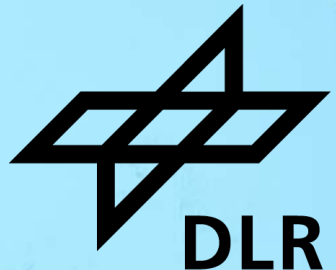


AN EXTENSION OF AGE-OF-INFECTION MODELS

A SECIR model based on integro-differential equations for epidemic outbreaks

Anna Wendler

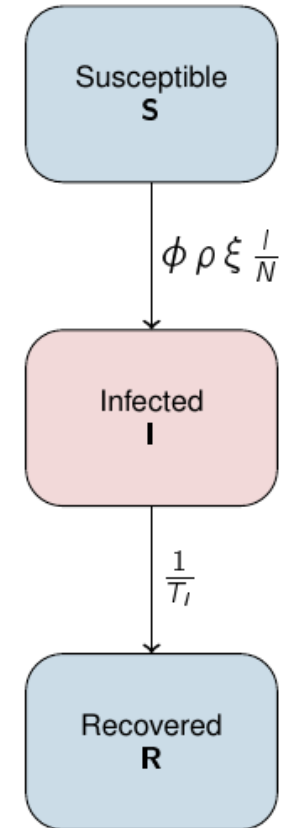
Joint work with Lena Plötzke, Hannah Tritschak and Martin J. Kühn



Ordinary-differential equation (ODE) based model

$$\begin{aligned}S'(t) &= -\frac{S(t)}{N} \phi(t) \rho(t) \xi(t) I(t) \\I'(t) &= \frac{S(t)}{N} \phi(t) \rho(t) \xi(t) I(t) - \frac{1}{T_I} I(t) \\R'(t) &= \frac{1}{T_I} I(t)\end{aligned}$$

$\phi(t)$	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
N	Total population



Motivation for age-of-infection models



- Simple ODE models assume exponentially distributed stay times
→ unrealistic assumption^{1,2}
- Choice of transition distributions impacts disease dynamics;
in particular at change points
 - Need for **flexible** choice of transition distributions
 - Linear Chain Trick allows Erlang distributed stay times³
 - For full flexibility: Model based on **integro-differential equations (IDE)**

¹ Wearing et al., Appropriate Models for the Management of Infectious Diseases, 2005. <https://doi.org/10.1371/journal.pmed.0020174>

² d'Onofrio, Mixed pulse vaccination strategy in epidemic model with realistically distributed infectious and latent times, 2004. [https://doi.org/10.1016/S0096-3003\(03\)00331-X](https://doi.org/10.1016/S0096-3003(03)00331-X)

³ Plötzke et al., Revisiting the Linear Chain Trick in epidemiological models: Implications of underlying assumptions for numerical solutions, 2025. <https://doi.org/10.1016/j.matcom.2025.07.045>

IDE-SIR model

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

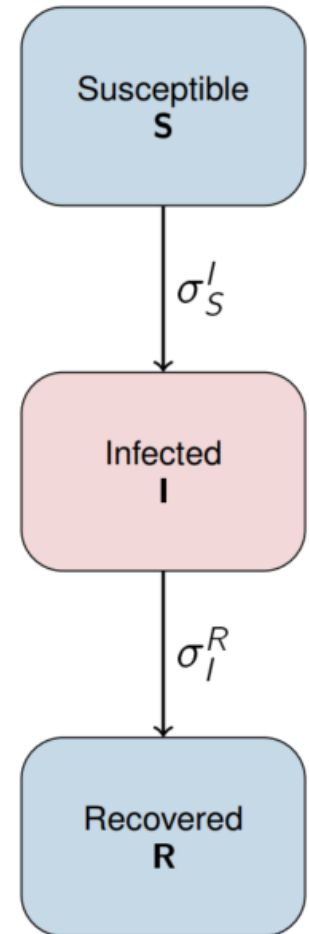
$\sigma_S^I(x)$	Number of individuals transitioning from S to I at time x
$\gamma_I^R(\tau)$	Mean proportion of individuals that are still infected at infection age τ
$\xi(\tau)$	Proportion of infected individuals that are not isolated at infection age τ
$\rho(\tau)$	Transmission probability at infection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

