MATHEMATICAL MODEL OF LYME DISEASE CAUSED BY THE BACTERIUM BORRELIA BURGDORFERRI

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Keywords: Delayed differential equations, Mathematical modelling.

If the antigen is Borrelia Burgdorferri which has 150 genes, in contact with antigen it may die or it may become resistant.

So we consider the classical Marchuk model but we must introduce a new variable W

$$\begin{cases} V'(t) &= (\beta - \gamma F(t))V(t) + \int_{-\infty}^{0} \rho(s)W(t+s)ds \\ W'(t) &= \beta_2(m(t))W(t) + \zeta V(t)F(t) - \int_{-\infty}^{0} \rho(s)W(t+s)ds \\ C'(t) &= \alpha\xi(m(t))(V(t-\tau) + W(t-\tau))F(t-\tau) \\ & \quad -\mu_C(C - C^*) \\ F'(t) &= \rho C(t) - (\mu_F + \eta\gamma V(t))F(t) \\ m'(t) &= \sigma(V(t) + W(t)) - \mu_m m(t) \end{cases} . \tag{1}$$

In (1) variable W denotes the level of immunized antigen, V is now the level of antigen that does not meet antibody yet.

In the Marchuk's model γ factor means the probability of meeting the antigen with the antibody. In the presented model, gamma is the probability of contact between the antigen and antibody. This contact is leading to elimination of antibody, and ρ probability of such contact will lead to its immunization

It should be mentioned that the integrals in the equation are only seemingly improper because the function ρ has the bounded support

Parallel Session

Epidemiology V

SHOULD I GET A FLU SHOT? HOW WELL DID THIS GO LAST YEAR?

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Keywords: Vaccination game, Imitation, Influenza.

The problem of how to induce people to make vaccination decisions that would be optimal from the point of view of the population has been widely studied over the last decade. When vaccination carries real or perceived costs, individual rational choices in the so-called vaccination game are known to lead to Nash equilibria that are suboptimal at the population level. In reality, the underlying assumption of perfect rationality is unrealistic; actual decision-making is more likely based on a mixture of rational calculations of (mis)perceived costs, imitation, and individual prior experience. We study models that incorporate some of these decision-making procedures, in particular, imitation. We were able to show that imitation can lead to near-optimal vaccination coverage if it is done sufficiently rarely. These findings contrast with results that were previously reported in the literature which show that frequent imitation leads to even lower vaccination coverage than Nash equilibria.

Parallel Session

Epidemiology V

VILLAGE-SCALE PERSISTENCE AND ELIMINATION OF HAT (*GAMBIENSE* HUMAN AFRICAN TRYPANOSOMIASIS)

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Keywords: HAT, Trypanosomiasis, Elimination.

Gambiense human African trypanosomiasis (HAT, sleeping sickness) is one of several neglected tropical diseases targeted for elimination as a public-health problem by the World Health Organization by 2020, and furthermore, HAT now has a complete elimination goal of 2030. Recent years have seen a substantial decline in the number of globally reported cases, largely driven by an intensive process of screening and treatment. However, this infection is highly focal, continuing to persist in small regions. Regional elimination, and ultimately eradication, rests on understanding the dynamics and persistence of this infection at the local population scale.

We develop a stochastic model of HAT dynamics, which is underpinned by screening and reporting data from one of the highest incidence regions, Kwilu Province, in the Democratic Republic of Congo. We use this model to explore the persistence of HAT across villages of different population sizes and subject to different patterns of active screening, and show how this low prevalence infection can still persist for long periods of time in relatively small populations. We highlight the impact of active screening, the risk of recrudescence following local elimination and consider how detecting zero cases with active screening informs on the probability of elimination. These quantitative results provide insights for public health policy in the region, particularly highlighting the difficulties in achieving and measuring the 2030 elimination goal.

Parallel Session

Epidemiology V

AN IMPULSIVE MODEL FOR DENGUE TRANSMISSION DYNAMICS WITH SEASONAL EFFECTS AND PESTICIDE CONTROL

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Keywords: Epidemic modeling, Mosquito-borne disease, Impulsive control.

