Integrating Spatial Resolution and Mobility Patterns in Models for Infectious Disease Dynamics

Martin J. Kühn

joint work with many others (see first slide)

Stakeholders' meeting for the R2M2P2 Consortium

Utrecht, The Netherlands, 2025/05/16

Gefördert durch:







HELMHOLTZ





The Team



Thanks to / joint work with:

Daniel Abele, Henrik Zunker, Julia Bicker, Sascha Korf, Anna Wendler, René Schmieding, Lena Plötzke, Patrick Lenz, Maximilian Betz, Carlotta Gerstein, Kilian Volmer, Hannah Tritzschak, Agatha Schmidt, Nils Waßmuth, Paul Johannssen, Julian Litz, Daniel Richter, Elisabeth Kluth...

and

David Kerkmann, Khoa Nguyen, Ralf Hannemann-Tamas, Wadim Koslow, Margrit Klitz, Achim Basermann, Sebastian Binder, Martin Siggel, Jan Kleinert, Kathrin Rack, Annette Lutz, Michael Meyer-Hermann, Jan Hasenauer, Alexander Heinlein...



Institute of Software Technology, Department High-Performance

Computing, Predictive Simulation Software

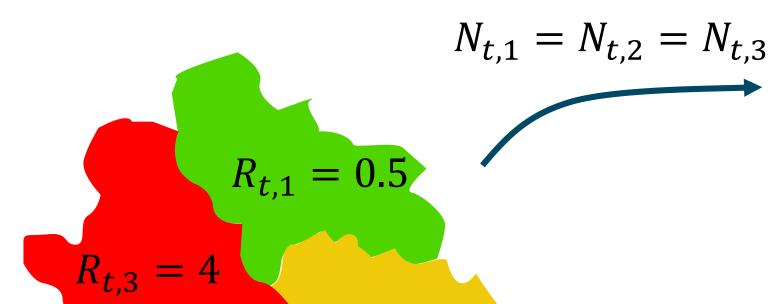


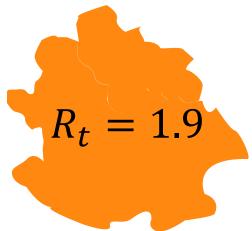
Life and Medical Sciences Institute and Bonn Center for Mathematical

Life Sciences, Mathematical-Epidemiological Modeling

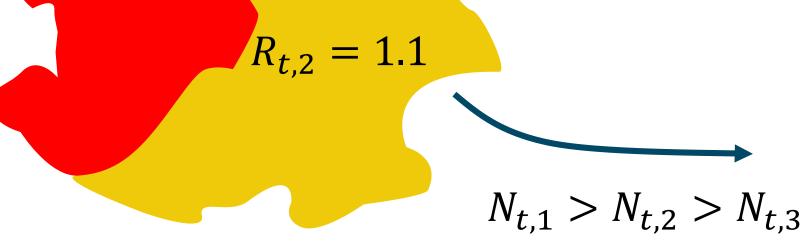
We care not enough about spatial resolution

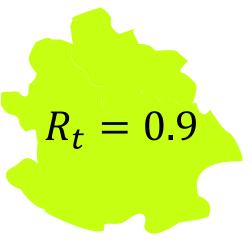




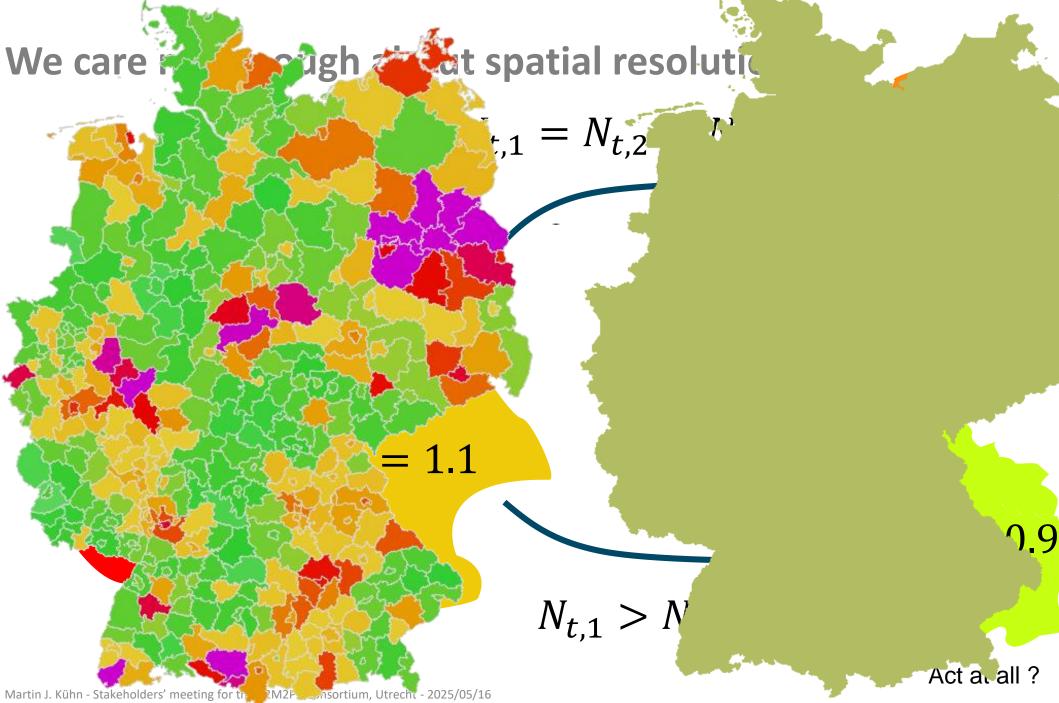


With which strictness to act?





Act at all?







$$N_{t,1}=N_{t,2}$$

Aggregated metrics...

