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LOKI
Pandemics



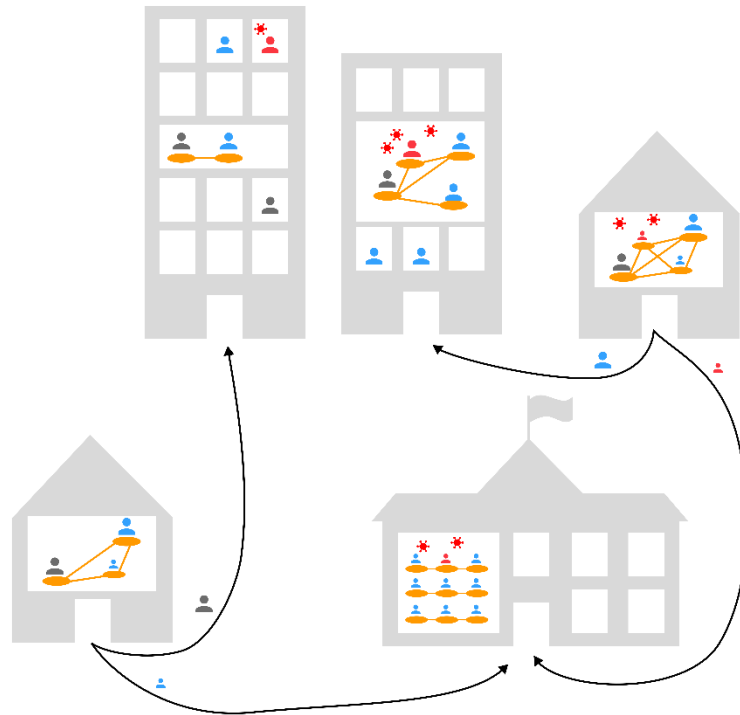
HYBRID EPIDEMIOLOGICAL MODELS FOR EFFICIENT INSIGHT ON THE INDIVIDUAL SCALE:

A CONTRIBUTION TO GREEN COMPUTING

2ND NATIONAL CONFERENCE ON INFECTIOUS DISEASE MODELING, 13 – 15 MARCH 2024

MARTIN J. KÜHN, GERMAN AEROSPACE CENTER & UNIVERSITY OF BONN
JOINT WORK WITH JULIA BICKER AND RENÉ SCHMIEDING

Why and why not agent-based modeling ?



Advantages

- Infectious disease transmission happens on individual scale
- Natural implementation of human contact behavior
- Allows explicit answers to, e.g., household transmission
- Includes stochastic effects

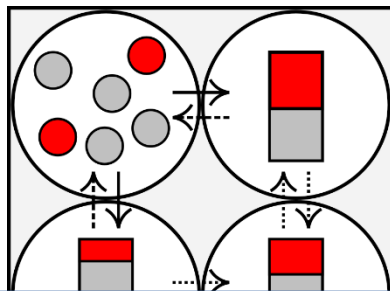
Disadvantages

- Stochasticity poses additional difficulties
- High computational complexity

How to define *hybrid* modeling ?

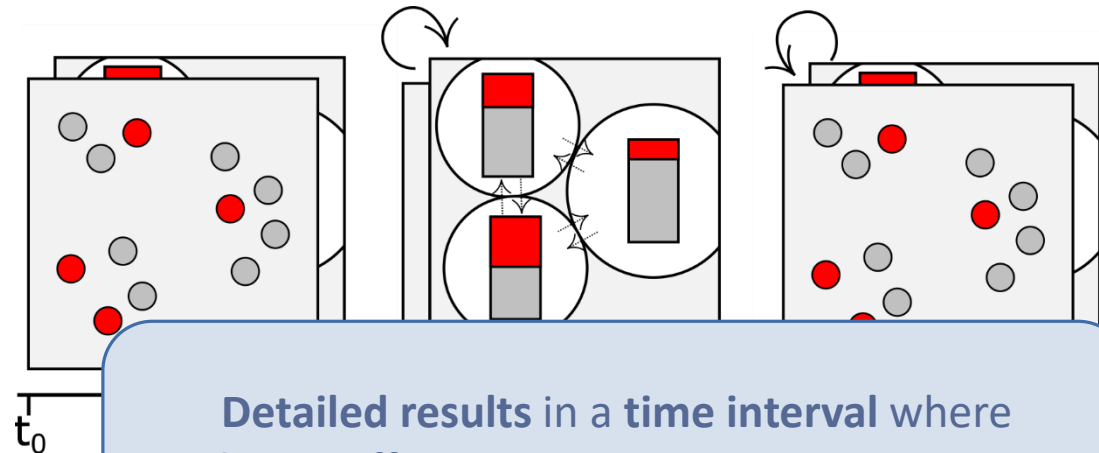
- Take the best out of the two „worlds“ of equation- and agent-based modeling
- Include complexity where necessary
- Reduce complexity where possible

