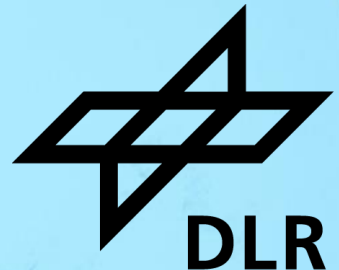


A HYBRID MODELING FRAMEWORK TO COMBINE AGENT- AND POPULATION-BASED MODELS

Julia Bicker

Predictive Simulation Software, German Aerospace Center

Joint work with René Schmieding, Michael Meyer-Herrmann and Martin Kühn



Motivation



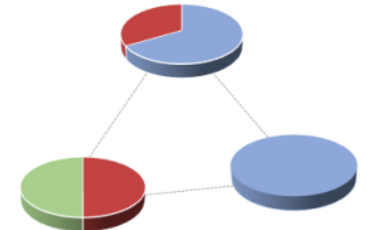
Agent-based models (ABM)



- 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

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

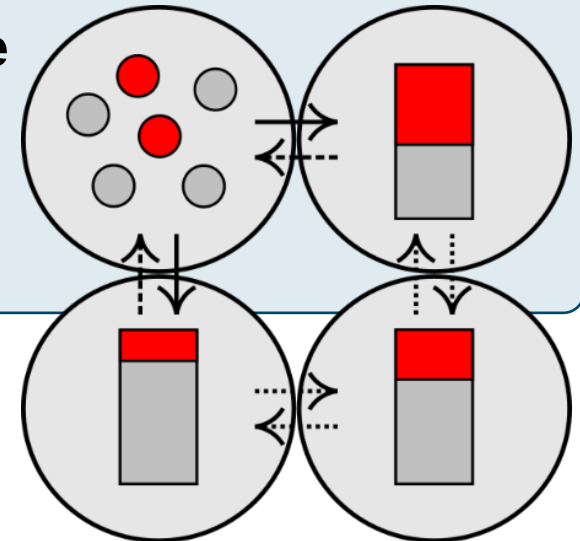


Motivation

- Interested in infection dynamics in a **particular region**
- Neighboring regions influence focus region through **commuting activities**
- Exclusive availability of **detailed data** in a particular region

Concept

- ABM in focus region and PBM for surrounding regions
- **Detailed results** in **focus region** while considering **influence of surrounding regions runtime efficiently**

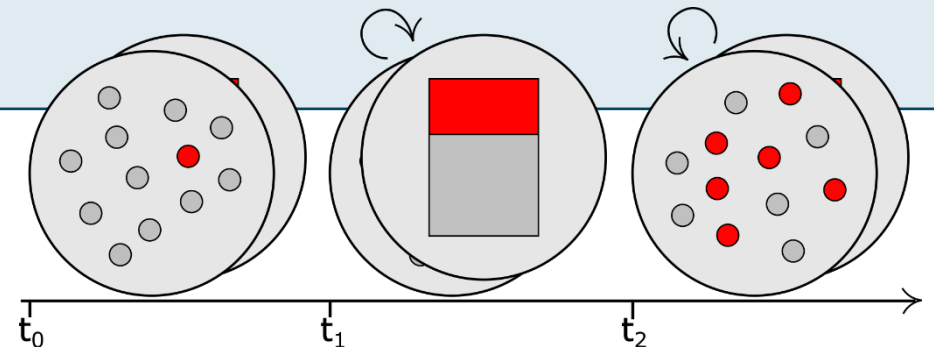


Motivation

- **Low case regime:** Results are highly **stochastic** and driven by **individual behavior**
- **High case regime:** Single simulation results are close to **averaged outcomes** and individual behavior is less influential

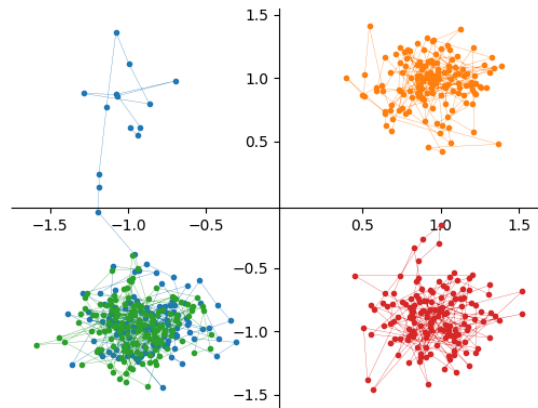
Concept

- ABM when case numbers are low and switch to PBM when case numbers exceed given threshold
- **Individual-level modeling** where necessary while using **runtime advantage** when possible



