With funding from the:
Federal Ministry of Research, Technology and Space

Comparing agent-based and population-based models with respect to their inherent assumptions

4TH (INTER-) NATIONAL CONFERENCE ON INFECTIOUS DISEASE MODELING

20 – 22 MAY 2026 IN HALLE (SAALE)

Julia Bicker, ***Anna Wendler***

Joint work with Lena Plötzke and Martin J. Kühn

Population-based vs. agent-based modeling

Population-based models (PBM)



- Aggregated results through modeling on compartment level
- Homogenous and well-mixed population
- Computationally efficient especially for large population size
- Low complexity and fewer parameters

Agent-based models (ABM)



- High level of detail through modeling on individual level
- Ability to capture heterogenous contact behavior and mobility patterns
- Computational complexity dependent on population size
- Many parameters and highly resolved data needed

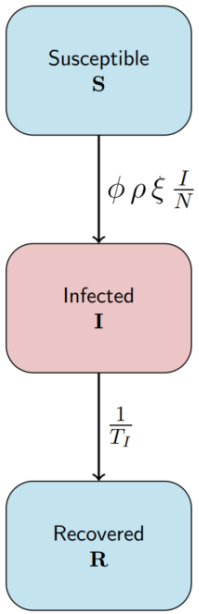
PBM using ordinary differential equations (ODEs)

$$S'(t) = -\frac{S(t)}{N}\,\phi(t)\,\rho(t)\,\xi(t)\,I(t)$$

$$I'(t) = \frac{S(t)}{N}\,\phi(t)\,\rho(t)\,\xi(t)\,I(t) - \frac{1}{T_I}\,I(t)$$

$$R'(t) = \frac{1}{T_I}\,I(t)$$

$\phi(t)$	Number of contacts at time t
$\rho(t)$	Transmission probability at time t
$\xi(t)$	Proportion of infected individuals that are not isolated at time t
T_I	Mean stay time in compartment I



PBM using the Linear Chain Trick (LCT)

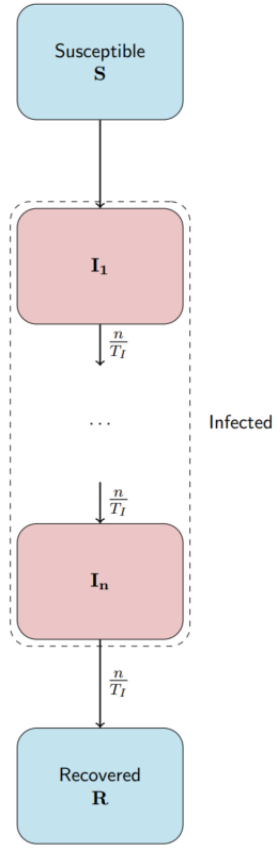
$$S'(t) = -\frac{S(t)}{N}\,\phi(t)\,\rho(t)\,\xi(t)\,I(t)$$

$$I_1'(t) = \frac{S(t)}{N}\,\phi(t)\,\rho(t)\,\xi(t)\,I(t) - \frac{1}{T_I}\,I_1(t)$$

$$I_j'(t) = \frac{n}{T_I} I_{j-1}(t) - \frac{n}{T_I}\,I_j(t), \qquad j \in \{2, \dots, n\}$$

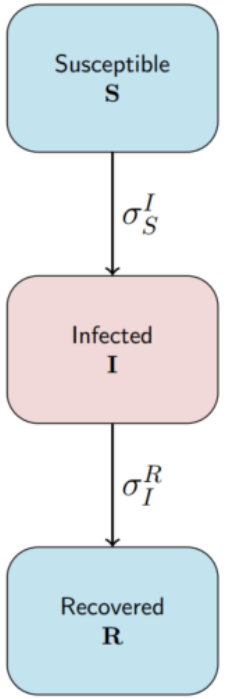
$$R'(t) = \frac{n}{T_I}\,I_n(t)$$

with $I(t) = \sum_{j=1}^{n} I_j(t)$



PBM using integro-differential equations (IDEs)

