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Modelling of Healthcare Associated Infections: A study on the dynamics of pathogen transmission by using an individual-based approach

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ABSTRACT

Prevention and control of Healthcare Associated Infections (HAIs) has become a high priority for most healthcare organizations. Mathematical models can provide insights into the dynamics of nosocomial infections and help to evaluate the effect of infection control measures. The model presented in this paper adopts an individual-based and stochastic approach to investigate MRSA outbreaks in a hospital ward. A computer simulation was implemented to analyze the dynamics of the system associated with the spread of the infection and to carry out studies on space and personnel management. This study suggests that a strict spatial cohorting might be ineffective, if it is not combined with personnel cohorting.

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1. Introduction

Healthcare Associated Infections (HAIs) are infections that are acquired in hospitals or as a result of healthcare interventions. HAI outbreaks can cause severe and costly disruption to services. Thus the prevention and control of HAIs has become a high priority for most healthcare organizations. In particular, hospitals worldwide are increasingly concerned by methicillin-resistant *Staphylococcus aureus* (MRSA). In many countries, recent decades have seen a rapid increase in the incidence and geographical range of MRSA infections [1–3].

Although various studies of HAIs have been carried out, the exact mechanism of pathogen transmission is still not fully understood. In the case of MRSA, the most likely mode of spread is by indirect transmission via a health-care worker acting as a 'transient carrier' and indirect acquisition by contact with a contaminated environment [3–8]. Several studies provide evidence that *S. aureus* is present in the environment or in the surrounding air and, as a result, both vehicle-borne and airborne transmission might also happen [9–12].

Outbreaks are usually contained with a package of infection control measures, which may include performing active surveillance cultures to identify colonized patients, improving hand hygiene compliance, contact-based infection control, barrier precaution policies, effective staff management, antibiotic policies, and, last but not least, education [2,13,14].

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2. HAI modelling

In the last century, a variety of mathematical models have been developed in order to improve understanding of epidemiology of infectious diseases [15–17]. However, their application to nosocomial epidemiology has been rather recent (for reviews of HAI modelling see [2,14,18,19]). After initial HAI studies based on a deterministic approach, almost all research groups have started to apply a stochastic approach to the HAI problem. In HAI modelling, a stochastic approach is desirable for the following reasons [16,20,21]: (a) the infection transmission is a discrete and random event; (b) the individuals are heterogeneous; (c) the population is small.

2.1. The state variable approach

Almost all of the HAI models, deterministic or stochastic, adopted since the 1990s can be described as *state variable* models. State variables, such as population densities, number of susceptible individuals, and number of infectious individuals, are used to represent the states of the system as a whole. Typically, the analysis of the system is carried out by using a set of ordinary differential equations (ODEs). These models are also called 'population-level' models.

The mass-action principle: One of the key assumptions in these models is the mass-action principle [22]. It states that the number of new infections per time period (transmission rate) is proportional to the number of susceptible individuals times the number of existing infectious cases.

The transmission rate tr is given by the following expression:

$$tr = \beta \times S \times I \tag{1}$$

 $\beta = \mathbf{c} \times \mathbf{t} \mathbf{p} \tag{2}$

where S is the susceptible population density, I is the infectious population density, β is the transmission coefficient, c is the contact rate (average number of contacts per individual per day), and tp is the transmission probability per contact. In general, the values for these parameters are derived directly from observational data or by using a parameterisation procedure. Typical values reported in the literature are listed in Table 1.

The limitations of the mass-action hypothesis have been highlighted in several studies [15,17,18,23,24]. First, this principle implies that the population mixes homogeneously and that each susceptible and infectious individual is accessible to all others at all times. However, in general, the hospital population shows heterogeneity—patients may be grouped based on sex, age, clinical specialty, severity of illness, given treatments; spatial and/or personnel cohorting may be applied. Second, the movement of each individual staff member within a ward or an intensive care unit cannot generally be consid-

Table 1 – Typical values for contact rate and transmission probability.

c = 1.38–7.60 [3,20,30,33] tp = 0.01–0.15 [3,20,30–34] ered as random—e.g. the health-care workers may carry out ward rounds on a regular basis and in a set pattern. Third, the transmission rate, as defined by Eq. (1), is a state variable and, as a result, it does not explicitly include the role of individual behaviour in the transmission process. As a result, the individual properties, such as the status or the actions of each agent, cannot be properly represented in this kind of modelling approach.

2.2. Exploring alternative approaches to HAI modelling. The individual-based approach

The *individual-based* approach has been proposed as an alternative way of investigating infectious disease outbreaks in hospitals and small communities [7,8,25–27]. The individualbased approach is 'bottom-up': it starts at the bottom level of the system investigated, i.e. at the individual (agent) level, and it treats the individuals as unique and discrete entities. The individuals are allowed to interact and the dynamics of the system as a whole depends on these interactions. Thus, the study and the analysis of the system is carried out from the individual level upwards, towards the population level.

Some of the recent models adopting an individual-based paradigm are based on Network Theory [8,27]. When a scalefree network is used to represent the interactions among the (susceptible and infectious) agents, several nodes, called 'hubs', have an unusually high number of connections [28]. If a simulation can show that a given 'hub' individual has an higher probability of becoming infectious, control measures, such as isolation or treatment, could be applied in a selective way and, as a result, spread can be contained or reduced significantly.

There are several potential benefits in adopting an individual-based approach for the HAI problem. An individualbased model might: (a) help to better understand the impact of the population heterogeneities and the spatial distribution of the agents (locations, movement); (b) provide a detailed description of the temporal evolution of individual interactions (proximity events, contacts), actions (agent behaviours, policies and control measures applied, treatments provided), and events (admission, discharge, readmission of the patients).

On the other hand, this kind of modelling approach presents several limitations.

Since it implies a mechanistic understanding of the dynamics of the system under analysis, in general, a detailed description is required. Detailed and reliable observational data are required for comparison and, as a result, parameterisation and validation procedures can be difficult to implement. In some cases, its complexity might even make the model difficult to implement or computationally prohibitive (parallel computing might be the only option for handling the problem).

3. Implementation of the model

The modelling approach adopted here can be described as individual-based and stochastic. In order to study and analyze the spread of HAIs (MRSA infections) a computer simulation Download English Version:

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