IDE-SIR model

$$S'(t) = -\frac{S(t)}{N} \phi(t) \int_{-\infty}^t \rho(t-x) \xi(t-x) \gamma_I^R(t-x) \sigma_S^I(x) dx$$

$$I(t) = \int_{-\infty}^t \gamma_I^R(t-x) \sigma_S^I(x) dx$$

$$R(t) = \int_{-\infty}^t (1 - \gamma_I^R(t-x)) \sigma_S^I(x) dx$$



IDE-SIR model

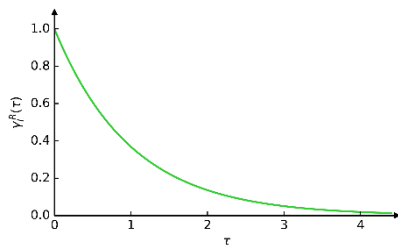
$$S'(t) = -\frac{S(t)}{N} \phi(t) \int_{-\infty}^t \rho(t-x) \xi(t-x) \gamma_I^R(t-x) \sigma_S^I(x) dx$$

$$I(t) = \int_{-\infty}^t \gamma_I^R(t-x) \sigma_S^I(x) dx$$

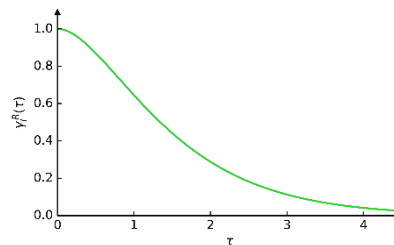
$$R(t) = \int_{-\infty}^t (1 - \gamma_I^R(t-x)) \sigma_S^I(x) dx$$

Flexible choice of transition distributions:

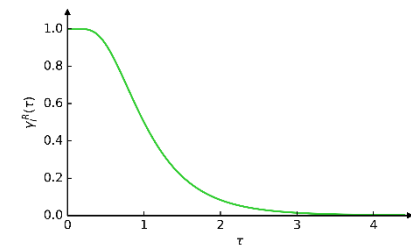
Exponential



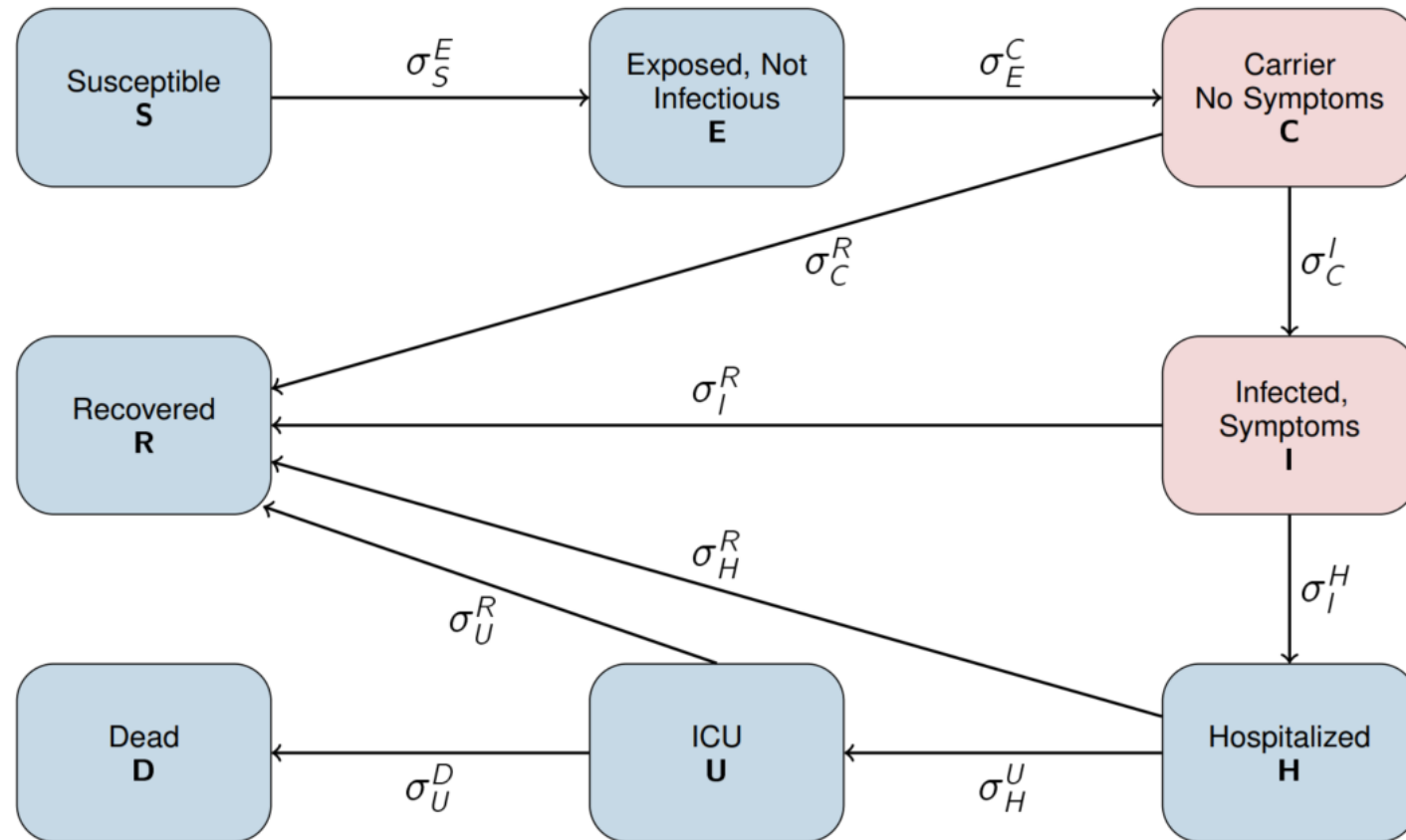
Gamma



Lognormal



Extension to IDE-SECIR model



Numerical scheme preserves biological properties



- Extension of nonstandard numerical scheme⁴ that preserves important biological properties:
 - Scheme is mass conserving

$$\hat{S}(t_n) + \hat{E}(t_n) + \hat{C}(t_n) + \hat{I}(t_n) + \hat{H}(t_n) + \hat{U}(t_n) + \hat{R}(t_n) + \hat{D}(t_n) = N.$$

- Susceptible compartment is monotonically decreasing and converges

$$\lim_{n \rightarrow \infty} \hat{S}(t_n) = \hat{S}_{\infty}(\Delta t).$$

- Recovered and Dead compartments are monotonically increasing and converge

$$\lim_{n \rightarrow \infty} \hat{R}(t_n) = \hat{R}_{\infty}(\Delta t), \quad \lim_{n \rightarrow \infty} \hat{D}(t_n) = \hat{D}_{\infty}(\Delta t).$$