Spatial hybridization



Detailed results in a **focus region** while considering the influence of **neighboring regions** in a **runtime efficient** manner.

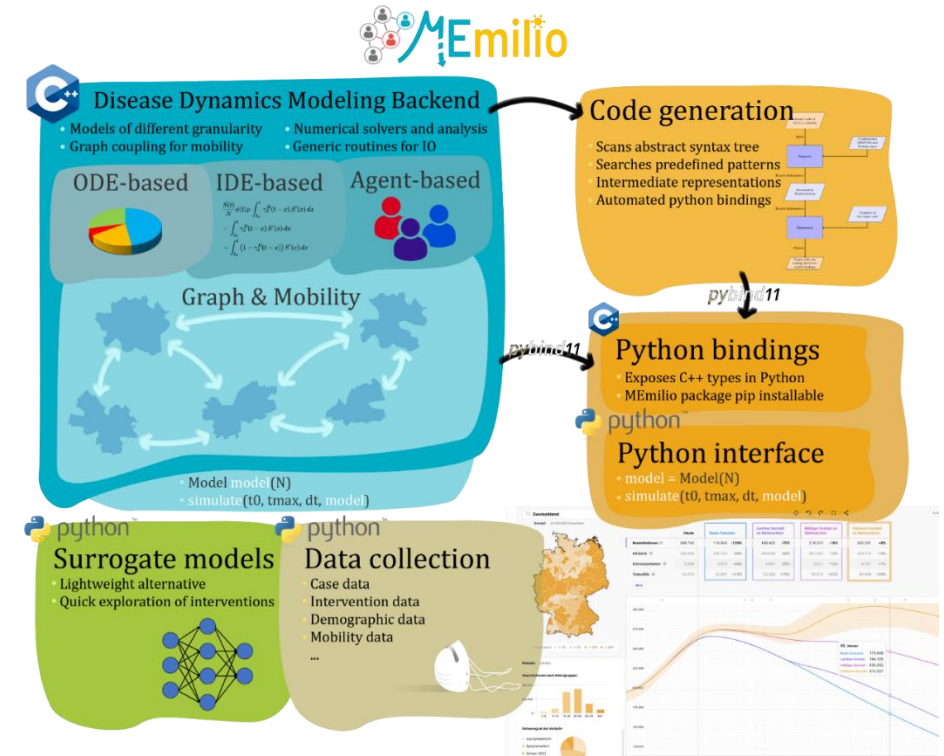
Temporal hybridization



Detailed results in a **time interval** where **stochastic effects** are **important**, **approximations** when **infection numbers** are **high**.

How to realize hybrid modeling ?

