

**INTRODUCTION TO THE PROCEEDINGS OF THE
INTERNATIONAL CONFERENCE ‘*ERICE MATHCOMPEPI 2015*
– INTERNATIONAL CONFERENCE ON MATHEMATICAL AND
COMPUTATIONAL EPIDEMIOLOGY OF INFECTIOUS
DISEASES: THE INTERPLAY BETWEEN MODELS AND
PUBLIC HEALTH POLICIES’, ERICE (ITALY)
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The mathematical and computational modelling of the spread of infectious diseases is a research field in applied mathematics that in the same time was both able to give an impetus to various areas of the dynamical systems theory and mathematical analysis, and to give an important contribution to the biological and epidemiological understanding of the spread of these diseases. National as well as Inter-National health authorities adopt routinely in the practice methodologies and concept that were born in the field of Mathematical and Computational Epidemiology (MCE) for assisting public Health decisions and policies. A major example is provided by the huge advancement in modelling and prediction on pandemic threats, and related preparedness plans for disease containment/mitigation. This operative influence in biomedicine is unparalleled in any other fields of mathematical and computational biology, with the possible exception of intra-host virus dynamics, whose models partly derive from those of MCE.

One of greatest challenges in modern MCE is finding ways to take into the account new complexity layers often ignored in classical MCE. For example, human behaviour and its relationship with the available information on the evolution of the epidemics, is an unsettled issue. It is fundamental to model the pseudo-rational objection to vaccinations and the response to pandemic threats.

In order to summarize the state of the art of Mathematical and Computational Epidemiology of Infectious disease we applied to a well-known institution working for the diffusion of the science, the *Ettore Majorana Institute for the diffusion of*

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scientific culture in order to organize a restricted conference in their Institute. Our proposal was accepted and so the *'Erice MathCompEpi 2015 – International conference on Mathematical and Computational Epidemiology of Infectious diseases: the interplay between models and public health policies'* was held at the 'Ettore Majorana' Institute at Erice (Italy) from August 30 to September 5 2015. Although the selection criteria of the 'Ettore Majorana Institute' are very strict, we had a large success and over 100 scientists attended our conference, which is a record for the Institute.

The aim of this international conference were twofold.

The first aim is to illustrate the major areas of research in MCE and the huge variety of tools and approaches that are currently employed, which mimic the disparate backgrounds of the scientists active in MCE. Models of various degrees of complexity are synergistically interplaying in this discipline. They are both needed and complementary, and in the Erice conference both were present.

The second and major aim, in line with the great tradition of the *International Centre 'Ettore Majorana'*, was to foster frank peer-to-peer discussions between expert outstanding researchers and more junior investigators as well as PhD students.

The papers presented here are only a partial slice of the many talks given at our conference. However, this proceedings qualitatively well mirrors the advancements that since 2015 our participants have obtained with respect to their talks in Erice. Moreover, also the thought-stimulating *peer-to-peer* mix of senior world-famous scientists with junior brilliant scientists – the real soul of all Erice conferences at the *International Centre 'Ettore Majorana'* – is equally represented here.

This special issue of Mathematical Biosciences and Engineering opens with a review paper by Capasso and Anita. This work summarizes the important contributes that their research groups have produced, starting from the largely influential pioneering works that prof Capasso published in early seventies of the past century. Some key concepts are deepened such as: the meaning and implication of the linear and non-linear force of infection; the transition from stochastic to continuous epidemic models; the role of the structure of epidemic models; the spatially distributed Men-Environment-Man (MEM) class of communicable diseases; the relevance of optimal control as public health tool. A particular emphasis is given to the concept that MEM diseases can be controlled in a given area by acting on a subset of it. In other words the control is obtained by following the principle of *Think globally act locally*[1] (one of Prof Capasso's favourite quotes !).

The infectious contamination of the environment is also at the core of the paper on Ebola Virus Disease by Berge, Bowong, Lubuma and Manyombe. In this paper the pollution is by infected animals, which is a further layer of complexity, which adds to the direct men to men contagion.

Animals and insects are vectors of many diseases. In particular one among the most important enemies of men is the mosquito, which is vector of a large number of infectious diseases such as: Malaria, Dengue, Zika fever, and so on. Thus it is important to investigate the population biology of mosquitos. This is what has been done in the paper by Okuneye, Abdelrazec and Gumel, who, in particular, investigate the impact of seasonal fluctuations of weather (temperature and rainfall) in the population dynamics of anopheles mosquitoes by using analytical tools. Realistic simulations are performed by using data for temperature and rainfall in some African cities.