Agent-based model

- Agent has position $x \in \mathbb{R}^2$ and infection state $z \in \{S, E, C, I, R, D\}$
- Position change is modelled with independent diffusion processes
- Infection state adoptions are modelled as stochastic jumps



Metapopulation model (PDMM)

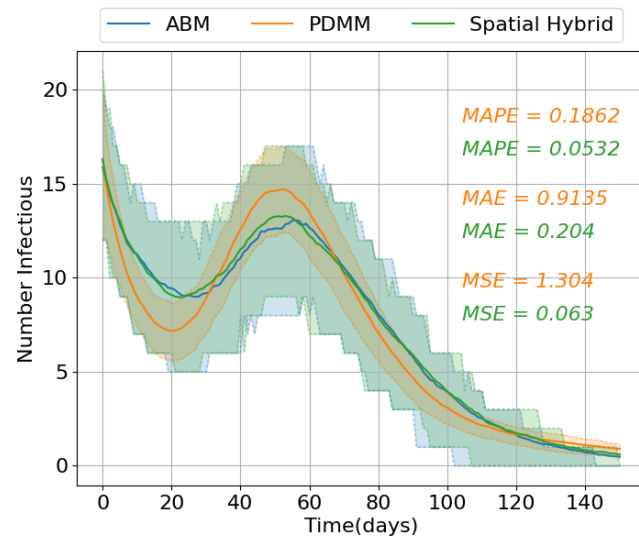
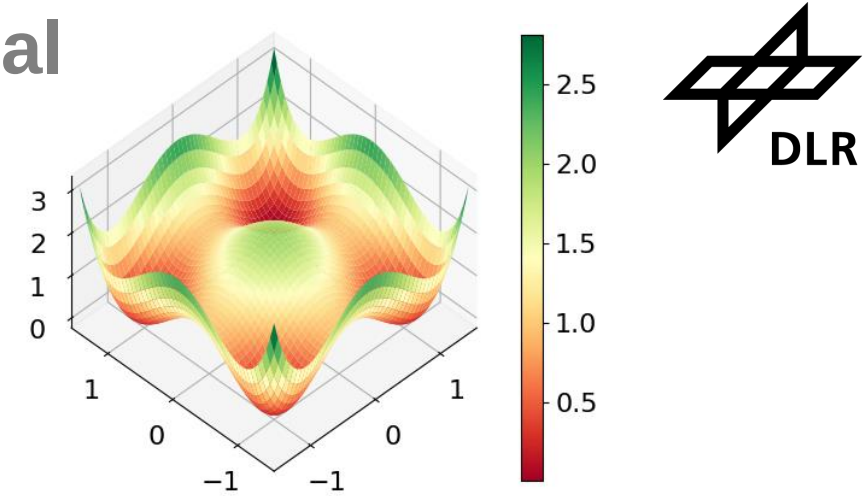
- Domain is split into disjoint regions and agents are aggregated by region and infection state
- Infection state dynamics modeled with a set of ordinary differential equations per region
- Movement between region is modelled as stochastic jumps

¹Winkelmann, Zonker, Schütte, Conrad: Mathematical modeling of spatio-temporal population dynamics and application to epidemic spreading. Mathematical Biosciences 336, 108619 (2021),

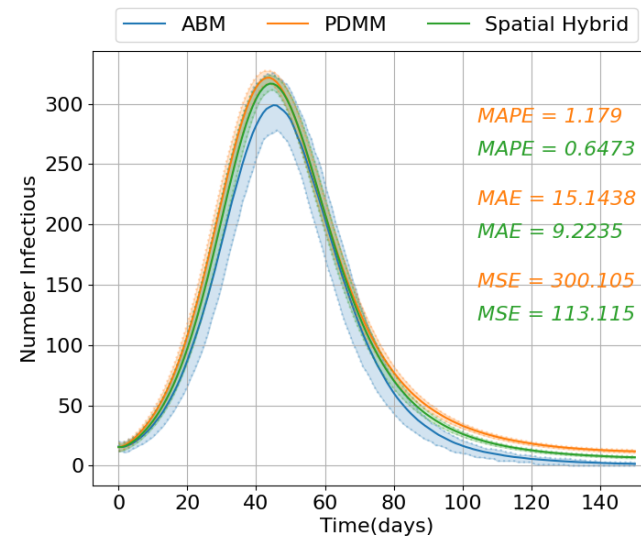
<https://www.sciencedirect.com/science/article/pii/S0025556421000614>