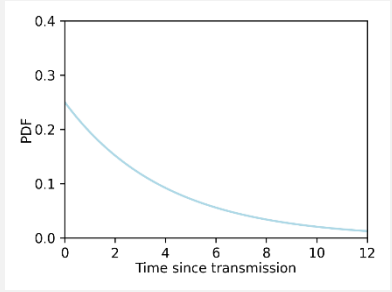
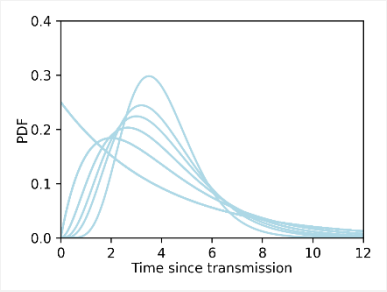
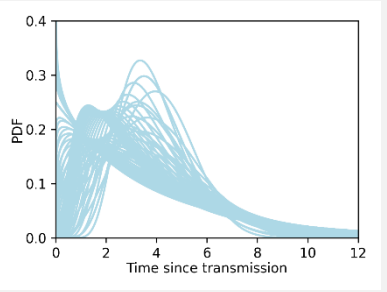
$$S'(t) = -\frac{S(t)}{N}\,\phi(t)\int_{-\infty}^{t}\rho(t-x)\xi(t-x)\,\underbrace{\gamma_I^R(t-x)\,\overbrace{\sigma_S^I(x)}^{\text{New infections at time } x}}_{\text{Individuals that are still infected at time } t}\,\mathrm{d}x$$



$\sigma_S^I(\mathrm{x})$	Number of individuals transitioning from S to I at time x
$\gamma_I^R(\tau)$	Mean proportion of individuals that are still infected at infection age τ
$\xi(t,\tau)$	Proportion of infected individuals that are not isolated at time t and infection age τ
$\rho(t,\tau)$	Transmission probability at infection age τ

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MODELING NETWORK for Severe Infectious Diseases

Overview PBMs

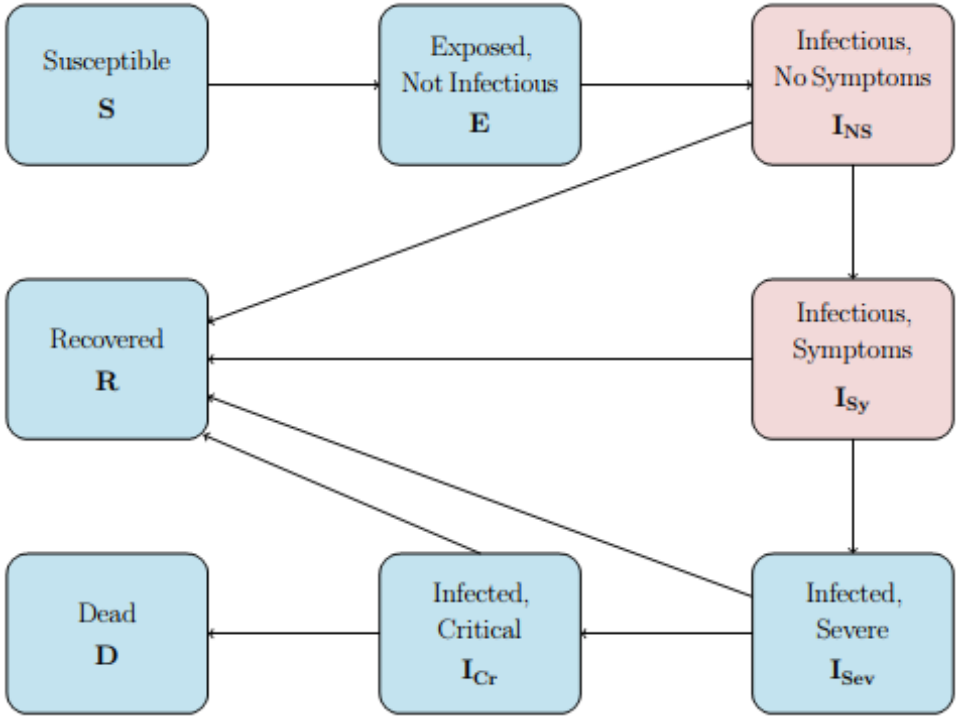
	ODE	LCT	IDE
Transition distribution	Exponential	Erlang	Arbitrary
$\mu = 4, \sigma^2 \in [2,18]$			
Computational complexity			

