11. A spatial model to simulate mosquito-borne disease transmission in the Netherlands

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Mosquito-borne diseases are prevalent across the world, with tropical regions experiencing the highest burden for human health. The Netherlands has recently seen the emergence of Usutu virus in 2016 and the first human West Nile virus cases in 2020. These two viruses are transmitted between birds and mosquitoes, and can occasionally infect humans and other mammals which could lead to severe disease in a small proportion of cases. Despite vector-borne diseases not forming a major threat for public health in the Netherlands at the moment, this situation is likely to change in the future under the influence of ecological changes, urbanisation, international travel, and changes in water management. It is this combination of factors that together determine the emergence and spread of these pathogens, making it difficult to assess the risks posed by new pathogens and the best strategies for preparedness and response. To overcome this challenge, we developed a spatial metapopulation model that stochastically simulates mosquito-borne disease transmission in the Netherlands, by building on the SimInf framework. This model can combine information on host abundance, mosquito abundance, animal dispersal, animal migration, birth rates, death rates, and virus transmission. It can be extended to include multiple host and vector species, and/or age groups. We also aim to add temperature effects into the model, by making parameters (e.g. virus replication in mosquitos) dependent on temperature. This model can be applied to different mosquito-borne pathogens and settings, by adapting the relevant input data and/or parameters. We will apply it to Usutu virus in the first instance by incorporating data on blackbirds and *Culex pipiens* mosquitoes and fitting it to surveillance data from 2016-2020. Surveillance data consists of PCR and serology testing in live wild birds, counts of dead birds and PCR results in a subset of those, all with a recorded date and location. These various data sources are integrated and used for model fitting using approximate Bayesian computation. This will result in a reconstruction of Usutu virus spread over the past few years. Subsequently, we will use the model to study the potential emergence and spread of other mosquito-borne pathogens, compare surveillance and control strategies by simulating their implementation, and study the effect of possible change scenarios while explicitly taking uncertainty into account.

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