- ...only give blurred information and intervention strictness is unclear
- ...do not allow for local action and targeted deployment of limited resources

7.9

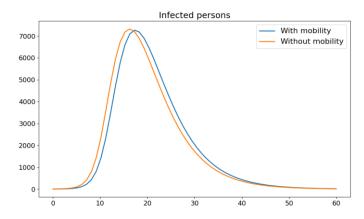
$$N_{t,1} > \Lambda$$

Act at all?

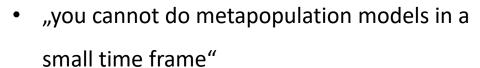


ODE*-SIR-type models are too easy to implement...

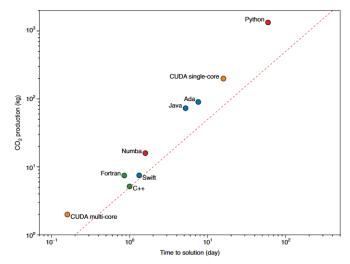
"in the end, it will arrive anyway…"



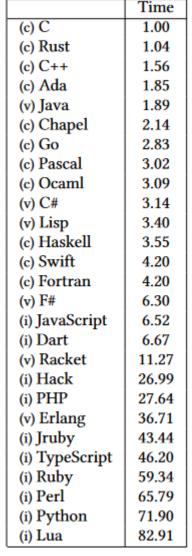
→ If it looks like that, you do not use the degrees of freedom and power in spatially resolved models



→ Do large-scale models in an efficient and scalable language (not R, not python...)

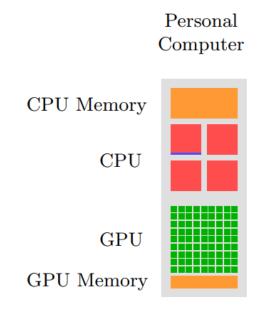


Portegies Zwart, Nature Astronomy (2020)