Comparing different transition distributions in PBMs

Scenario 1.1: Exponential distributions in all models

Scenario 2.1: Different distributions per model

- Assumed groundtruth: Lognormal distribution
- IDE : Use groundtruth directly
- ODE and LCT:
  Choose exponential and Erlang distributions as close as possible (w.r.t. mean and variance) to groundtruth



Comparing different transition distributions in PBMs

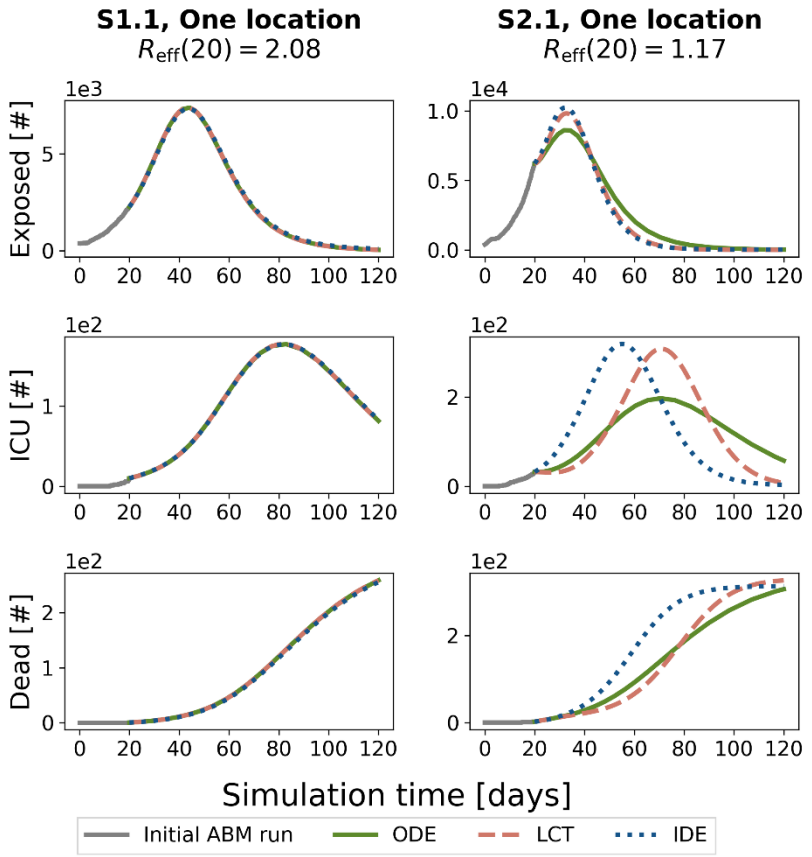
Scenario 1.1: Exponential distributions in all models

- Initialization based on one ABM trajectory
- Sanity check: Results coincide

Scenario 2.1: Different distributions per model

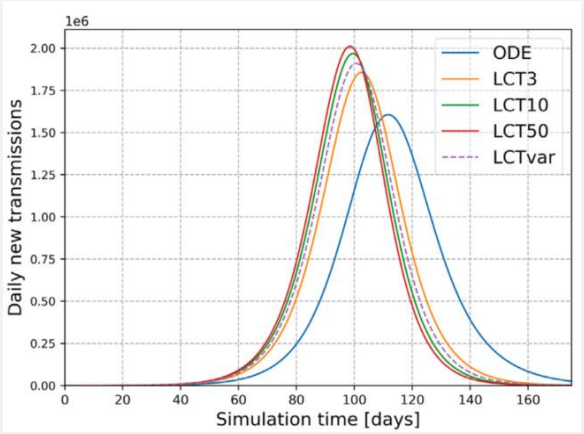
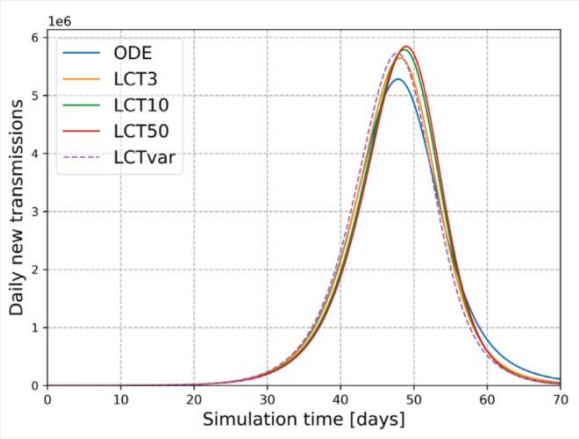
- Assumed groundtruth: Lognormal distribution
- IDE : Use groundtruth directly
- ODE and LCT:
  Choose exponential and Erlang distributions as close as possible (w.r.t. mean and variance) to groundtruth

