Data-driven agent-based modeling for infectious diseases

Development of a high performance application to analyze and predict the spread of infectious diseases with applications to SARS-CoV-2.

sascha.korf@dlr.de

Sascha Korf*, David Kerkmann†, Martin Kühn*, Achim Basermann*, Alexander Mitsos§, Andreas Schuppert‡

* High Performance Computing, German Aerospace Center, 51147 Cologne, Germany † Systems Immunology, Helmholtz Centre for Infection Research, 38124 Braunschweig, Germany ‡ Institute for Computational Biomedicine, RWTH Aachen University, 52056 Aachen, Germany § AVT-Aachener Verfahrenstechnik, RWTH Aachen University, 52056 Aachen, Germany

Background

- Pathogens are a pending threat for the human population.[1]
- Interventions can mitigate the impact of a pandemic.[2]
- Mathematical models can inform decision makers.[3]
- A large amount of data is required to calibrate the models.

Methods

- Analysis of pathogen, mobility and intervention data sets.
- Combination of expertise from immunology, epidemiology and scientific computing.
- Efficient use of resources and parallel computing.

Develop a data-driven HPC epidemic simulation model.[4]

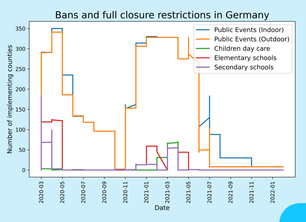
Schematic overview of the agent-based model with important Data Sources

Mobility data

- Daily routines of individual agents, e.g., about one million trips in the region of Braunschweig

INTERVENTION DATA

- Reported interventions for the 400 German counties
- Correlation-based clustering
- Assessment of the impact of intervention clusters



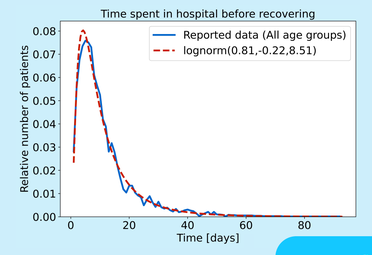
corona daten plattform

Geographic data

- Extraction of facilities such as workplaces from OpenStreetMap
- Deduction of capacities
- Use of demographic data such as households from Zensus

Pathogen-related data

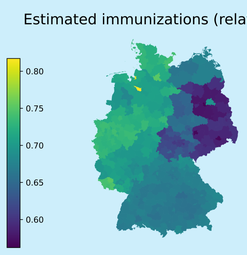
- Gather individual infection data
- Fit data to distributions
- Derive individual course of the disease



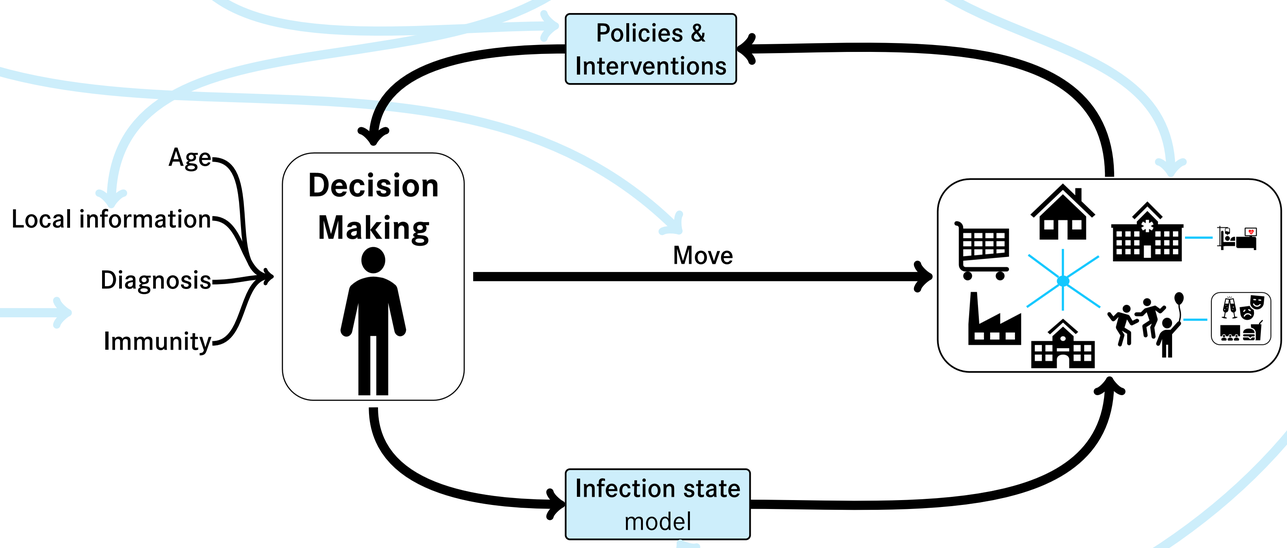
LEOSS

Public Health DATA

- Number of daily infection cases
- Number of vaccinations and immunity levels
- Hospital and ICU occupancy



ROBERT KOCH INSTITUT



First results

- Simple interventions can be simulated and compared by a prototypic model.
- The effect of different vaccination levels can be visualized.
- A general test-and-isolate strategy was implemented.
- An enhanced model for the transition of the infection state was implemented.

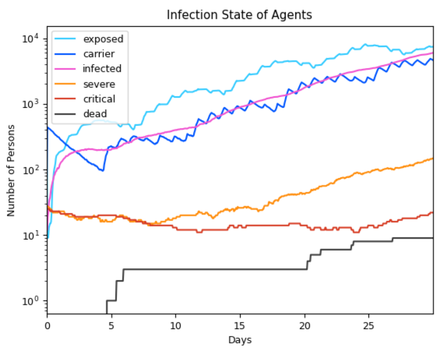


Figure: One run of the ABM showing the amount of people in several infection states.

Github Code Repository: MEmilio

REFERENCES

1. Daszak, P. *et al.* *Workshop Report on Biodiversity and Pandemics of the Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES).* en. Tech. rep. (Oct. 2020).
2. Walker, P. *et al.* *Report 12: The global impact of COVID-19 and strategies for mitigation and suppression.* Tech. rep. (Imperial College London, Mar. 2020).
3. Berndt, J. O. *et al.* *Szenarien für den Verlauf der SARS-CoV-2-Pandemie im Winter 2022/23 - Ergebnisse eines Workshops des Modellierungsnetzes für schwere Infektionskrankheiten (Modellierungsnetz).* de. Tech. rep. Version Number: 1.0 (Zenodo, Sept. 2022).
4. Kühn, M. J. *et al.* *MEmilio - a high performance Modular EpideMIcs simuLatIOn software.* 2022.