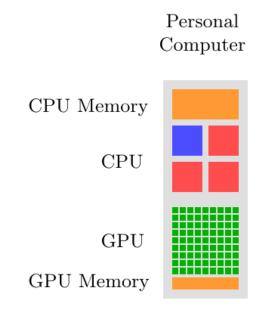


^{*} ODE: Ordinary differential equations

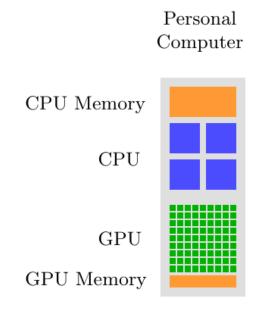






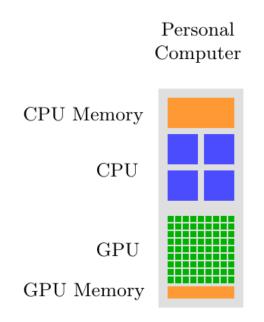


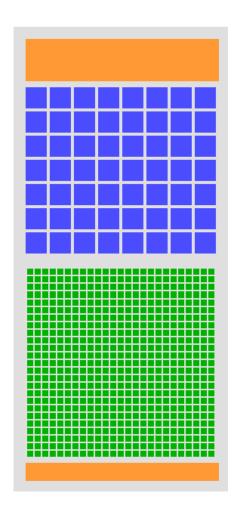




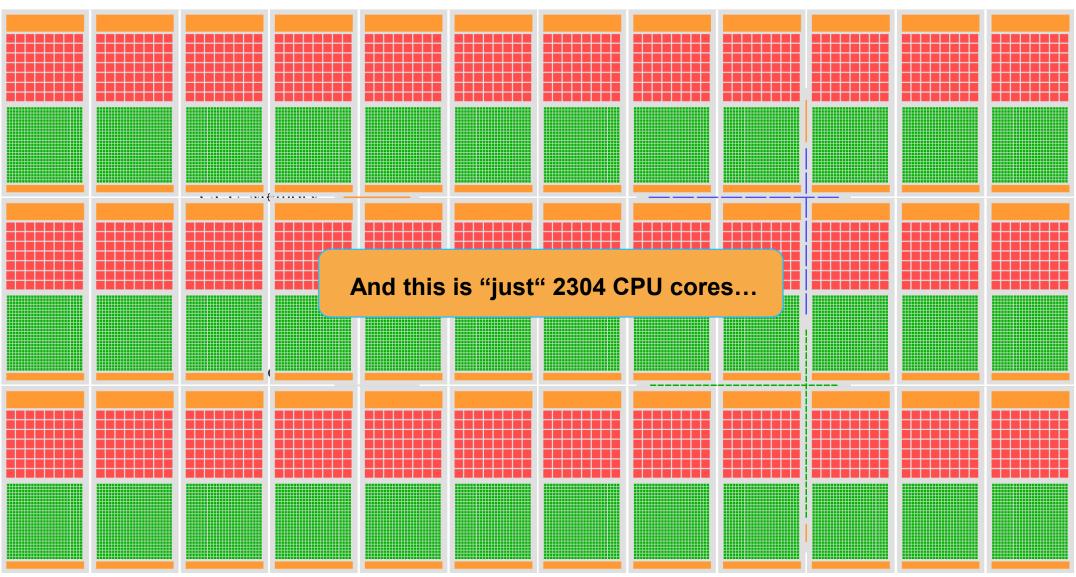


HPC Node

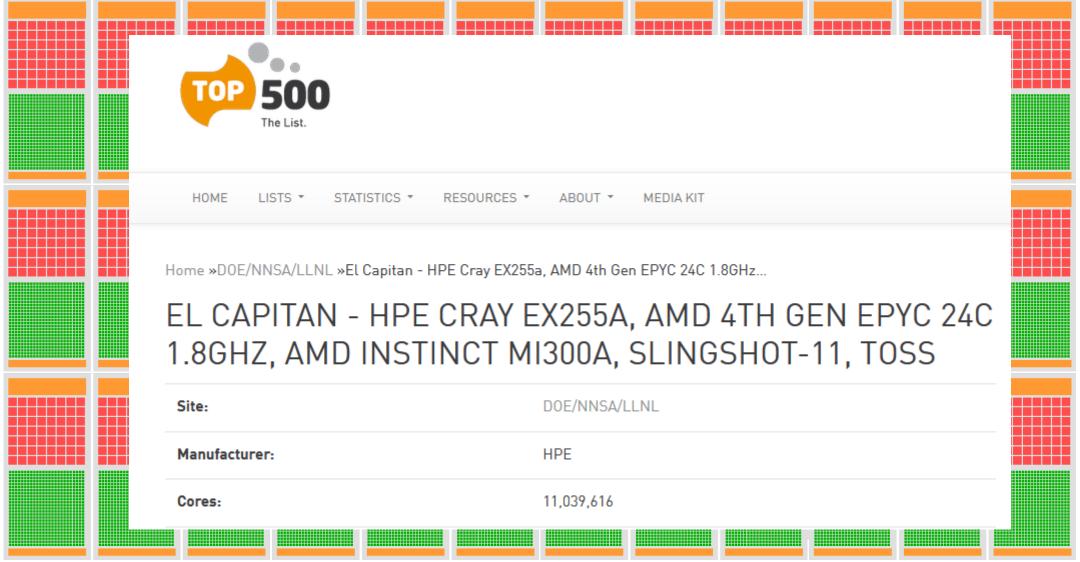




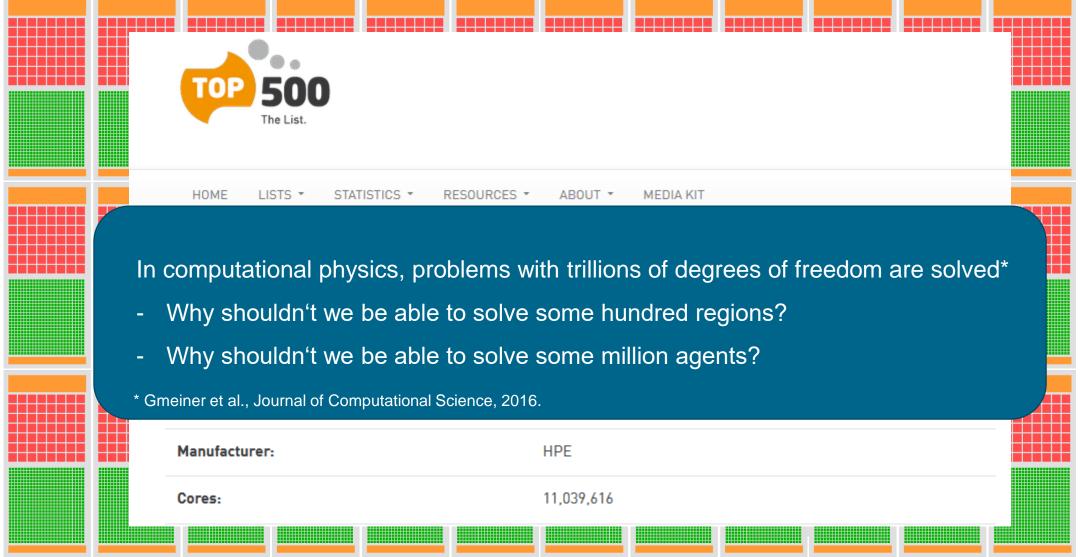




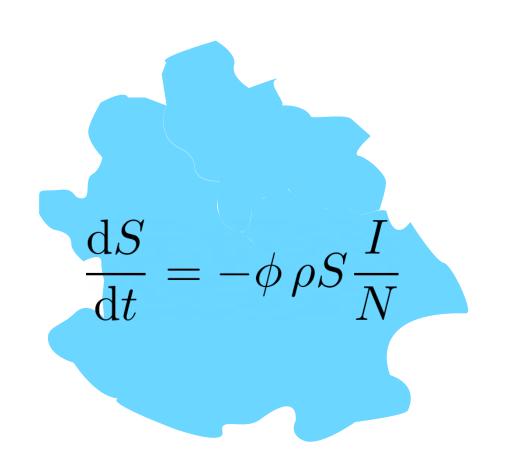












S: Susceptible population

I: Infected/Infectious population

N: Total population

 ϕ : Contact rate

 ρ : Transmission probability



$$\frac{\mathrm{d}S_1}{\mathrm{d}t} = -\phi \,\rho S_1 \frac{I_1}{N_1}$$

$$\frac{\mathrm{d}S_3}{\mathrm{d}t} = -\phi \,\rho S_3 \frac{I_3}{N_3}$$

$$\frac{\mathrm{d}S_2}{\mathrm{d}t} = -\phi \,\rho S_2 \frac{I_2}{N_2}$$



$$\frac{\mathrm{d}S_1}{\mathrm{d}t} = - \underbrace{A}_{\text{No commuting}} - \underbrace{B}_{\text{Commuting}}$$

$$\frac{\mathrm{d}S_3}{\mathrm{d}t} = -\underbrace{A}_{\text{No commuting}} - \underbrace{B}_{\text{Commuting}}$$

$$\frac{\mathrm{d}S_2}{\mathrm{d}t} = -\underbrace{A}_{\text{No commuting }} - \underbrace{B}_{\text{Commuting }}$$



$$\frac{\mathrm{d}S_1}{\mathrm{d}t} = -\underbrace{\frac{1}{2}\phi\rho\frac{I_1}{P_1}S_1}_{\text{No commuting}} - \underbrace{B}_{\text{Commuting}}$$