➢ Different peak sizes and timings for different distributions assumptions



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Epidemic peak behavior depending on R_{eff}

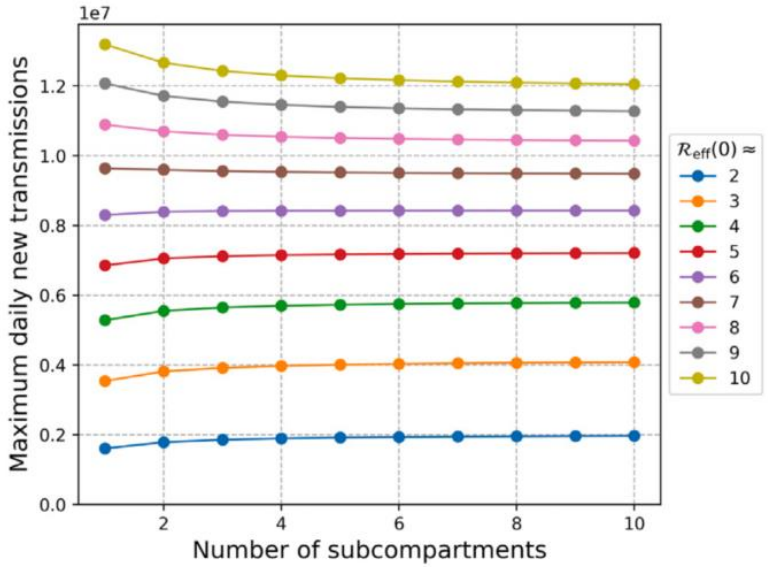
$R_{eff}(0) = 2$	$R_{eff}(0) = 4$
	
The more subcompartments, the **higher** the peak	
The more subcompartments, the **earlier** the peak	The more subcompartments, the **later** the peak

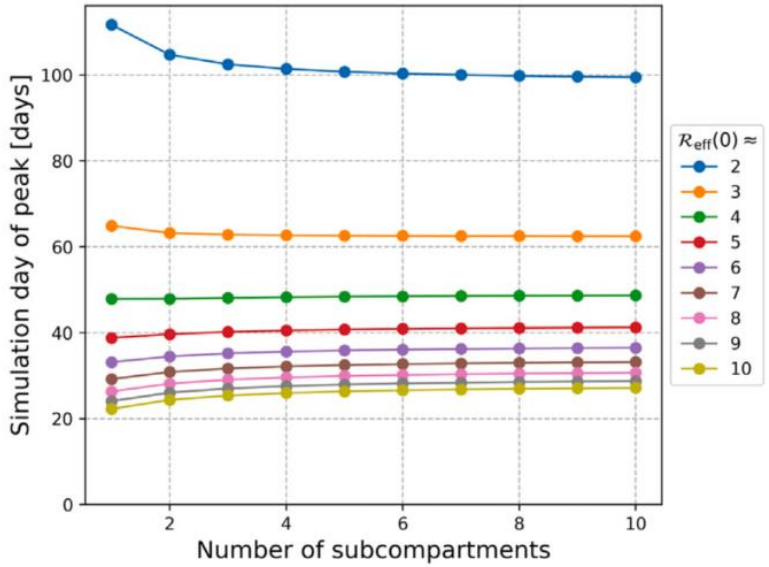
➢ We cannot draw clear conclusions from distribution alone, R_{eff} needs to be considered!

