

Parallel Session  
Epidemiology III

## EVOLUTIONARY VACCINATION DYNAMICS

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*Keywords:* Vaccination, SIRI model.

In this work, we consider a vaccination game where people have to choose between to vaccinate or not to vaccinate, depending on the morbidity risks from the vaccine and the morbidity risks from the infection. We introduce the evolutionary vaccination dynamics for the reinfection SIRI model and we prove that it is bistable. The bistability of the evolutionary dynamics indicates that the damage provoked by false vaccination scares can be much higher and much more persistent than in the SIR model [1].

## References

- [1] J. Martins, A. Pinto. (2017). *Bistability of Evolutionary Stable Vaccination Strategies in the Reinfection SIRI Model*. *Bulletin of Mathematical Biology*, 79, 853–883.

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### **LEARNING STRATEGIES IN A RUMOR SPREADING MODEL BASED ON THE SIR EPIDEMIC MODEL**

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*Keywords:* SIR model, Rumors.

Based on the classical epidemiological SIR model, we propose a similar model to analyze the spreading of a false rumor in a homogeneous mixing population. Regarding the rumor, individuals can be ignorants, believers or unbelievers. Assuming that the rumor is false, we will study its spreading depending on the level of the real information attained by the individuals. Since the search for information can have costs but can also be very advantageous to an individual, we will introduce the expected learning payoff and we will compute the Nash and the evolutionary stable information search strategies.

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## RATIONAL BEHAVIOR AND SOCIAL COST FOR VACCINATION IN CHILDHOOD DISEASES

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*Keywords:* Rational behavior, Age-structured population.

The aim of our work is to understand what happens when a typical child disease that has almost none complications for children but significant complications for adults is prevented with vaccination at birth. It is expected that the vaccination decreases the rate of infection, and, as side effect, increase the age at infection. This last effect is enhanced if the vaccine loses efficacy over time.

For levels of vaccination below the herd-immunity threshold, as the disease has more complications for adults, the total cost of disease treatment for the society may be bigger of that it would have with no vaccination. We show that, from the point of view of the society, there is a threshold for the level of vaccination, and that below this threshold the cost for society is bigger with vaccination than without. Moreover, individuals may or not vaccinate their children according to their perceptions of expected cost, originating another threshold for the level of vaccination, now from the individual point of view, below which individuals don't vaccinate.

We consider an age-structured population divided in two groups: juveniles and adults. Each individual is vaccinated at birth with a certain probability  $p$ . Also, the vaccine is imperfect, because it only confers life-long immunity with probability  $\lambda$ , while with probability  $1 - \lambda$  the immunity lasts only during the juvenile phase. We define the social cost and the individual joint costs of disease and vaccination.

Our aim is to describe the sets of parameters  $\{p, \lambda\}$  where is better or worst to vaccinate, both from the point of view of the society or individuals and how these sets overlap. From here we study the Nash equilibria that occur and describe possible actions to attain such an equilibrium that benefits both the society and individuals.

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**EPIDEMICS ON NETWORKS WITH SOCIAL DISTANCING**

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*Keywords:* Networks, Infectious disease dynamics, Behaviour change, Preventive social distancing, Individual vs. population.

In the presence of an epidemic in a population, individuals may decide to take preventive measures to avoid infection. This could lead to changes in the contact pattern in the population over the course of an epidemic. In this talk we look at social distancing as one such preventive measure. We consider an epidemic on a social network whose structure changes as the epidemic evolves. Susceptible individuals may distance themselves from infectious neighbours to avoid infection. They may choose to drop the connection completely and thereby reduce their number of neighbours. Alternatively, they may replace the social connection with another individual in the population in their desire to maintain their number of social contacts. From an *individual-level* perspective, social distancing cannot increase one's risk to become infected. However, social distancing can have negative consequences for *population-level* epidemic outcome.

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## HOUSEHOLD MODELS FOR ENDEMIC DISEASES

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*Keywords:* Epidemiology, Childhood diseases, Population dynamics, Household models.

Many developing countries are undergoing demographic transition, with birth rates decreasing and life expectancy increasing, changing the age profile and household structure of these countries. Both age structure and household structure are known to profoundly influence infection dynamics and the actions of disease control measures, meaning that changes to these demographic characteristics are likely to significantly impact the burden of disease. Our work extends household models for epidemics to an endemic setting by including natural demographic processes to generate a mathematical model which can address the problems associated with demographic transition.

Our framework combines a demographic model describing the evolution of a household structure in terms of children being born, aging, and leaving home as adults, and an epidemic model describing the transmission of a disease. The disease follows Markovian SIR dynamics within the household, and the age profile of the children within the household is inferred from the demographic state in order to model age-structured interactions between distinct households with contact intensities which could be chosen from population data sources such as POLYMOD. Our model includes vaccination at birth with the potential for vaccination behaviour to be correlated between households, allowing us to model household-based vaccination strategies or anti-vaccine sentiment.

We calculate the endemic equilibrium of the system and early growth indicators such as  $R_0$  as functions of the model parameters and demonstrate that incorporating age structure increases the population-level burden of disease and concentrates this burden in households with younger children. Population data and epidemiological data is incorporated in order to make comparisons between our results for different countries and diseases. We use the model to compare the efficacy of a clustered vaccination strategy in which vaccine is given to all children within a certain proportion of households to that of an unclustered strategy in which vaccine is given to a fixed proportion of children in every household. We find that the unclustered strategy reduces growth rate, household-level reproductive number, and disease burden more effectively than the clustered strategy, with less vaccine needed for eradication of the disease.

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## OPTIMAL CONTROL OF A SIQRB CHOLERA DELAYED MODEL

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*Keywords:* Cholera, Stability of disease-free and endemic equilibria, Optimal control.

Cholera is a bacterial disease provoked by the bacterium *Vibrio cholerae*, which lives in an aquatic organism. Cholera outbreaks can be caused by ingestion of contaminated water and through the contact with infected individuals. If an infectious individual does not have treatment becomes dehydrated, suffering of acidosis and circulatory collapse. This situation can lead to death, within 12–24h. Cholera continues to kill a significant number of people and mathematical modelling gives useful information how its development can be stopped. We revisit the SIQRB model studied in [1] by adding a delay that translates the time between the instant in which an individual becomes infected and the instant in which he can transmit the virus. We analyse the stability of the disease-free and endemic equilibria in function of the delay. An optimal control problem is investigated to obtain a successful treatment through quarantine. A numerical simulation of a cholera outbreak in Haiti is carried out, illustrating the usefulness of the proposed model.

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## References

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