$$\frac{\mathrm{d}S_3}{\mathrm{d}t} = -\underbrace{\frac{1}{2}\phi\,\rho\frac{I_3}{P_3}S_3}_{\text{No commuting}} - \underbrace{B}_{\text{Commuting}}$$

 h_{ij} : Commuter from region i to j

 I^c : commuting infectious

 I^r : remaining infectious

$$P_i = \sum_{j=1}^n h_{ij}$$

$$N_i = P_i - \sum_{j \neq i} h_{ij} + \sum_{j \neq i} h_{ji}$$

$$\frac{\mathrm{d}S_2}{\mathrm{d}t} = -\underbrace{\frac{1}{2}\phi\rho\frac{I_2}{P_2}S_2}_{\text{No commuting}} - \underbrace{B}_{\text{Commuting}}$$



$$\frac{\mathrm{d}S_{1}}{\mathrm{d}t} = -\underbrace{\frac{1}{2}\phi\rho\frac{I_{1}}{P_{1}}S_{1}}_{\text{No commuting}} - \underbrace{\frac{1}{2}\left(\phi\rho\frac{I_{1}^{r}}{N_{1}}S_{1}^{r} + \phi\rho\frac{I_{1}^{c}}{N_{1}}S_{1}^{r} + \phi\rho S_{1}\sum_{j\neq 1}\frac{h_{1j}}{P_{1}}\frac{I_{j}^{r} + I_{j}^{c}}{N_{j}}\right)}_{\text{Commuting}}$$

$$\frac{\mathrm{d}S_3}{\mathrm{d}t} = -\underbrace{\frac{1}{2}\phi\,\rho\frac{I_3}{P_3}S_3}_{\text{No commuting}} - \underbrace{\frac{B}{\mathrm{Commuting}}}_{\text{Commuting}}$$

 h_{ij} : Commuter from region i to j

 I^c : commuting infectious

 I^r : remaining infectious

$$P_i = \sum_{j=1}^n h_{ij}$$

$$N_i = P_i - \sum_{j \neq i} h_{ij} + \sum_{j \neq i} h_{ji}$$

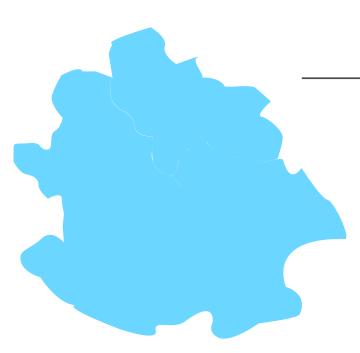
$$\frac{\mathrm{d}S_2}{\mathrm{d}t} = -\underbrace{\frac{1}{2}\phi\,\rho\frac{I_2}{P_2}S_2}_{\text{No commuting}} - \underbrace{B}_{\text{Commuting}}$$

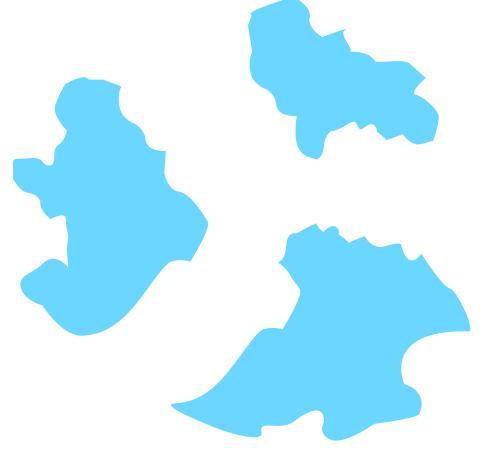


→ For uniformly distributed cases, the models should return the same output

Basic reproduction numbers for different numbers of regions.

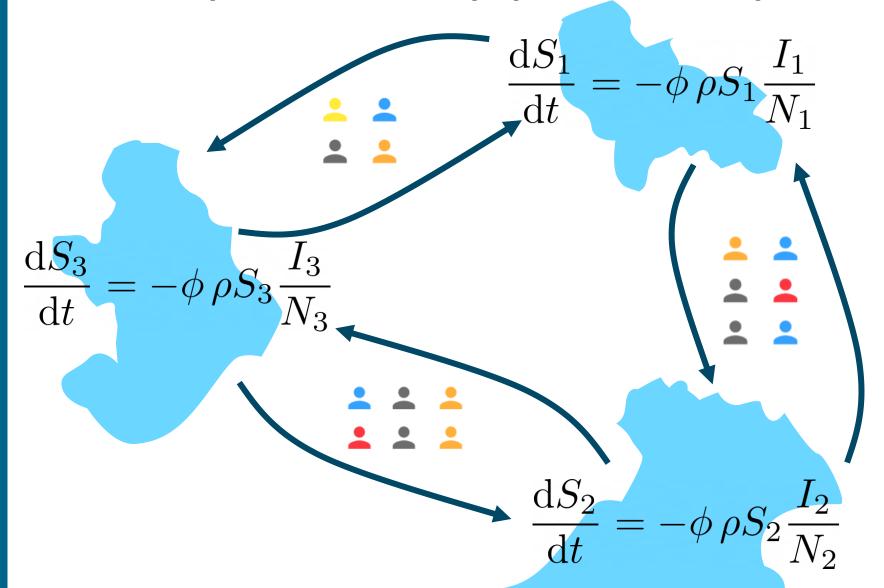
Number of Regions	Model A	Model B	Model C
1	4.48161	4.48161	4.48161
2	4.48161	6027	4.48161
5	4.48161	6.2 43	4.48161
10	4.48161	6 3 54	4.48161
20	4.48161	.6105	4.48161
50	4.48161	6.67782	4.48161





From simple ODE to metapopulation: A Graph-ODE alternative





- Use a graph with regions as nodes
- One edge per, e.g., pair (infection state, age group)
- Advance nodes in parallel from t to t+0.5 and from t+0.5 to t+1