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Epidemic peak behavior depending on R_{eff}

Systematic investigation of peak size and timing for different values of R_{eff}:





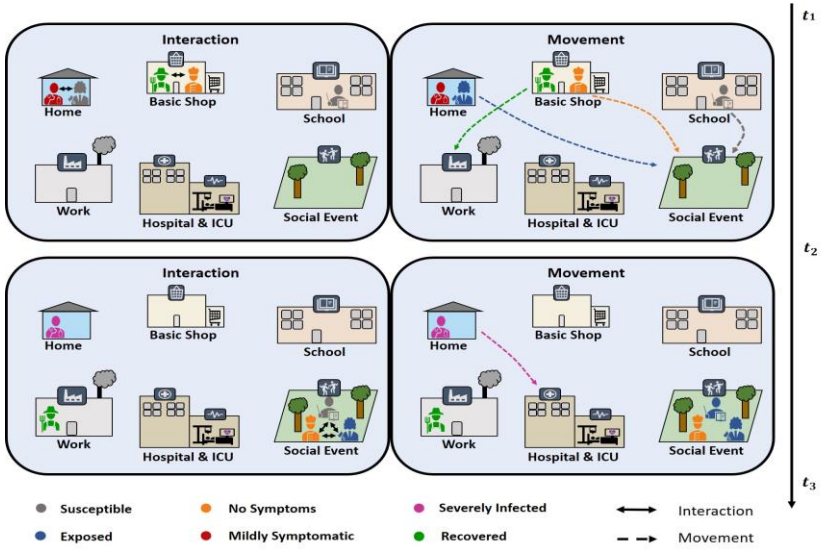
➢ Different tendencies for different R_{eff}

LCT Paper

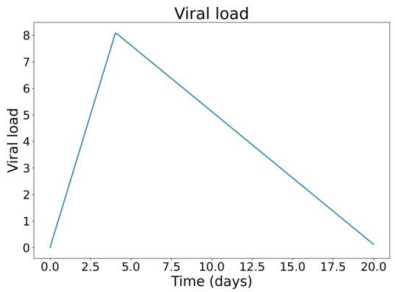
Plötzke et al., Mathematics and Computers in Simulation, 2026.

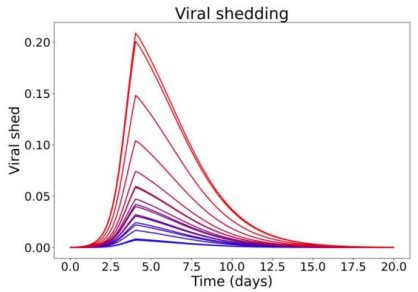
Agent-based model (ABM)

- Activity/mobility based model
- Different location types (Home, School, Work, Event, Shop)



- Disease progression of individuals is drawn from distribution
  - Waiting time until transmission: exponentially distributed
  - Subsequent transition distributions: can be chosen arbitrarily
  - In contrast to PBMs: Stochastic model
- Modeling of viral load/viral shedding