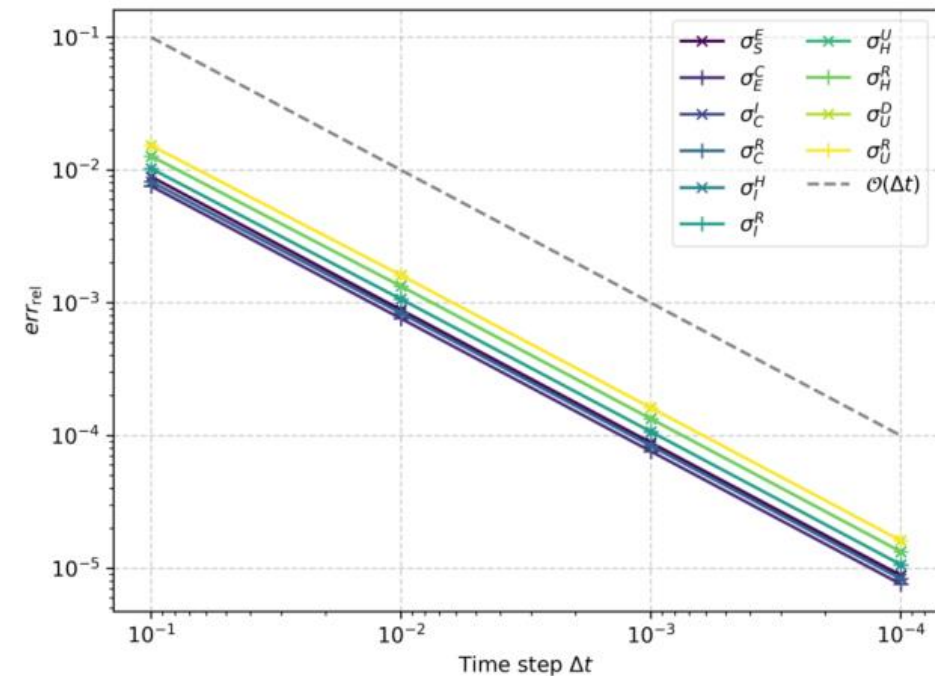
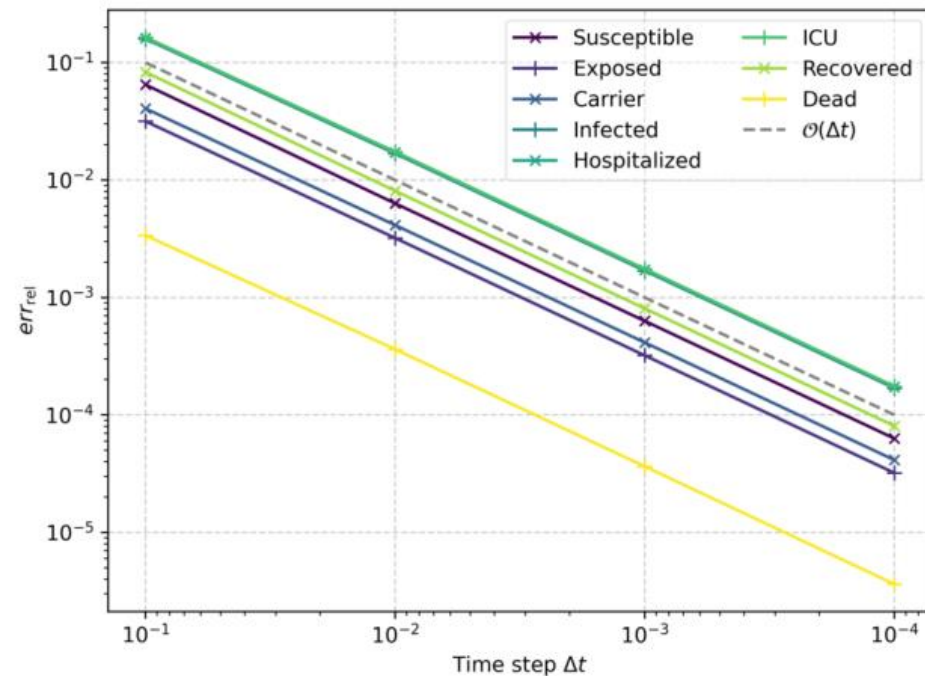
- Flows converge to zero

$$\lim_{n \rightarrow \infty} \hat{\sigma}_{z_1}^{z_2}(t_n) = 0.$$

⁴ Messina et al., A non-standard numerical scheme for an age-of-infection epidemic model, 2022. <https://doi.org/10.3934/jcd.2021029>

Nonstandard numerical scheme

- Linear convergence of solver:



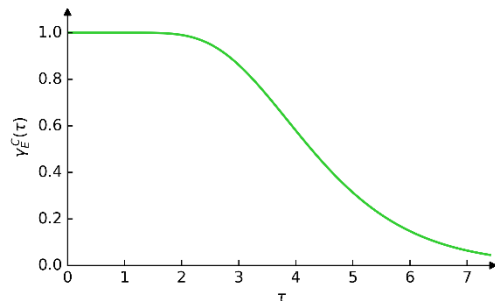
Current goal: Implement higher order solver

Numerical comparison of IDE and ODE models

Assess impact of distribution by comparing IDE-SEIR model with a corresponding ODE model:

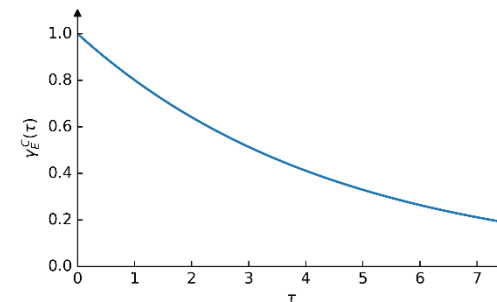
IDE model:

- Use **lognormal distributions** according to data on COVID-19⁵



ODE model:

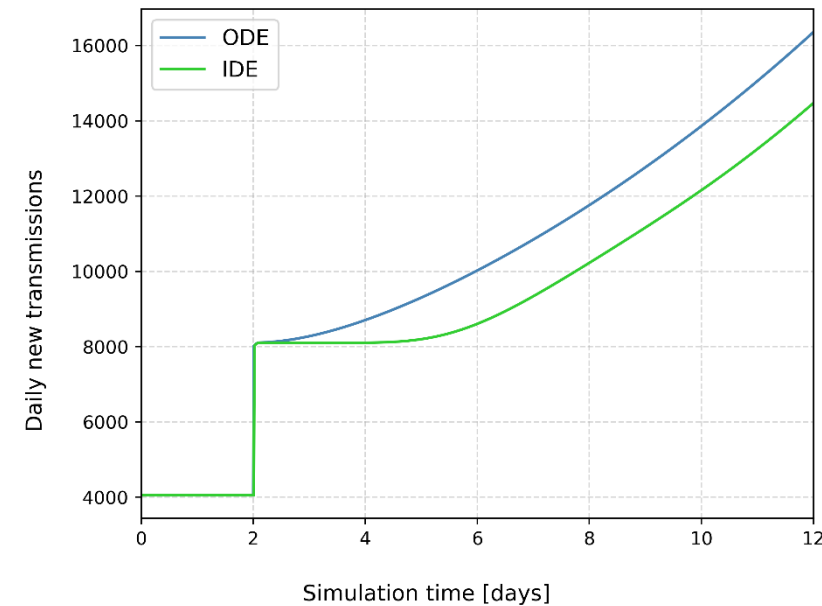
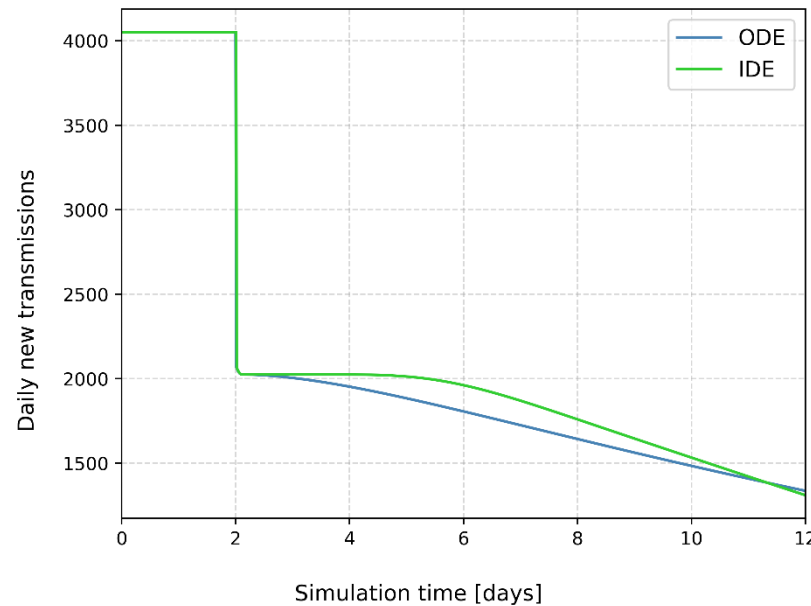
- Use **exponential distributions** with corresponding mean stay times



⁵ Kerr et al., Covasim: An agent-based model of COVID-19 dynamics and interventions, 2021. <https://doi.org/10.1371/journal.pcbi.1009149>

