



# Summer Solstice 2018 Conference on Discrete Models of Complex Systems

Gdańsk, June 25-27, 2018

## Healthcare system network model for simulations of inter-hospital multidrug-resistant pathogen spread

Konrad Sakowski, *Institute of High Pressure Physics, PAS*

Monika Piotrowska, *Institute of Applied Mathematics and Mechanics, University of Warsaw*

Widespread use of medicines and antibiotics in modern treatment leads to development of resistance of pathogens to some drugs due to natural selection. Such effect is particularly noticeable in the hospital environment. Spread of the multidrug-resistant Enterobacteriaceae (MDR-E) became an important problem for European healthcare systems. The standard approach to this problem is to focus on preventing of transmission of MDR-E locally, on the single facility level. However, there is growing evidence that the inter-hospital patient transfers may be the an important factor contributing to the MDR-E spread within healthcare systems. In this study, we present a network model of patient traffic in healthcare systems, which can be a basis of systematic study of transmission dynamics of MDR-E and the effectiveness of infection control strategies to prevent their spread through these systems. This model takes into account direct transfers between healthcare facilities as well as indirect transfers, where the patients stay at home for some time between discharge and readmission. To model the pathogen spread within single facilities, we use standard SIS differential model. We show results of simulations preformed with the proposed model and we show what is the impact of various model parameters on the MDR-E transmission dynamics. An important problem in this study is how to build a network corresponding to a realistic healthcare system having access only to limited (privacy reasons) patient hospitalization records. We would like to present the problems and limitations of recovering of patient transfer network from such records. Examples of derived networks will be presented and discussed.

Acknowledgements: This work was supported by grant no. 2016/22/Z/ST1/00690 of National Science Centre, Poland within the transnational research programme JPI-EC-AMR (Joint Programming Initiative on Antimicrobial Resistance).