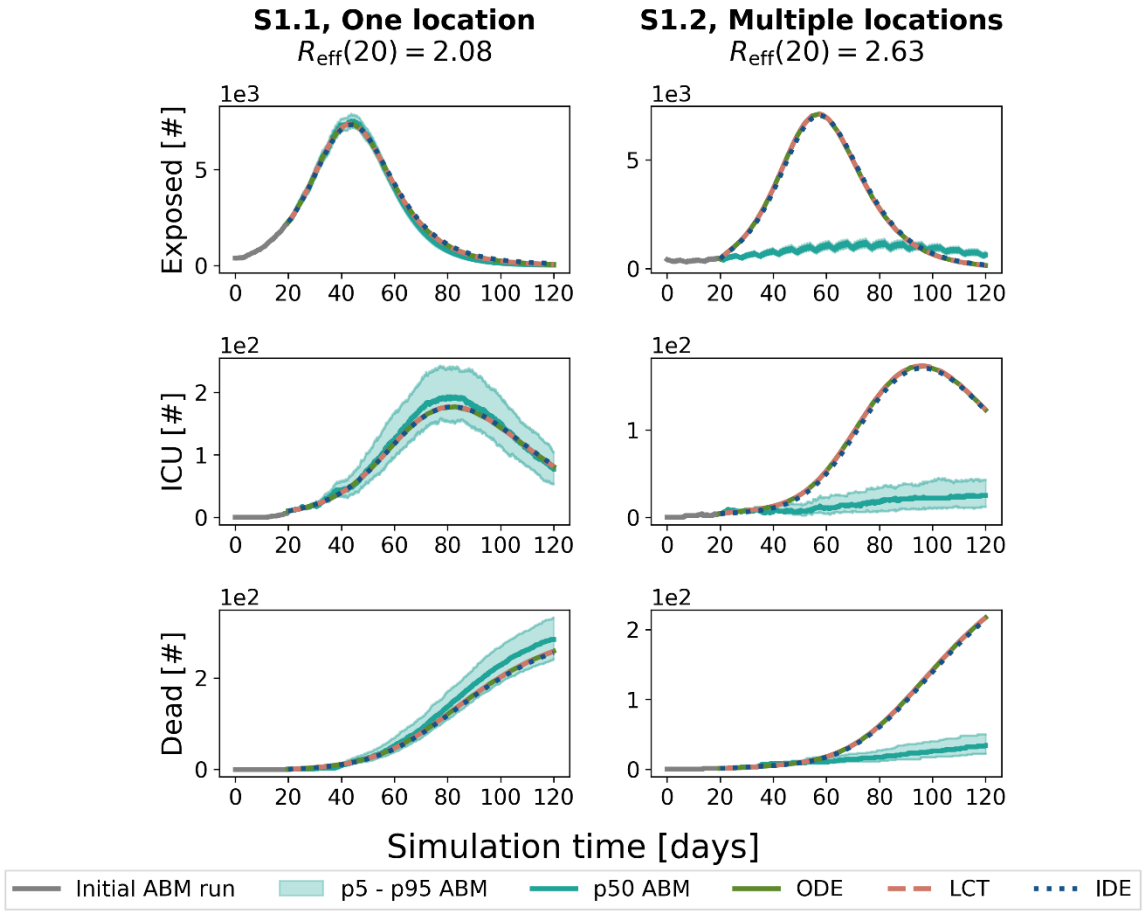


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Comparison of ABM and PBMs: Exponential transition distributions

Bicker et al., arXiv, 2026.