Advantage:

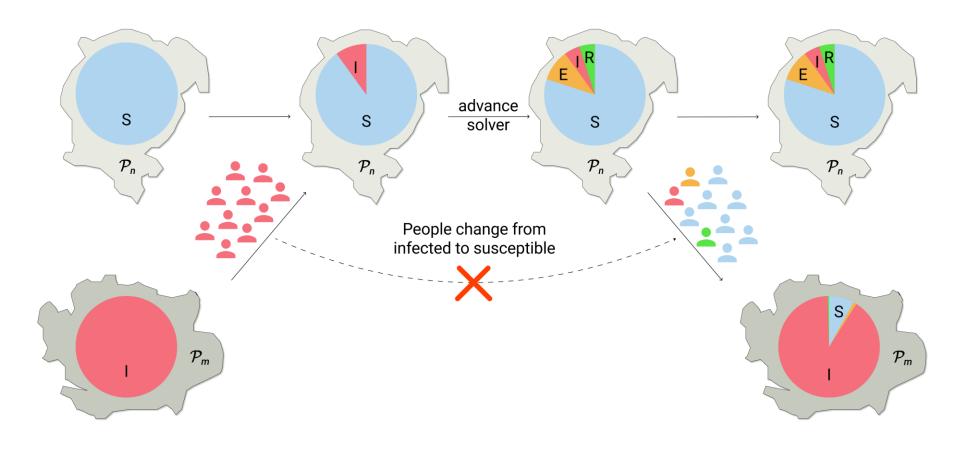
Parallelism

Disadvantage:

- Returning commuters need to be approximated
- Theory more complex

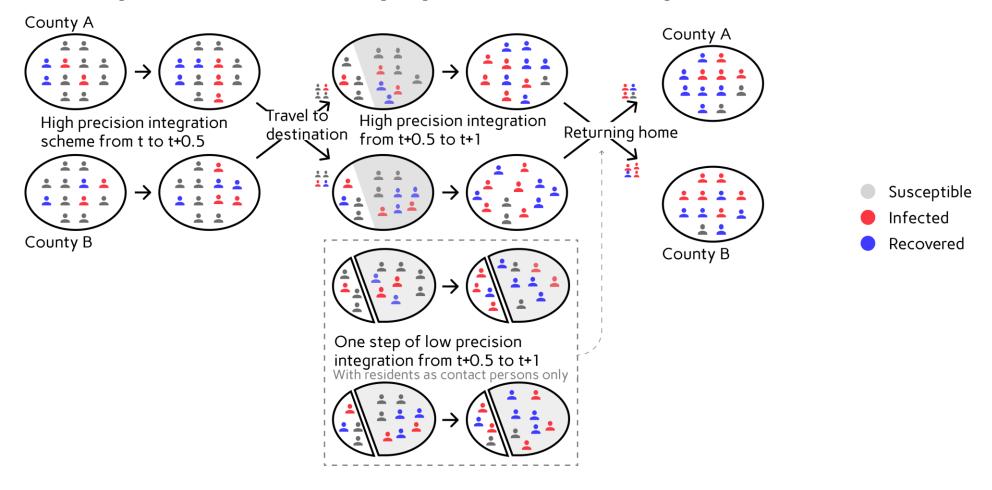
From simple ODE to metapopulation: A Graph-ODE alternative





From simple ODE to metapopulation: A Graph-ODE alternative

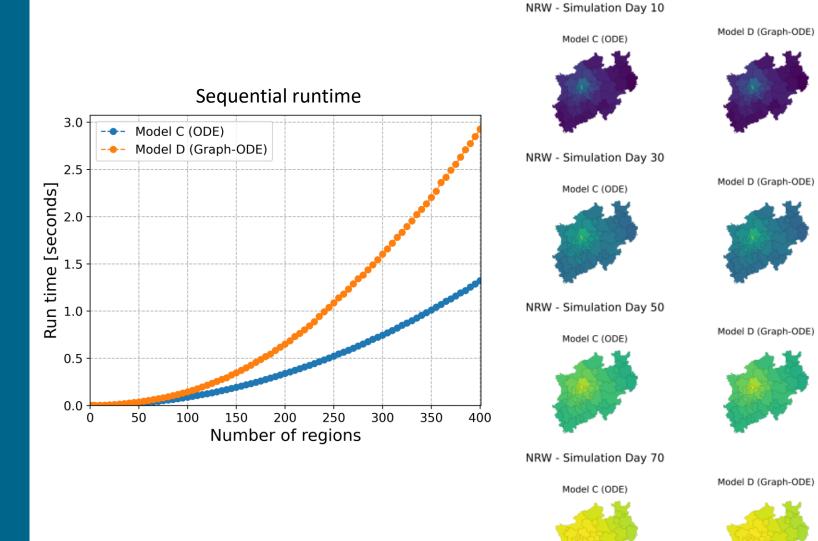


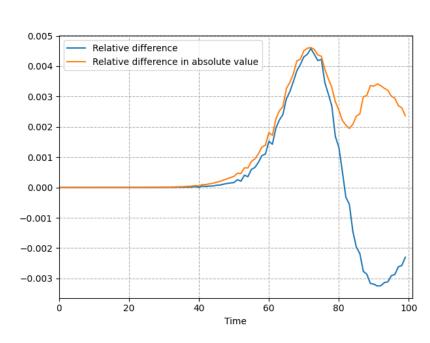


- Commuter return overshoots if number of commuters relative large; take from largest compartment
- Improvement to commuter extrapolation in development: Zunker et al, In preparation, 2025