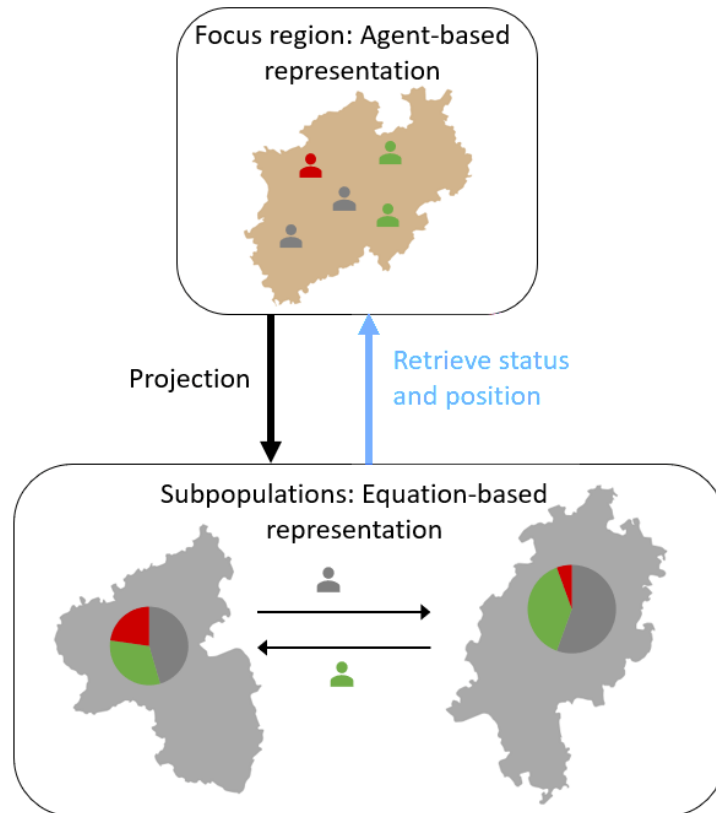
- Modular software design as much as *possible*
 - Flexible model structures for demography and spatial resolution
 - Flexible mobility patterns
 - Joint structures for parameters
 - Joint structures for IO and visualization
- High-performance computing for agent-based model



Funded by



A spatial-hybrid model and exchange of *individuals*



- Agents can be projected to equation-based models (EBMs)
- Exchange between EBMs can be realized by multiple approaches
 - Direct modeling inside singular/unified EBM (J Liu et al., Transportation Research Part A (2022))
 - Stochastic jump processes outside multiple EBMs (S Winkelmann et al., Mathematical Biosciences (2021))
 - Commuter exchange outside multiple EBMs with approximative backtracing (MJ Kühn et al., Mathematical Biosciences (2021))
 - ...
- Exchange from EBM to ABM open research question
 - model-dependent problem
 - here, sampled uniform in region
 - how much information to retain ?

A spatial-hybrid model for Munich and its neighboring counties

Full scale ABM

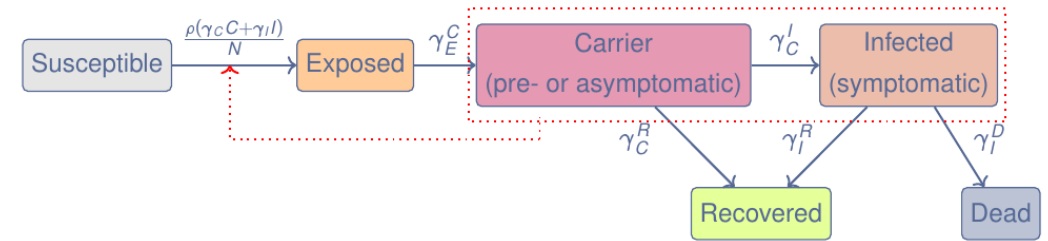


versus

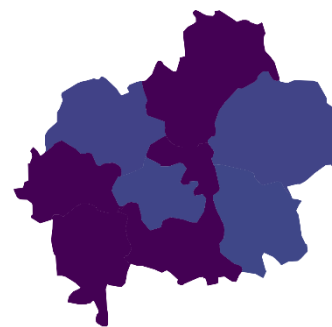


Spatial-hybrid ABM-EBM

Transmission model



Results of the hybrid model (map view)



