The SILAS-Model: Sexual Infections as Large-Scale Agent-based Simulation

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Introduction

The spread of infectious diseases not only depends on the course of the disease, but also on the population structure and on behavioural aspects relating on the heterogeneity of patients or patient groups. Therefore, effects caused by certain individuals may not be covered by the models mostly used in epidemiology or public health, as only expected values of a population are incorporated in those models (i.e. Markov, dynamic transmission). A famous example to demonstrate the influence of the non-average behavior of a single individual is the spread of HIV in the US via a flight attendant in the 1980's. (**?**, see) Modeling the spread of HIV using only expected values regarding mobility and number of sex-partners would have failed to include this kind of behavior and therefore the spread of the disease would have been underestimated. Agent-based modeling (ABM) can incorporate the heterogeneity of individuals and the variety of their behaviors.

This paper presents first results from the *Sexual Infections as Large-Scale Agent-based Simulation* (SILAS)-model, on the spread of Syphilis in Germany. As additional feature to existing literature on ABM in STDs, which reports results for the subgroup of men who have sex with men (MSM)(**?**,), the agent population in SILAS is representative for the whole German population.

Simulating the spread of syphilis

The SILAS-model is implemented in the FLAME-framework (**?**,). Each agent has a set of 21 memory variables (e.g. age, sex, sexual orientation and relationship status) with its individual value sets. Following the X-machine framework (**?**,), within each model iteration (one day) agents update their memory variables, determine if they want to show a certain behavior (e.g. break-up their relationship), communicate with other agents via the FLAME-messageboard (e.g. inform their partner about the break-up) and update their memory variables according to the information received over the messageboard.

The agent behavior is modeled stochastically and is estimated based on data of the German federal statistics office, the Robert Koch-Institute (**?**,) the PAIRFAM panel dataset (**?**, ; **?**,) and published literature. Several generalized additive and linear models have been estimated using the panel-dataset under the assumption of a zero-one-inflated beta distribution (**?**,) for probabilities and Weibull-distributions for durations of relationships. A multinomial logit-model was estimated for the parameters of contraception use of the agents. Contraception options include no contraception, condoms, birth control pill or both of the latter. All parameters (e.g. mean and variance) of the according distributions are estimated using the GAMLSS- (**?**,) or mlogit-package (**?**,) for R (**?**,) and define the stochastic behavior rules of the agents. Hence, the agents behavior is sampled from an individual probability distribution dependent on the individual value set of an agent.

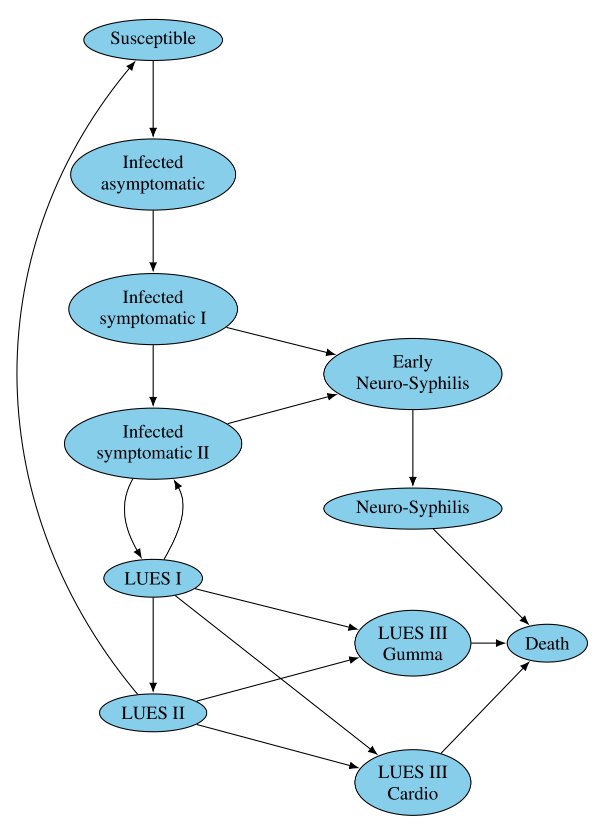

Figure 1: Course of the disease of syphilis within the SILAS model. Each node represents a Markov-state arrows denote direction agents can move between the states.

Agents of the starting population have an age-, sex- and sexual orientation-specific probabilities of syphilis infection. The course of the disease itself is modeled as a Markov-model within each agent as depicted in figure 1. Once the simulation started, the spread of the disease is only governed by the behavior rules and interactions of the agents. Depending on the health state of the agent, different probabilities of transmission by unprotected sexual contact between agents and age- and sex-specific diagnosis and treatment rates are applied from reported data. (**?**,) Furthermore, congenital transmission at birth is modeled explicitly.

As the FLAME-framework produces XML-files for each model iteration, the resulting panel-dataset can be used for the analysis and visualization (see figure 2) of the disease spread in the agent society. Additionally, each infected agent memorizes the ID of the infecting agent. This allows to draw infection paths between the agents, to identify super-spreaders of the disease (and their particular characteristics) and to analyze bridging of the disease from MSM to the heterosexual population via bisexual individuals or between other parts of the population.

`/home/stefan/SyphNetwork.pdf`

Figure 2: Infection path between agents from the SILAS-model

Concluding Remarks

The SILAS-model shows that the spread of infectious diseases can be modeled bottom-up using ABM. One of the advantages of this method is the incorporation of a wide range of agent characteristics and related behavior patterns. Therefore tailored public health or medical interventions can be built upon the detailed results of the model. As one of the disadvantages of ABM is claimed to be relying on assumptions (**?**,), we want to emphasize that given sufficient data supply, many assumptions could be avoided in the SILAS model. It is rather possible to overcome many of the simplifications and assumptions, e.g. the use of expected (mean) values, or technical boundaries of other modeling techniques. For example, to re-build the SILAS-model as dynamic transmission model would require at least 48.000 compartments to cover the main agent characteristics which additionally need to be solved on a daily basis.

Nevertheless, it should be stated that the agent-behavior does not rely on theoretical, economic or sociological models or utility-functions. However, the current state of the SILAS-model would allow for their integration, and furthermore, it can easily be supplemented by a spatial distribution of the agents, the simultaneous simulation of several STDs or the extension of social networks from families and partnerships to more complex networks like friends and work. Hereby, the use of parallelization allows for large-scale agent populations. Also the adaption of the model to populations of other countries is possible.

Acknowledgements

This paper uses data from the German Family Panel pairfam, coordinated by Josef Brüderl, Karsten Hank, Johannes Huinink, Bernhard Nauck, Franz Neyer, and Sabine Walper. pairfam is funded as long-term project by the German Research Foundation (DFG)

References