Spatial hybridization – A quadwell potential

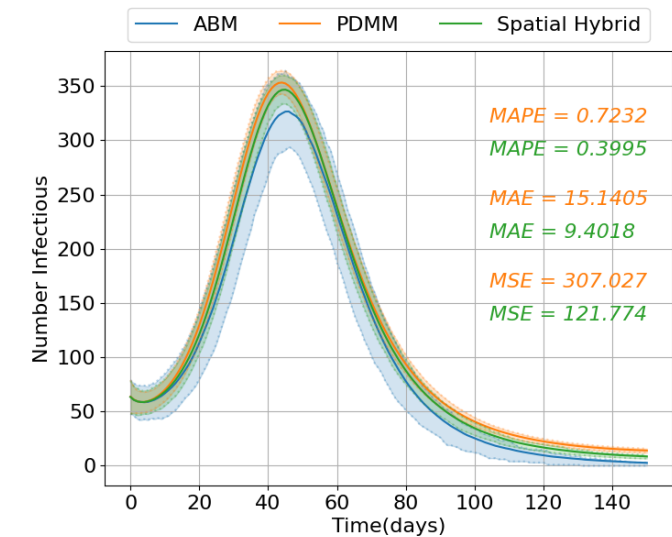
- 8000 agents, 1% of population initially infected
- Transmission rate in region 2 (next to focus region) 3-times higher than in other regions



Focus region



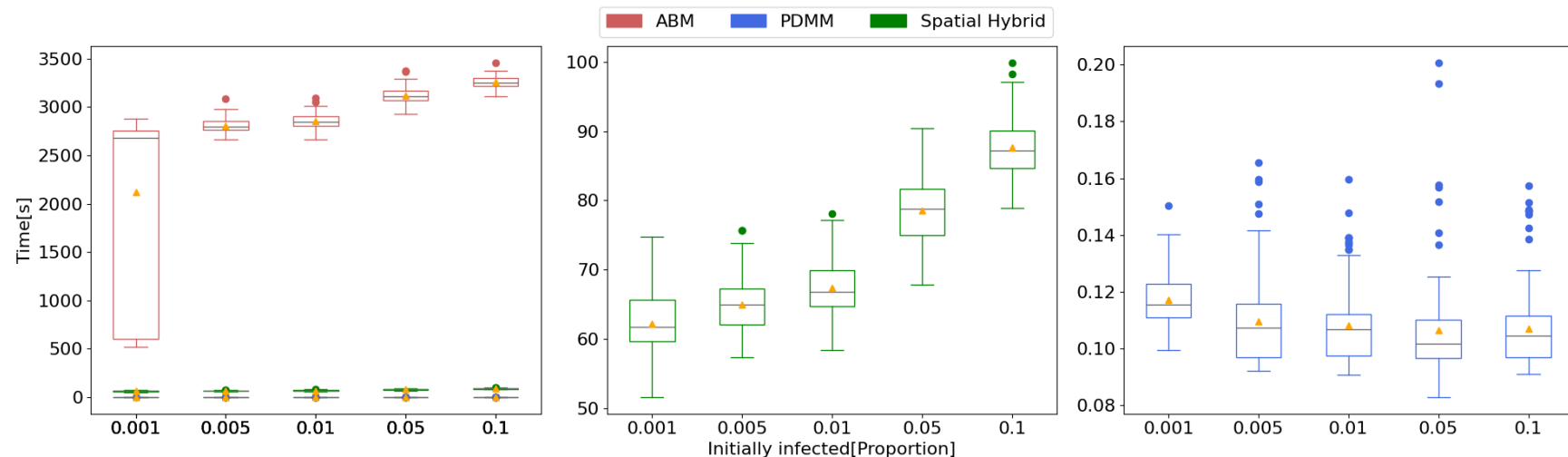
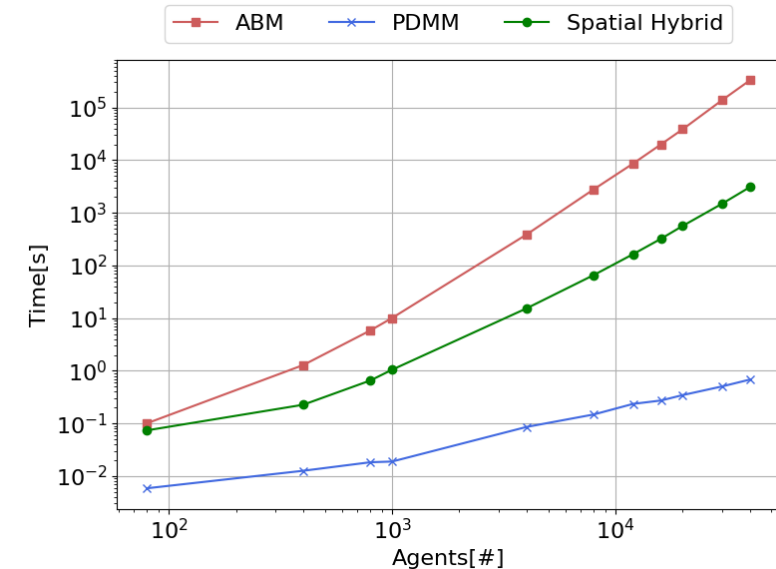
Region 2