ODE metapopulation vs. Graph-ODE metapopulation

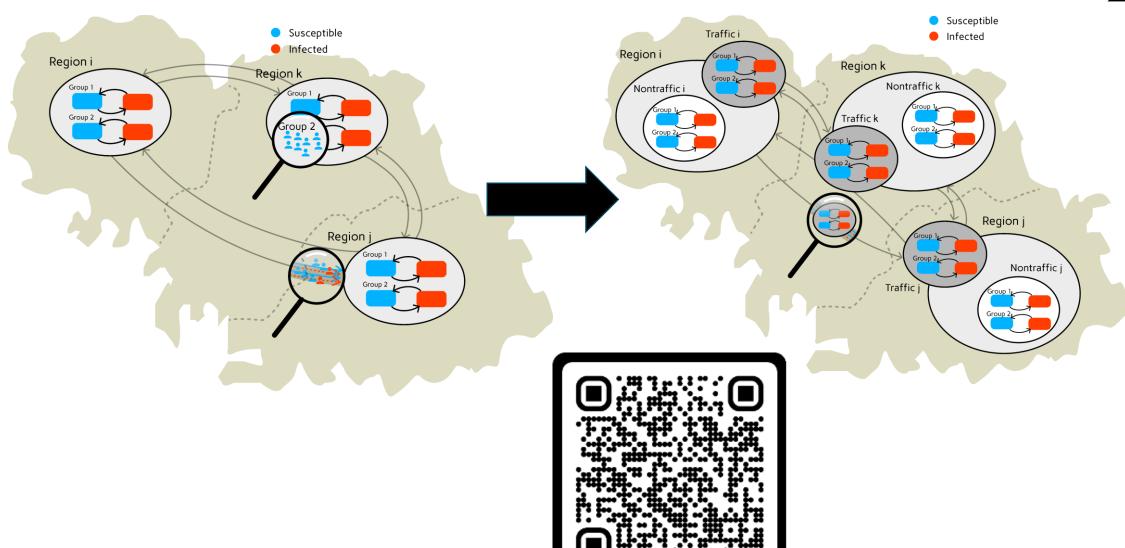






Extension to travel-time aware Graph-ODE metapopulation model





Metapop (2024)

Zunker et al., PLOS Comp Bio, 2024.

Al-based on-the-fly computation for web applications

Days ®



- Simulate spatially resolved expert models
- Train spatially resolved AI surrogates (Graph Neural Networks) on expert model' outcomes

→ Enables low-barrier web access for decision makers

.767

10¹

12.238

22.928

25.723

33.004

→ Timely reaction for pandemic mitigation

0.045

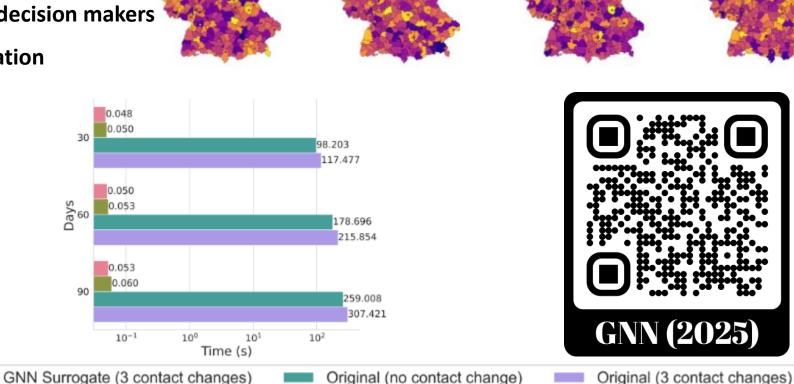
0.046

0.047

0.049

0.049

 10^{-1}





Schmidt et al. - Graph Neural Network Surrogates to leverage Mechanistic Expert Knowledge towards Reliable and Immediate Pandemic Response (2025)

GNN Surrogate (no contact change)

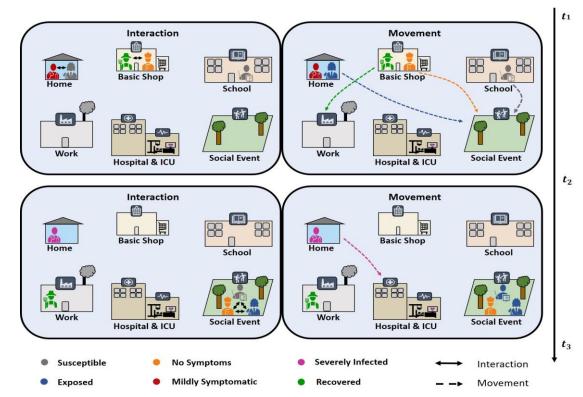
 10^{0}

Time (s)

Agent-based modeling



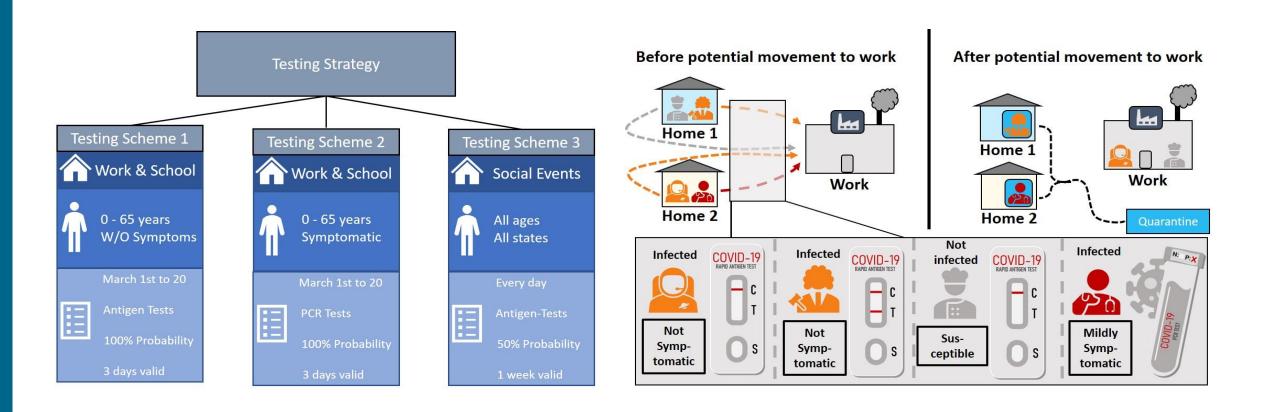
- Model individuals (or households) as individual agents
- Study and answer research questions on a "microscopic" level (e.g. individual decisions, test strategies, viral load...)
- Computational cost scales (super)linearly with number of agents