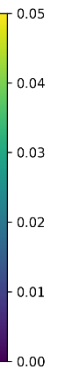
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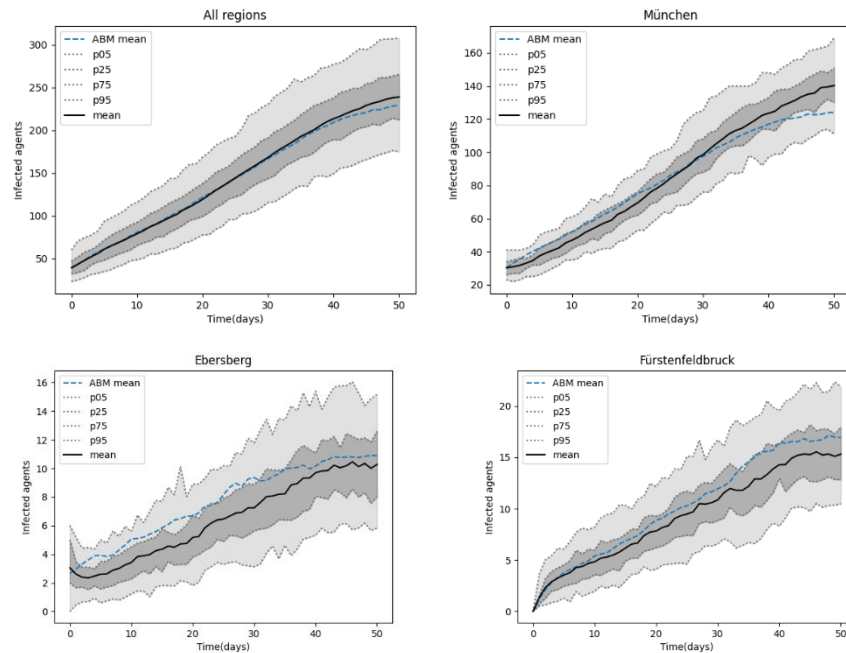


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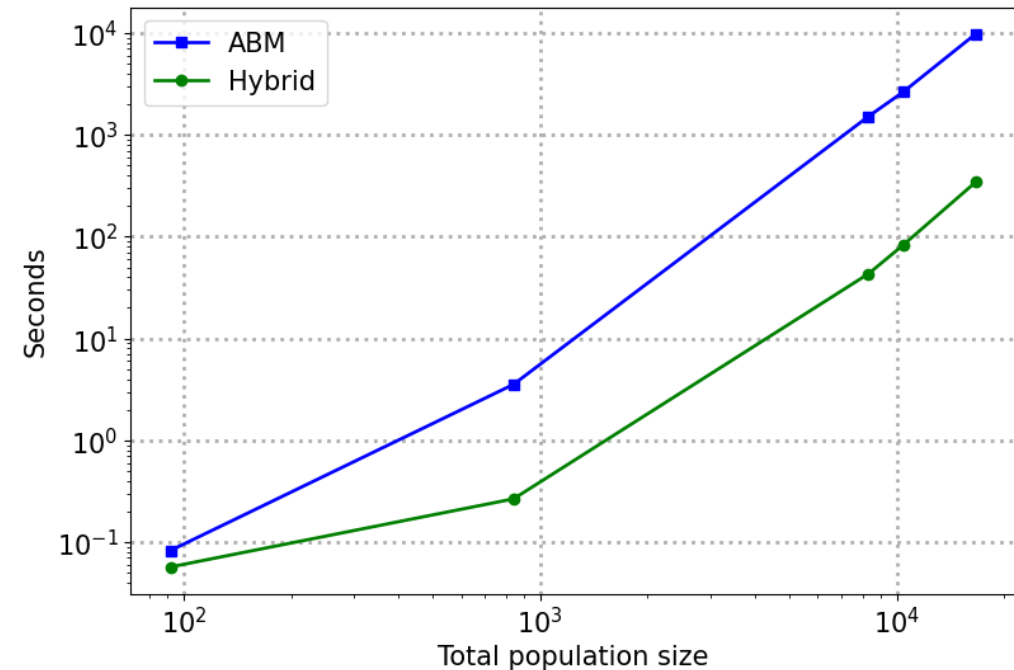


A spatial-hybrid model for Munich and its neighboring counties

Detailed results



Runtime comparison



→ Hybrid model reduces runtime by 96.5 % for 17,000 agents

Bicker et al., Hybrid metapopulation agent-based epidemiological models for efficient insight on the individual scale: a contribution to green computing. To be submitted, 2024.

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Thank you for your attention !