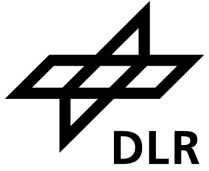
Whole domain

Spatial hybridization – Runtime

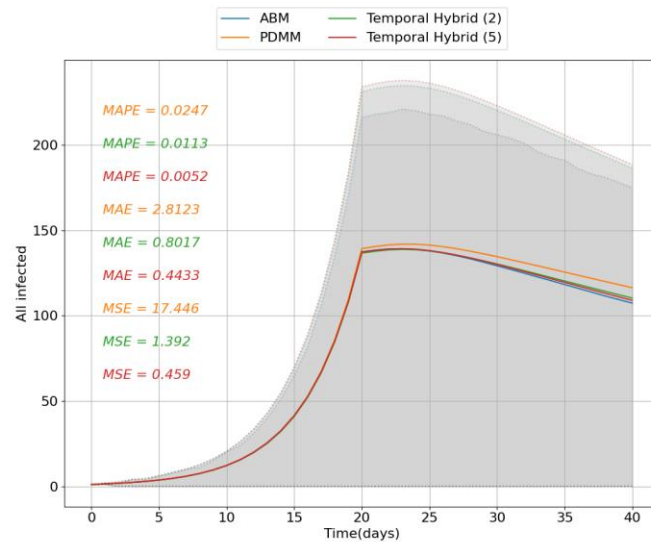
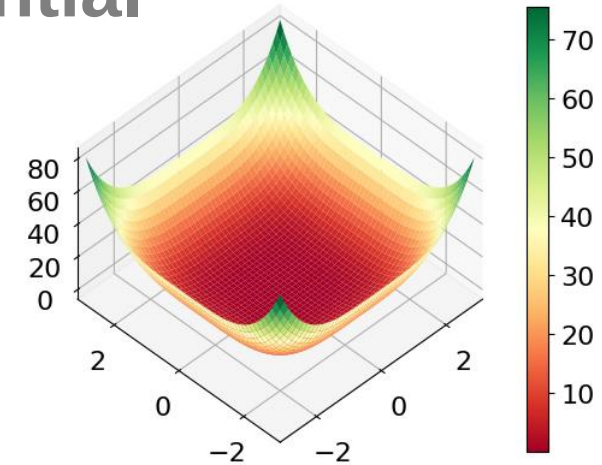
- Spatial-hybrid has same scaling behavior like ABM
- Spatial-hybrid and ABM runtime increase with increasing proportion of initially infected, while PDMM runtime is independent of initially infected
- Spatial-hybrid **up to 98% faster** than ABM



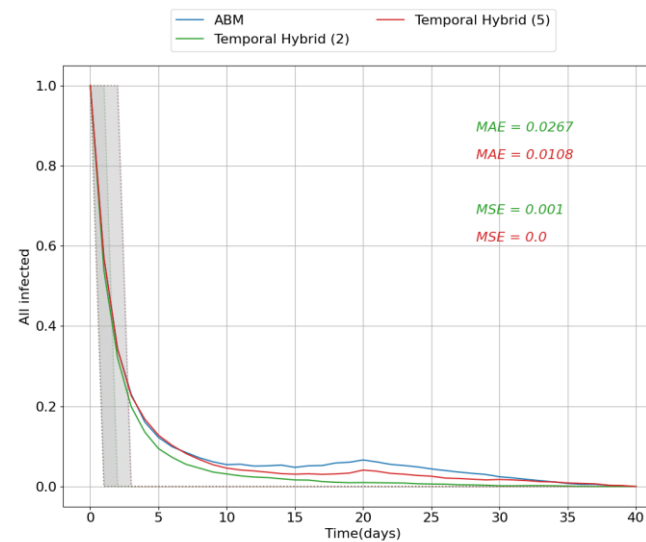
Temporal hybridization – A singlewell potential



