfolding of vector-borne diseases dynamics in a particular region. We developed approximation models to describe the biological processes of the vector population and the development of the pathogen within the host. Each one of these models is temperature dependent. Our methodology facilitates the quantification of implementing vector life-shortening intervention on areas with emerging or reemerging vector-borne diseases. Further, vertical transmission data reported from experiments on infectious vectors were used to design a computational vertical transmission model to express the presence of vector-borne disease after periods of vector unfavorable weather conditions. In Figure 1 the stochastic computational model capturing the multipopulation interaction is depicted; squared elements represent individuals in the human population and circular elements represent the vector population. An interaction in the form of a vector's blood meal can occur between an infectious vector and a susceptible human or vice versa. Each interaction can result in the transmission of the infectious agent into the susceptible host. In In the figure, susceptible (S) mosquito population is represented by \$\frac{M_i}{S}\$, likewise infected (I) by \$\frac{M_i}{I}\$. The upper component in red represents the interaction between susceptible vectors and humans, whereas the lower component in yellow represents the interactions of infectious vectors and humans. Allowing this distinction during simulation, the time complexity of generating these interactions in the GSCM outperforms a \textit{naive} stochastic implementation; hence, reducing computational overhead. In this research, a study of dengue disease was conducted for a region in Thailand. Thailand weather data were used to provide the input for the thermal model. In addition, five years of monthly dengue cases were used to corroborate our computational model. Our contribution is an efficient and high fidelity vector-borne disease model, GSCM-DEN, that has been validated using existing data. Further, GSCM-DEN has the flexibility to represent any vector-borne disease providing the corresponding thermal model and historical data for validation.

An infectious disease model on empirical networks of human contact: bridging the gap between dynamic network data and contact matrices

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Background:
The integration of empirical data in computational frameworks designed to model the spreading of infectious diseases poses a number of challenges that are becoming more and more pressing with the increasing availability of high-resolution information on human mobility, contact, and behavior. In particular, wearable sensor networks and mobile devices allow to measure human contact networks from the geographic scale to the level of individual face-to-face interactions, with unprecedented temporal resolution. On the one hand, this deluge of data has the potential to revolutionize the computational efforts aimed at simulating scenarios, designing containment strategies and understanding their efficacy. On the other hand, integrating highly detailed data sources yields models that are unavoidably less transparent and general in their dynamics. Hence, given a specific diseases model, it is crucially important to assess what are the representations of the raw data that work best to inform the model, striking a balance between simplicity and detail.

Methods and Findings:
We consider high-resolution data on the face-to-face interactions of individuals in a general pediatrics hospital ward, obtained by using a wireless sensor network of wearable devices that sense face-to-face proximity. We simulate the spreading of a disease in this community by using an SEIR model on top of different mathematical representations of the empirical contact patterns computed from the raw data. At the most detailed level, we take into account all the contacts between individuals, together with their exact temporal ordering and timing. Then, we build increasingly coarse-grained representations of the contact patterns, that preserve only partially the temporal and structural information available in the data. We compare the dynamics of the SEIR model across these representations and show that a contact matrix that only takes into account the average contact duration between role classes fails to reproduce the size of the epidemic obtained using the high-resolution contact data. We introduce a contact matrix of probability distributions that takes into account the heterogeneity of contact durations between (and within) classes of individuals and show that this representation yields a good approximation of the epidemic size obtained by using the high-resolution data.

Conclusions:
These results have important implications for understanding the level of detail that is needed to correctly inform computational models for the study and management of real epidemics. In particular, they mark a first step towards the definition of strategies for the synopsis of high-resolution dynamic contact networks, providing a compact representation of contact patterns that, in simulation, preserves quantitative features of the epidemic that are central for decision-making.

Exploring spatio-temporal diffusion patterns from the London riots to investigate contagion in civil unrest

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Taking place predominantly in high population areas, such as London, Manchester and Birmingham, the civil unrest that occurred in the UK in August 2011 spread across the country, and it is generally perceived that the outbursts exhibited strong spatial and temporal clustering. It is widely considered that a social contagion process was at least partly responsible for the severe escalation and perseverance of clusters of unrest in space and time. Indeed, London's Metropolitan Police Service have since attributed the severity of unrest to unprecedented planning and communication via social media between people intent on causing disruption. They also state that the ability of gangs to co-ordinate widespread crime quickly via the Internet was a new phenomenon. However, to date, the precise space-time patterns of events have not been quantified in a systematic way.

In this paper, we investigate the diffusion patterns exhibited by the unrest in London, using high-resolution offence data. A fine-grain area-level analysis is performed to understand the precise patterns that emerged. We ask, on the one hand, whether outbreaks of unrest were more likely to occur in contiguous areas throughout London, perhaps implying proximity is the major factor in a process of geographic contagion, or, on the other, if 'flashpoints' of unrest in geographically distinct areas are more likely to occur. The latter may imply that a different type of mechanism is responsible, perhaps a form of social contagion facilitated by the Internet and social media.

We develop a statistical approach to quantify the observed diffusion patterns of unrest and test theoretical expectations - each with varying assumptions on how the unrest spread. Monte Carlo simulations are then used to test hypotheses. Finally, we relate our findings to the mechanisms claimed responsible for the apparent contagion behaviour during the unrest.