MEmilio Paper



Scenario 1: Exponential transition distributions

Scenario 1.1: One location per type

- ABM very similar to PBMs

Scenario 1.2: Multiple locations per type

- Less infections in ABM than in PBMs

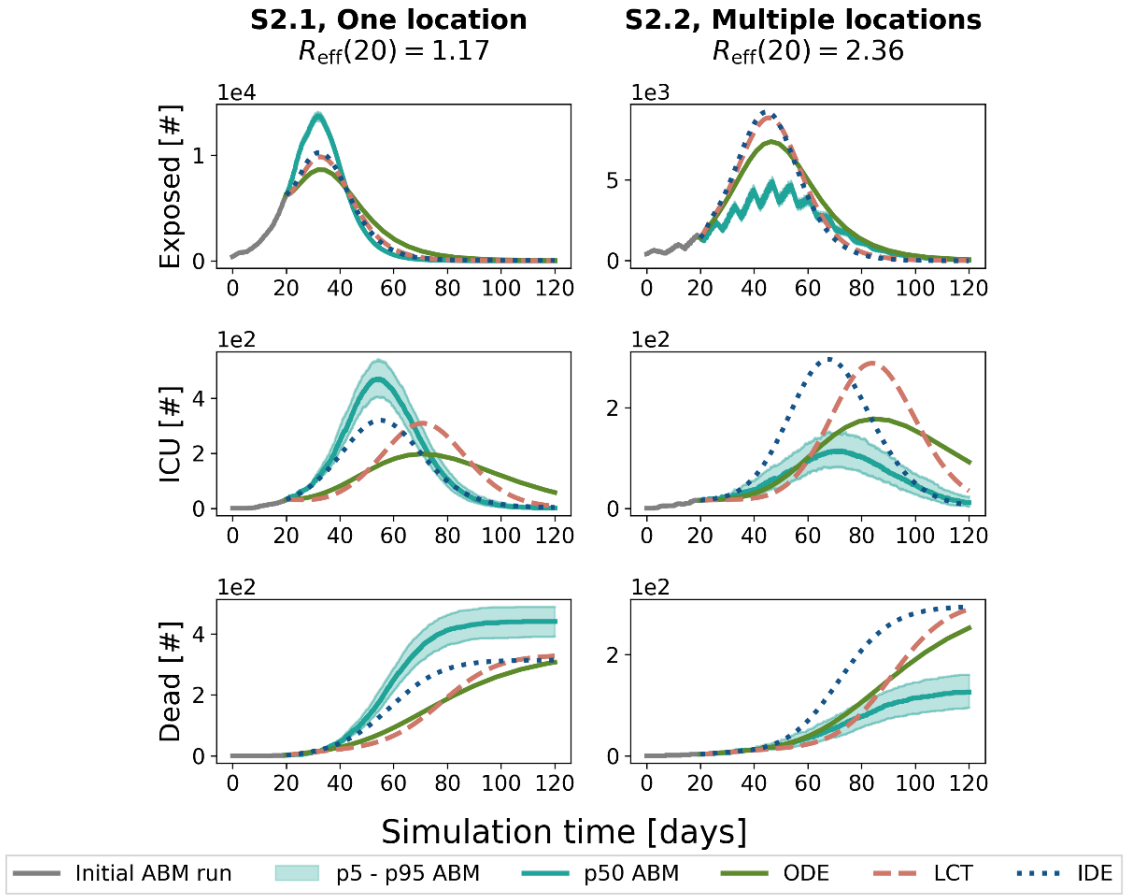
- ➢ Homogeneous mixing assumption in PBMs and within locations, i.e. all individuals have contact with each other
- ➢ Contact networks are more heterogeneous in ABM with multiple locations
  - ➢ Less transmission events

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Comparison of ABM and PBMs: Different transition distributions

Bicker et al., arXiv, 2026.

MEmilio Paper



Scenario 2: Different transition distributions

- ABM and IDE: Lognormal
- LCT and ODE: Erlang and exponential

Scenario 2.1: One location per type

- Peak timing of IDE and ABM very similar
- Peak size ABM higher than IDE (and other models)

➢ Possibly due to different transmission mechanisms in ABM (exponential) and IDE (depending on transition distributions between infectious compartments)

Scenario 2.2: Multiple locations per type

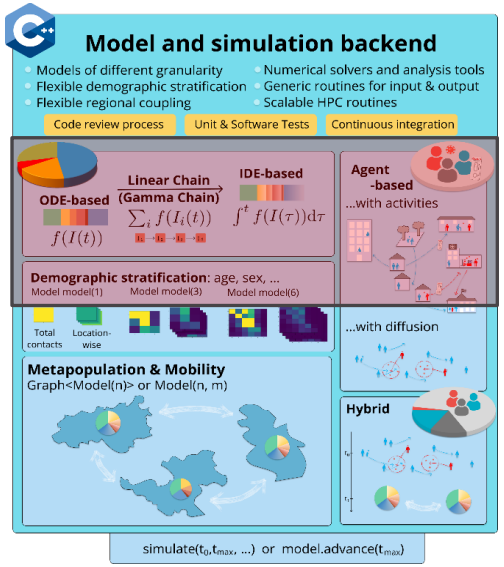
- Less infections in ABM than in PBMs (as before)

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LCT Paper

- **Substantial difference** in modeling outcome when using different transition distributions
- **Impact** of different assumptions **cannot be stated generally** by, e.g., higher or earlier peaks; case-by-case consideration necessary
- More advanced models need **advanced numerical solvers** and **scientific computing**



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Thank you for your attention!