In this talk we will introduce an SIR epidemiological model describing the vector-to-host and host-to-vector transmission dynamics of Dengue [1]. The proposed model includes vector control in terms of pesticide applications, mathematically described as impulsive perturbations in the system, thereby accounting for reductions of the vector population in very short time intervals. In addition, seasonality is incorporated into the model via a sinusoidal forcing mimicking periodic regimes of the intensity of vector-to-host and host-to-vector infections, as well as vector growth. A detailed numerical analysis of the model is carried out via path-following techniques for non-smooth systems, implemented via the software COCO [2]. The numerical study also considers the optimization of the times at which pesticide is applied.

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Parallel Session

Epidemiology V

DYNAMIC MODELLING OF HEPATITIS C TRANSMISSION AMONG IDUS: REVEALING THE UNDIAGNOSED AND IMPACT OF INTERVENTIONS

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Keywords: Dynamic modelling, Hepatitis C, Treatment, Surveillance data, Shiny app.

To reach the WHO goal of hepatitis C elimination by 2030, it is essential to identify the number of undiagnosed cases and to investigate the impact of interventions such as drug treatment and needle exchange programs on the disease transmission dynamics. In most developed countries, the primary route of hepatitis C transmission is via contaminated needles shared by injecting drug users (IDUs). However, high uncertainty regarding the size of the IDU population and difficulty detecting hepatitis C in the early stages of the disease make it challenging to estimate the number of undiagnosed cases. We present a novel, multi-layered dynamic transmission model for hepatitis C transmission within an IDU community that accounts for disease stage (acute and chronic), IDU status (current and former IDU), status of diagnosis (diagnosed and undiagnosed) and country of disease acquisition (within or outside the country under consideration). First, based on this model and using routine surveillance data, we estimate the number of undiagnosed IDUs, the basic reproduction number, the time until diagnosis and associated uncertainties. Second, we examine the impact of two interventions on disease dynamics: 1) direct-acting antiviral drug treatment, which is characterized by high success rates but substantial costs, and 2) needle exchange programs. We illustrate our approach for Swedish data, however, our modelling approach can also be applied to other countries with a similar disease burden. To support communication of our results with public health decision makers, the model and its outputs are made accessible through a shiny app.

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Parallel Session

Epidemiology V

MODELING THE IMPLEMENTATION OF DENGUE VACCINE

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Keywords: Epidemic models, Dengue Fever, Vaccination, Chaos and parameter estimation, Prediction and predictability.

Developed by Sanofi Pasteur, a tetravalent dengue vaccine, Dengvaxia, was recently recommended by the World Health Organization (WHO) Strategic Advisory Group of Experts (SAGE) on Immunization, based partially on modeling results, to be used in countries with high dengue endemicity as evidenced by seroprevalence in the targeted age group of more than 50% (preferably 70%) [1].

Analyses of clinical trial data demonstrate that individuals who were seronegative (never infected with a dengue virus prior to vaccination) when vaccinated routinely develop non-protective dengue antibodies [2, 3]. Surprisingly, despite high rates of overt disease among vaccinated seronegative persons, mathematical models of populations with a seroprevalence of 70% have estimated an overall reduction of dengue hospitalizations on the order of $10-30\%$ over a period of 30 years, with 80% vaccine coverage of 9 year-olds [1, 4]. It should be noted that accurate predictions in complex systems such as described in [4] can be only made for short periods of time. A 20-30-year prediction horizon puts in doubt the beneficial results of vaccine administration [5].

In this talk I will present an age structured model that was developed based on the WHO-SAGE recommendation to vaccinate persons age 9-45 years in dengue endemic countries. The model was used to explore the clinical burden of two vaccination strategies: 1) Vaccinate individuals, ages 9-45 years, seropositives and seronegatives, and 2) vaccinate individuals, ages 9-5 years, who are dengue immune only [6]. A sensitivity analysis of the proposed model will be discussed.

Our mathematical model finds that significant reduction of hospitalizations can be only achieved when vaccine is directed exclusively to seropositive individuals [6]. When using a more recent data set by age and serostatus from the combined CYD14, CYD15, CYD57 trials, as reported in Table 1 in Martinez-Vega et al. [7], we confirm statistically the vaccine induced risk in seronegative individuals [8],[9].

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