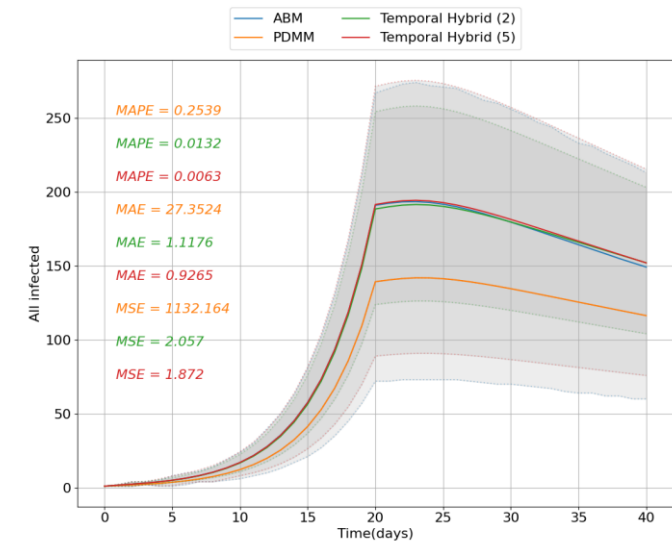
- 10,000 agents, 1 initially infected, small contact radius
- High initial transmission rate and reduction of transmission rate by 80% after 20 days
- Two switching thresholds in temporal-hybrid (2 and 5 infected)



All runs

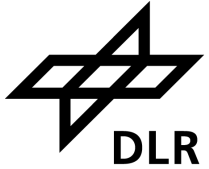


Extinction runs



Survival runs

Temporal hybridization – Runtime



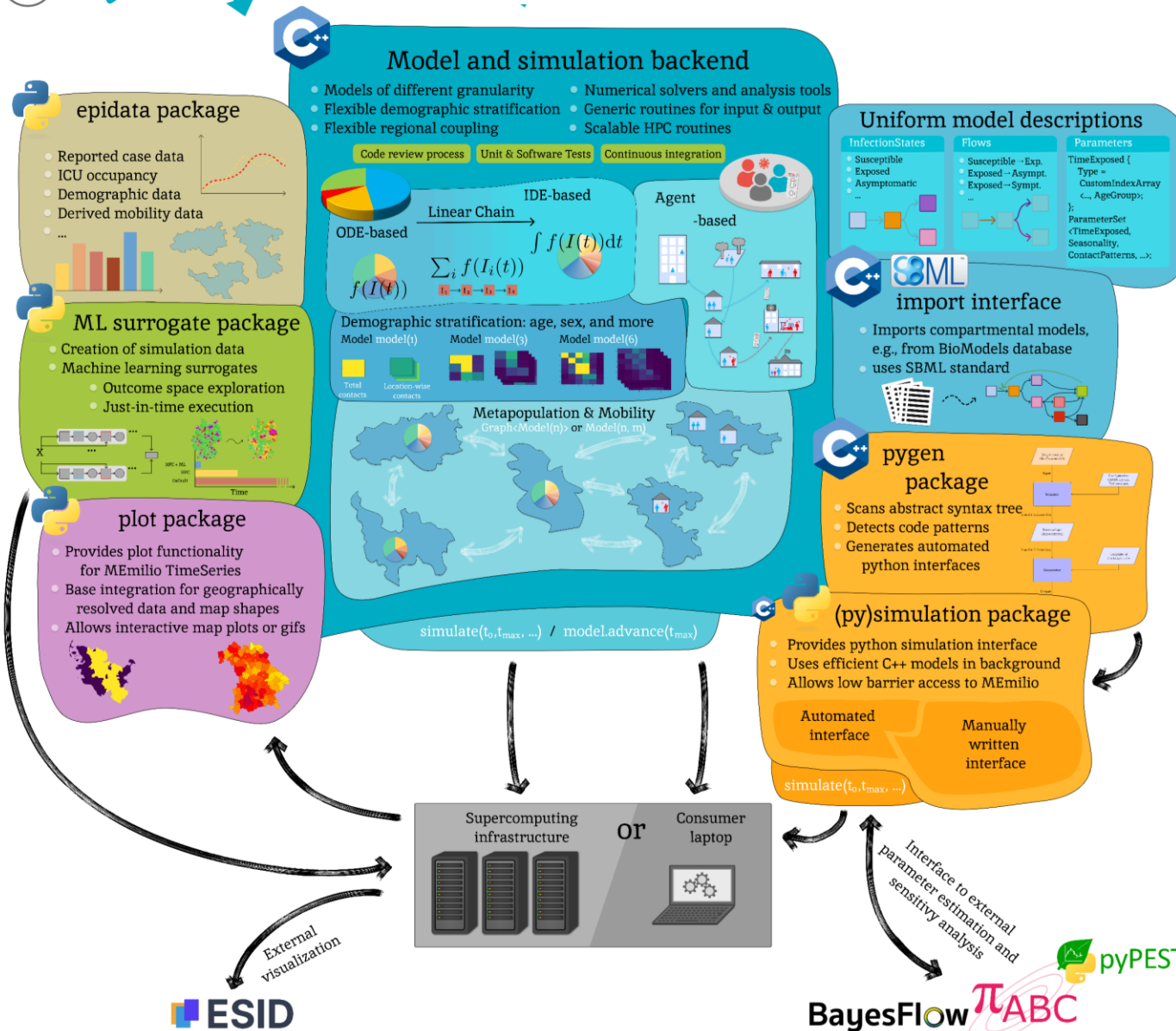
- Temporal-hybrid with threshold 2 is on average **41 times faster** (9 times for extinction runs and 49 times for survival runs)
- Temporal-hybrid with threshold 5 is on average **20 times faster** (8 times for extinction runs and 22 times for survival runs)