Algorithm 1: Trip-based agent-based simulation 1 $t \leftarrow t_0 \in \mathbb{R}$ 2 while $t \leq t_{\text{max}}$ do 3 | for each location do 4 | Execute agents' interactions 5 | for each agent do 6 | Perform individual movement 7 | $t \leftarrow t + \Delta t$

Agent-based modeling: Testing strategies

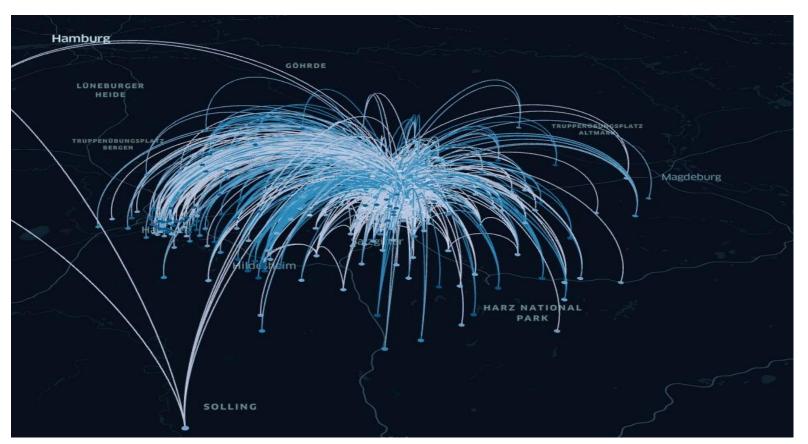




Agent-based modeling: Application to city-scale



- Approximately 370.000 persons from Brunswick and the surrounding area
- Over 1.3 million trips per day

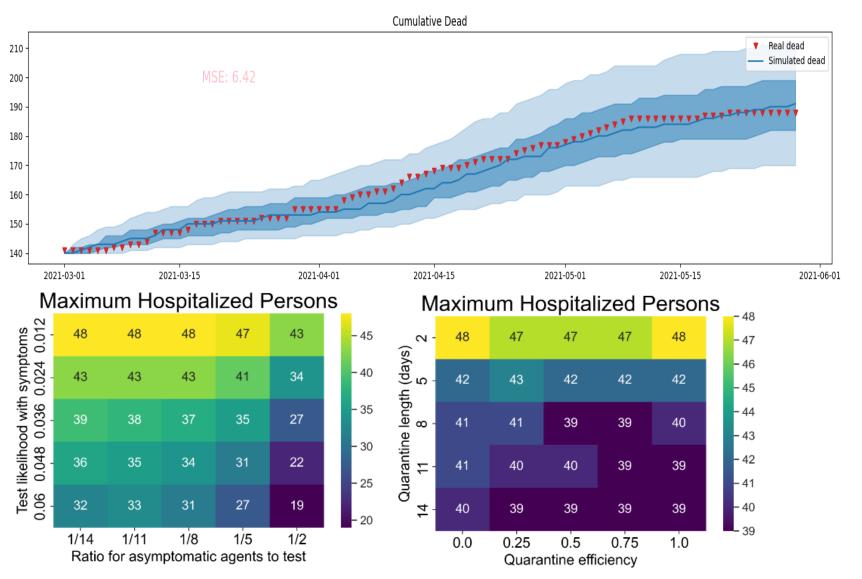




Kerkmann, Korf et al., Accepted for Computers in Biology and Medicine, 2025

Agent-based modeling: Application to city-scale







Kerkmann, Korf et al., Accepted for Computers in Biology and Medicine, 2025

Hybrid agent-metapopulation models: Spatial hybrid

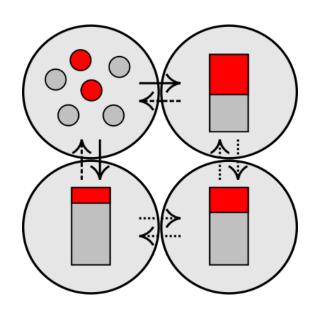


• Idea:

- Interest in infection spread in particular region
- Exclusive availability of data in specific region (or computational resources limited)

Concept:

- Agent-based model in region of interest (focus region)
- ODE-based models for connected regions
- → Detailed results in focus region while considering influence of connected regions in runtime efficient manner

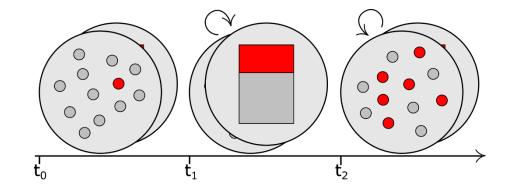


Hybrid agent-metapopulation models: Temporal hybrid



Idea:

- Low case numbers:
 High stochasticity and individual behavior is important
- High case numbers:
 Individual behavior is less influential and single simulation outcomes are close to averaged results



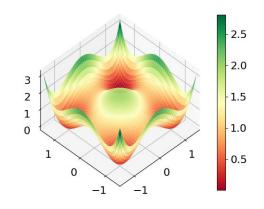
Concept:

