Lessons from a Systematic Review (2006-2015) on Individual-Based Models for Infectious Disease Transmission

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Introduction

The (re)emergence of pathogens (e.g., pandemic influenza, bioterrorism) and final stages of elimination (e.g., polio, measles) are driven by stochastic events and heterogeneity. Mathematical models at the individual-level are suited to capture this stochasticity and heterogeneity, and can be valuable tools to grasp transmission dynamics and inform policy makers.
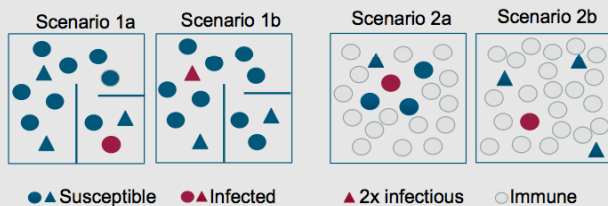

Figure 1: Possible initial conditions for (re)emerging diseases (left) and final stages of elimination (right) with one index case, which will most likely lead to different outcomes, to illustrate the potential effect of heterogeneity.

Methods

We systematically identified original research papers published between 2006 and 2015 using an IBM with a focus on infectious disease transmission in humans. We use individual-based model (IBM) as the overarching term for models at the individual-level.

Individual-based model "Computer simulation for the creation, disappearance and movement of a finite collection of interacting individuals or agents with unique attributes regarding spatial location, physiological traits and/or social behavior".

We searched Web of Science and PubMed using keywords listed in Table 1. The first selection was made on title/abstract/keywords screening, and fulltext if necessary. Secondly, we extracted detailed modeling features from papers on established vaccine-preventable childhood diseases based on full-text screening.

Table 1: Search query keywords by category, which are combined with "AND".

Category	Keywords (hyphens are ignored by the search engines)
model	model* OR simulat*
infectious disease	disease OR infect* OR transmi* OR epidem*
individual-based model	agent-based OR individual-based OR individual-level OR multi-agent OR actor-based OR micro-simulation OR microsimulation OR cel* automata OR (stochastic AND individual*)

Results

We observed a variety of descriptions for models simulating transmission events between humans at the individual-level. Figure 3 summarizes the query terms in all unique hits and for the selected subset of IBMs for infectious disease transmission.
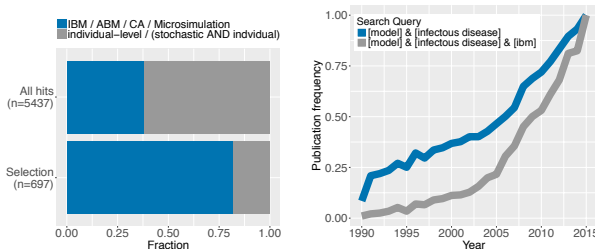

Figure 2: Presence of "individual-based model" terms in all unique hits or in the selected subset of after screening (left). Relative publication frequency over time (reference = 2015), based on the search query with and without the "individual-based model" category (right).
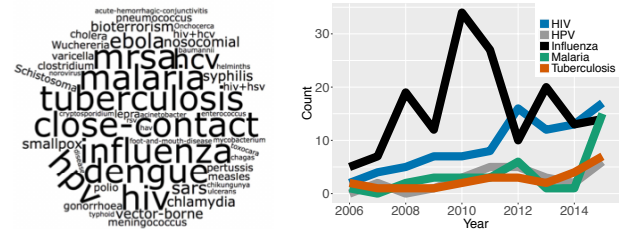

Figure 3: Disease topics with the font size corresponding to the number of publications (left) and the number of studies over time (right).

Table 2: Model details.

Topic	Details
purpose	between- and within-host dynamics, targeted vaccination campaigns, adaptive behavior, serotype carriage and replacement
lowest level	a "person" with a health state
other state variables	age, gender, spatial location, social mixing behavior, compliance, cellular immunity, etc.
population size	ranged from 38 infants in a hospital setting up to 48 million inhabitants of England and Wales
population dynamics	static (i.e. constant) or dynamic with aging, mortality, newborns, new households, etc.
time horizon	from 60 days up to 320 years, with steps of 30 min up to 1 month
realizations	3x - 1000x - unknown
model names	STDSIM, EPISIMS, EMOD, ONCHOSIM, HPV-ADVISE, FRED, Openmalaria platform, FluTE, etc.
other	the amount of missing information on technical details is noteworthy

Table 3: Observed modeling platforms.

Platform	Advantages	Limitations
IBM software e.g., Netlogo, Gama, AnyLogic	person-level functions graphical interface	specific skillset scaling & performance
Mathematical software e.g., Matlab, Mathematica, R	generic skillset post processing	not object-oriented
C++	scaling & performance	programming effort

Summary

Observed reasons for choosing an IBM:

- To model **heterogeneous between-host interactions** regarding social mixing behavior, age, demography, clustering, compliance to mitigation strategies and spatial distribution.
- To model **heterogeneous within-host processes** in combination with between-host interactions .
- To obtain **stochastic individual-level information** on the disease burden to inform economic analyses or other post-processing.

We advocate the exchange of (preferably open-source) platforms and stress the need for consistent "branding". The application of (existing) conventions and reporting protocols would stimulate cross-fertilization between research groups and fields, and ultimately policy making in decades to come.

Acknowledgments

References

Willem, L., Verelst, F., Bilcke, J., Hens, N., & Beutels, P. (2017). Lessons from a decade of individual-based models for infectious disease transmission: a systematic review (2006-2015). BMC Infectious Diseases, 17(1), 612.

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