Model	All simulations		
	min	mean	max
<i>ABM</i>	41.80	331.76	1835.93
<i>PDMM</i>	0.00040	0.00047	0.01140
<i>Temporal-hybrid s = 2</i>	0.5587	8.4082	92.6604
<i>Temporal-hybrid s = 5</i>	0.5591	16.6405	104.497

Model	Extinction simulations			Survival simulations		
	min	mean	max	min	mean	max
<i>ABM</i>	41.80	48.77	109.147	91.07	442.20	1835.93
<i>PDMM</i>	-	-	-	0.00040	0.00047	0.01140
<i>Temporal-hybrid s = 2</i>	0.5587	5.4414	85.2773	0.8115	9.5341	92.6604
<i>Temporal-hybrid s = 5</i>	0.5591	6.2384	99.2354	2.9843	20.7604	104.497



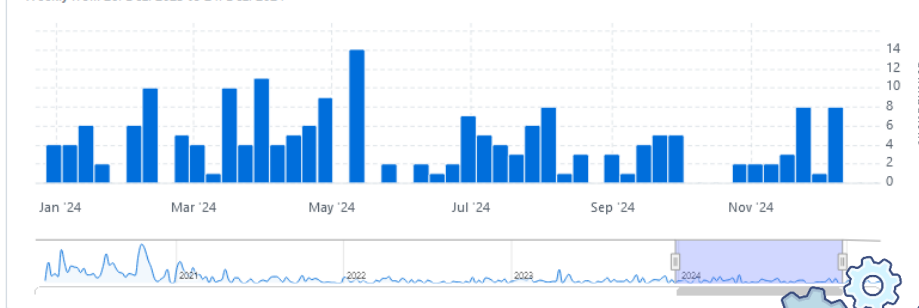
A high performance Modular EpiDeMics simuLatOn software



CI passing codecov 97%

Commits over time

Weekly from 26. Dez. 2023 to 24. Dez. 2024



Contributors

- 2024: 20
- Overall: 40



Activity (on main) August 2025

- 20 active pull requests (12 merged)
- 31 active issues (22 closed)
- 18 active authors

Software & Unit Tests

- C++: ca. 650 (2023: ca. 300)
- Python: ca. 230 (2023: ca. 200)

Thank you for your attention!



- **Paper:** Bicker et al., 2025, <https://doi.org/10.1016/j.idm.2024.12.015>



- Paper simulations: <https://github.com/reneSchm/memilio/releases/tag/hybrid-paper-v2>

- **MEMILIO** software framework: <https://github.com/SciCompMod/memilio>



GEFÖRDERT VOM



Bundesministerium
für Bildung
und Forschung

Gefördert durch:



Bundesministerium
für Digitales
und Verkehr



HELMHOLTZ