Optimizing surveillance for livestock disease spreading through animal movements

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[7] *ISI Foundation, Italy*

The spatial propagation of many livestock infectious diseases critically depends on the animal movements among premises; so the knowledge of movement data may help us to detect, manage and control an outbreak. The identification of robust spreading features of the system is however hampered by the temporal dimension characterizing population interactions through movements. Traditional centrality measures do not provide relevant information as results strongly fluctuate in time and outbreak properties heavily depend on geotemporal initial conditions. By focusing on the case study of cattle displacements in Italy, we aim at characterizing livestock epidemics in terms of robust features useful for planning and control, to deal with temporal fluctuations, sensitivity to initial conditions and missing information during an outbreak. Through spatial disease simulations, we detect spreading paths that are stable across different initial conditions, allowing the clustering of the seeds and reducing the epidemic variability. Paths also allow us to identify premises, called sentinels, having a large probability of being infected and providing critical information on the outbreak origin, as encoded in the clusters. This novel procedure provides a general framework that can be applied to specific diseases, for aiding risk assessment analysis and informing the design of optimal surveillance systems.

Activity driven modeling of dynamic networks

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Network modeling plays a critical role in identifying statistical regularities and structural principles common to many systems. The large majority of recent modeling approaches are connectivity driven. The structural patterns of the network are at the basis of the mechanisms ruling the network formation. Connectivity driven models necessarily provide a time-aggregated representation that may fail to describe the instantaneous and fluctuating dynamics of many networks. We address this challenge by defining the activity potential, a time invariant function characterizing the agents' interactions and constructing an activity driven model capable of encoding the instantaneous time description of the network dynamics. The model provides an explanation of structural features such as the presence of hubs, which simply originate from the heterogeneous activity of agents. Within this framework, highly dynamical networks can be described analytically, allowing a quantitative discussion of the biases induced by the time-aggregated representations in the analysis of dynamical processes.

Building an Agent-based Model for assessing Default Contagion in Financial Networks

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In financial systems, agents can borrow from or lend money to other agents in order to match their investment and debt maturities. If a stress occurs for one or few agents, it can rapidly spread into the system through these creditor-debtor relationships as one's default might trigger the default of some of its creditors, which, in turn, might propagate the stress to their own creditors, and so on. This phenomenon is known as Default cascades. In order to analyze the dynamics of such contagion process, we introduce an agent-based model inspired by the analytical model proposed by Battiston. We first confirm the matching between the results retrieved by our model and the analytical one and, then, investigate to what extent does the topology of a financial network (i.e., the way links are distributed among the agents) play a role in the propagation of a stress. An important advantage of the model is its possibility to be run over empirical data without any change.

DebtRank: Too Central to Fail? Financial Networks, the FED and Systemic Risk

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Systemic risk, here meant as the risk of collapse of a large portion of the financial system, depends on the network of financial exposures among institutions. However, there is no widely accepted methodology to determine the systemically important nodes in a network. Moreover, exposures are seldom disclosed. To fill this gap, we introduce, DebtRank, a novel measure of systemic impact inspired by feedback-centrality. As an application, we analyse a new and unique dataset on the USD 1.2 trillion FED emergency loans program to global financial institutions during 2008-2010. We find that a group of 22 institutions, which received most of the funds, form a strongly connected graph where each of the nodes becomes systemically important at the peak of the crisis. The system is even vulnerable to small, dispersed shocks. The results suggest that the debate on too-big-to-fail institutions should include the even more serious issue of too-central-to-fail.

Relevance of SIR Model for Real-world Spreading Phenomena: Experiments on a Large-scale P2P System

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Understanding the spread of information on complex networks is a key issue from a theoretical and applied perspective. Despite the effort in developing theoretical models for this phenomenon, gauging them with large-scale real-world data remains an important challenge due to the scarcity of open, extensive and detailed data. In this paper, we explain how traces of peer-to-peer file sharing may be used to this goal. We first describe the structure and properties of the underlying network and observed information spreading cascades. Performing simulations on this network we assess the relevance of the standard SIR model to mimic key properties of observed spreading cascades -- in particular we examine the impact of the network topology on the spreading cascade properties. Finally we turn to the evaluation of two heterogeneous versions of the SIR model, in which the spreading probability depends on the node behavior and on the information being transmitted. We conclude that all the considered models failed to reproduce key properties of such cascades: typically real spreading cascades are relatively "elongated" compared to simulated ones and also denser. We have also observed interesting similarities common to these models.

Effect of bursty communication patterns on contagion in a threshold-based epidemic dynamics

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Records of interactions between individuals provide us with new sources of data for understanding how interaction patterns affect collective dynamics. Such human activity patterns are often bursty, implying short periods of intense activity followed by long periods of silence. The bursty property has been considered to affect spreading phenomena, speeding up epidemic spreading in some cases and slowing down in other cases. In this presentation, we investigate a model of history dependent contagion. Our model assumes that repeated exposures of susceptive individuals to infected individuals in a short period of time is needed for contagion. By carrying out numerical simulations on real temporal network data, we find that bursty activity patterns facilitate epidemic spreading in our model.