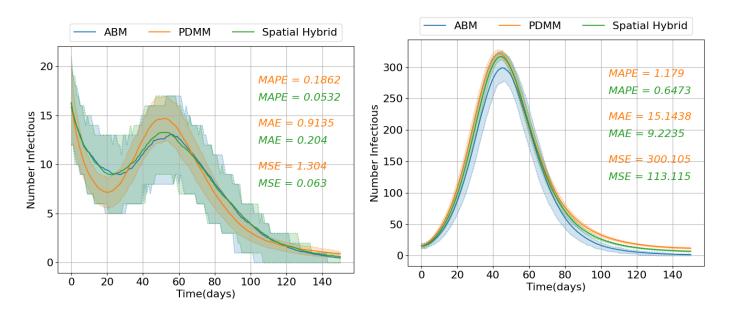
- Switch between agent-based and ODE-based model during the simulation according to a threshold value
- → Capture stochasticity and individual behavior when necessary for accurate outcomes while using runtime advantage when possible

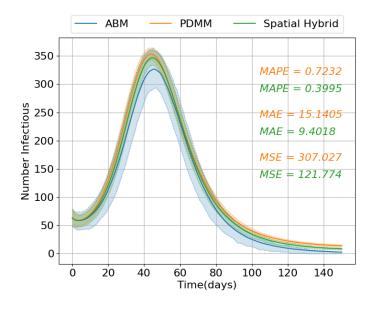
Proof-of-concept spatial hybrid model



- Setup: 8000 agents, 1% of population initially infected
- Focus region: $\Omega_1 = (-\infty, 0) \times (0, \infty)$
- Transmission rate in $\Omega_2=(0,\infty)\times(0,\infty)$ corresponding to $R_0=2.4$
- Transmission rate in other regions corresponding to $R_0=0.8$





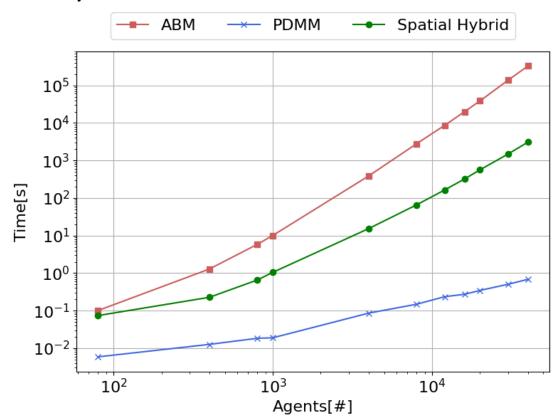


Bicker, Schmieding et al., Infectious Disease Modelling, 2025

Proof-of-concept spatial hybrid model



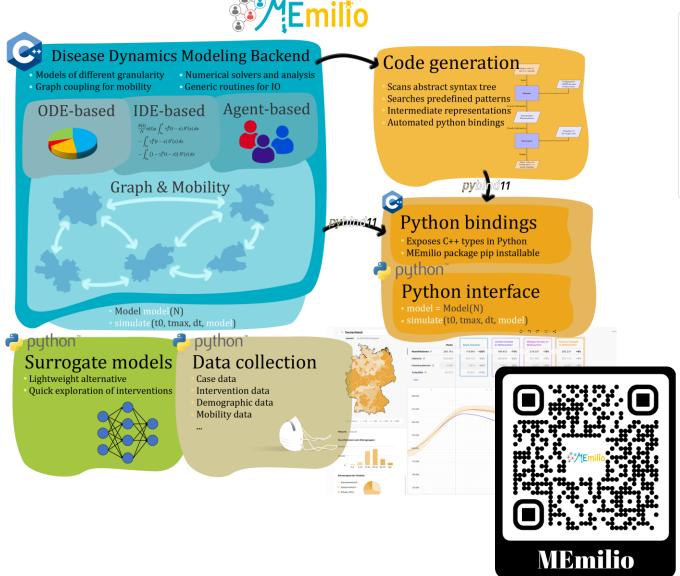
- Spatial-hybrid has same scaling behavior like ABM
- For 400 agents: Runtime of spatial-hybrid 1 order of magnitude lower than for ABM
- For **40,000 agents**: Spatial-hybrid reduces runtime by **98%**



MEmilio:

A high performance Modular EpideMIcs simuLatIOn software







Activity (on main) December 2024

- 11 active pull requests (5 merged)
- 13 active authors

Software, Unit Tests, Comments

- C++: ca. 650 (2023: ca. 300)
- Python: ca. 230 (2023: ca. 200)
- Code lines vs comments: 83k vs 31k













Thanks to our funders! / Thank you for your attention!

UNIVERSITÄT BONN

Further reading:

- Gerstein et al., Comparison and performance of metapopulation models (working title), In preparation, 2025
- → Let me know if you want to be informed on preprint
- Zunker et al., Commuter exchange in Graph-ODE models (working title), In preparation, 2025
- → Let me know if you want to be informed on preprint
- Kerkmann, Korf et al. **Agent-based modeling for realistic reproduction of human mobility and contact behavior to evaluate test and isolation strategies in epidemic infectious disease spread**, *Accepted for publication in Computers in Biology and Medicine* (2025)
- Bicker et al., Hybrid metapopulation agent-based epidemiological models for efficient insight on the individual scale: a contribution to green computing. Infectious Disease Modelling, 10(2), 571 (2025)
- Zunker et al., Novel travel time aware metapopulation models and multi-layer waning immunity to assess late-phase epidemic and endemic scenarios. PLOS Computational Biology 20(12): e1012630 (2024)
- Schmidt et al., Graph Neural Network Surrogates to leverage Mechanistic Expert Knowledge towards Reliable and Immediate Pandemic Response (2024)
- Kühn et al., Assessment of effective mitigation and prediction of the spread of SARS-CoV-2 in Germany using demographic information and spatial resolution. *Mathematical Biosciences* 339 (2021): 108648

Application: Numerical assessment of the control strategy