Among the animal diseases that can be transmitted to humans, the hantavirus-related diseases exhibit large fatality rates. The paper by Bürger, Chowell, Gavilán, Mulet and Villada focuses on the investigation of the spatio-temporal spread of hantavirus among rodents. The authors propose gender-structured spatiotemporal models (as well as the numerical schemes to simulate them) with not only diffusion but also convection. This additional spatial component is caused by the fact that movement of males is assumed to be influenced by local or nonlocal variations of the densities of the group of females.

Gender-structured modelling of some infectious diseases is also the topic investigated in the paper by Pugliese, Gumel, Milner and Velasco-Hernandez. This work focuses on the effect of genders in asymmetric heterosexually transmitted SIS diseases epidemics, with possible further direct or vector-mediated components of transmission. The above-mentioned asymmetry lies in a marked difference of the probability of contagion between the two sexes. In particular, the authors investigate which is the impact of the asymmetry in the attack rates.

Mathematical models for quantitatively controlling the spread of communicable diseases have to be validated with real-world data. Given the nonlinearity of ME models the development of new methodologies.

The paper by Widder is based on the concept that the parameters of models in ME are not exactly known. Thus, the control engineering approaches based on the concept of set-membership can be usefully adapted in ME to estimate the state of the system. The methodology allows to infer best and worst cases scenarios as well as the conditions determining them.

In the context of disease control, surveillance data are of primary relevance. The paper by Gerberry proposes new methodologies to calibrate ME models to those data, reaching high degrees of matching. The proposed calibration tools are applied by the author to explore the correspondence of model of HIV, HSV, and of their co-presence, to the related epidemiological data.

The matching with available epidemiologic data and the forecast of the future evolution of an epidemic is at the basis of the work by Papa, Binda, Felici, Franzetti, Gandolfi, Sinisgalli and Balotta, who propose a model of HIV epidemic in Italy. The model investigated in this paper is characterized by some noteworthy features: i) the inclusion of immigration and emigration; ii) the realistic distribution of intra-host disease progression; iii) a time-varying exit rate modelling the treatment failures and/or voluntary exit from the therapy. The forecast predicted by the model stress the very positive impact of an early initiation of the anti-retroviral therapy.

Data forecast based on partial observations is also the focus of the paper by Leonenko and Ivanov, which investigate the forecast of peaks of acute respiratory infections in some important Russian cities by comparing the SEIR epidemic model with the discrete-time Baroyan-Rvachev model.

A third paper devoted to the study of a major epidemic in a specific country, namely: Tuberculosis (TB) in India, is the one by Pandey and Venturino. This work focuses on some hot topics such as the diagnosis rate in private vs public healthcare centres. The model is highly complex both in its structure and behaviour (e.g. its solution can exhibit backward bifurcations, i.e. bistability involving the disease-free state). The results of Pandey and Venturino suggest that eradication of TB in India would be very difficult if not at all impossible, a conclusion that might trigger discussion in the Public Health community.

To reach the control of disease spread in a target populations, analytical and computational tools for resource allocation are of course of primary relevance. This is the topic faced in the article by Kassa, who proposes a three-levels hierarchical decision making approach for resource allocation for HIV.

As far as control is concerned, an increasingly important phenomenon is the reduced compliance of individual to the suggested interventions. A further layer of complexity that reduce the success of intervention is the heterogeneity of the exposure to the infectious agent. The paper by Yan focuses on these important questions by using frailty models, a classical tool of mathematical statistics, and quarantine isolation as case study of Public Health (PH) intervention.

Another example of non-compliance to PH intervention is the observed reduced propensity to vaccinate children against paediatric infectious diseases, which is the ultimate case of the resurgence of such diseases worldwide, as shown by a number of outbreaks. This phenomenon is one of the pillars of the new branch of Behavioural epidemiology of infectious diseases. As shown in [2] for SIR-type infectious diseases, actions of PH system to favour vaccine propensity can greatly improve vaccination levels, and even induce eradication of the target disease. In this Special Issue the paper by Buonomo, Carbone and d'Onofrio extends [2] by focusing on the co-presence of two important factors: i) the presence of latent subjects; ii) the seasonal fluctuations of the transmission rate (TR). The authors show that the knowledge of the average TR is not enough to make inferences on the global stability of the disease-free state. Indeed, the amplitude of the oscillations paradoxically favours the eradication. The paradox is only apparent: it is a beneficial effect of the phase when the TR is under its average value, over-compensating the TR increase during periods of intense contacts.

Immunization against measles of children is the topic of the paper by Chladna. Focusing on cost-effectiveness of possible interventions in Slovakia, Chladna adopts a tool of stochastic analysis in finance, the *real options*, to assess the time of first intervention and the level of vaccination rate at which it is optimal to perform intervention. Early intervention with large vaccination rates are suggested by the model.

The papers that were accepted and above illustrated show, it is correct, a large variety of mathematical and computational tools of interest. However, which is more important, all share a common awareness: MCE must have as their main aim to help the global and local Public Health interventions.

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