Behavior at change points

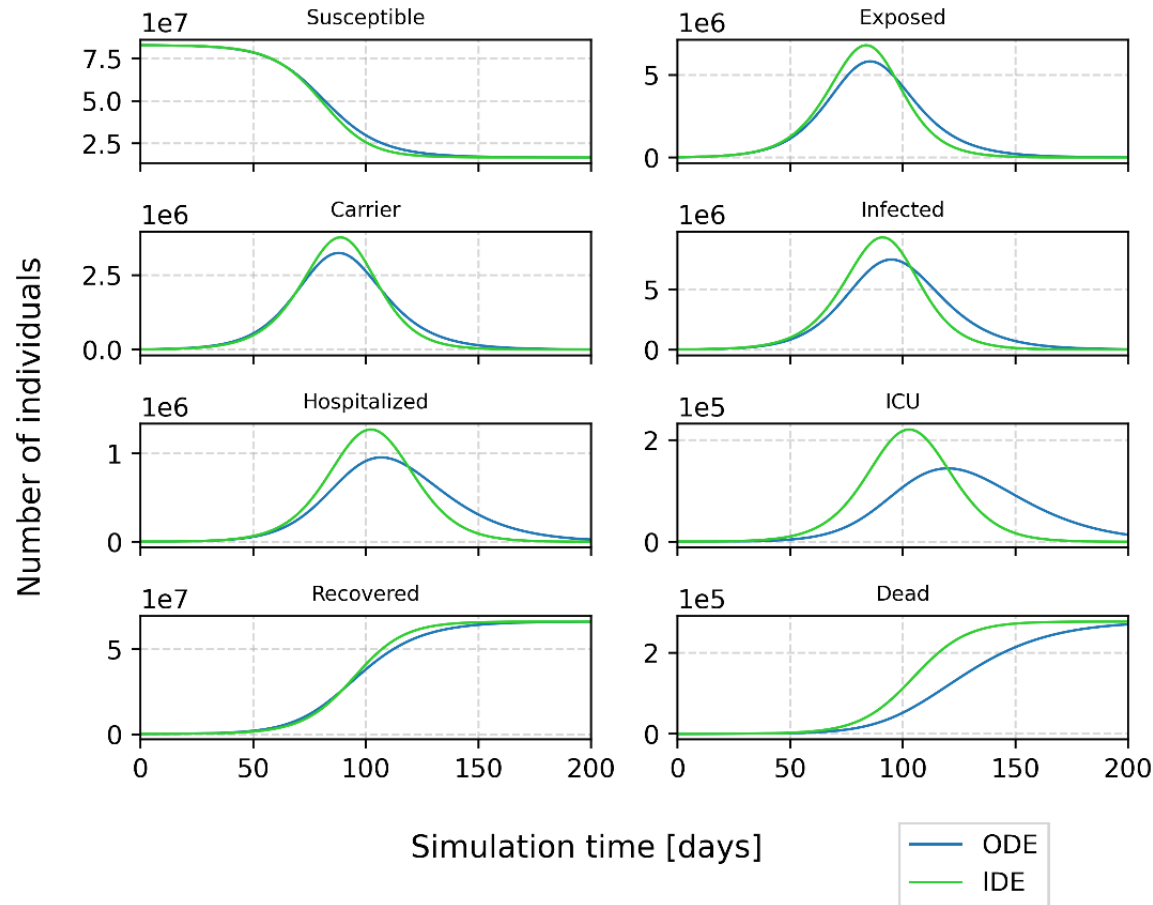
- IDE model reacts slower to change in contact rate than ODE model, in agreement with literature^{6,7}
- Important for timing of mitigation action



⁶ Dey et al., Lag time between state-level policy interventions and change points in COVID-19 outcomes in the United States, 2021. <https://doi.org/10.1016/j.patter.2021.100306>

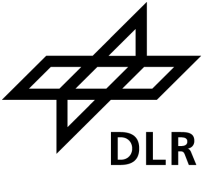
⁷ Guglielmi et al., Identification of time delays in COVID-19 data, 2023. <https://doi.org/10.1515/em-2022-0117>

Epidemic peak behavior

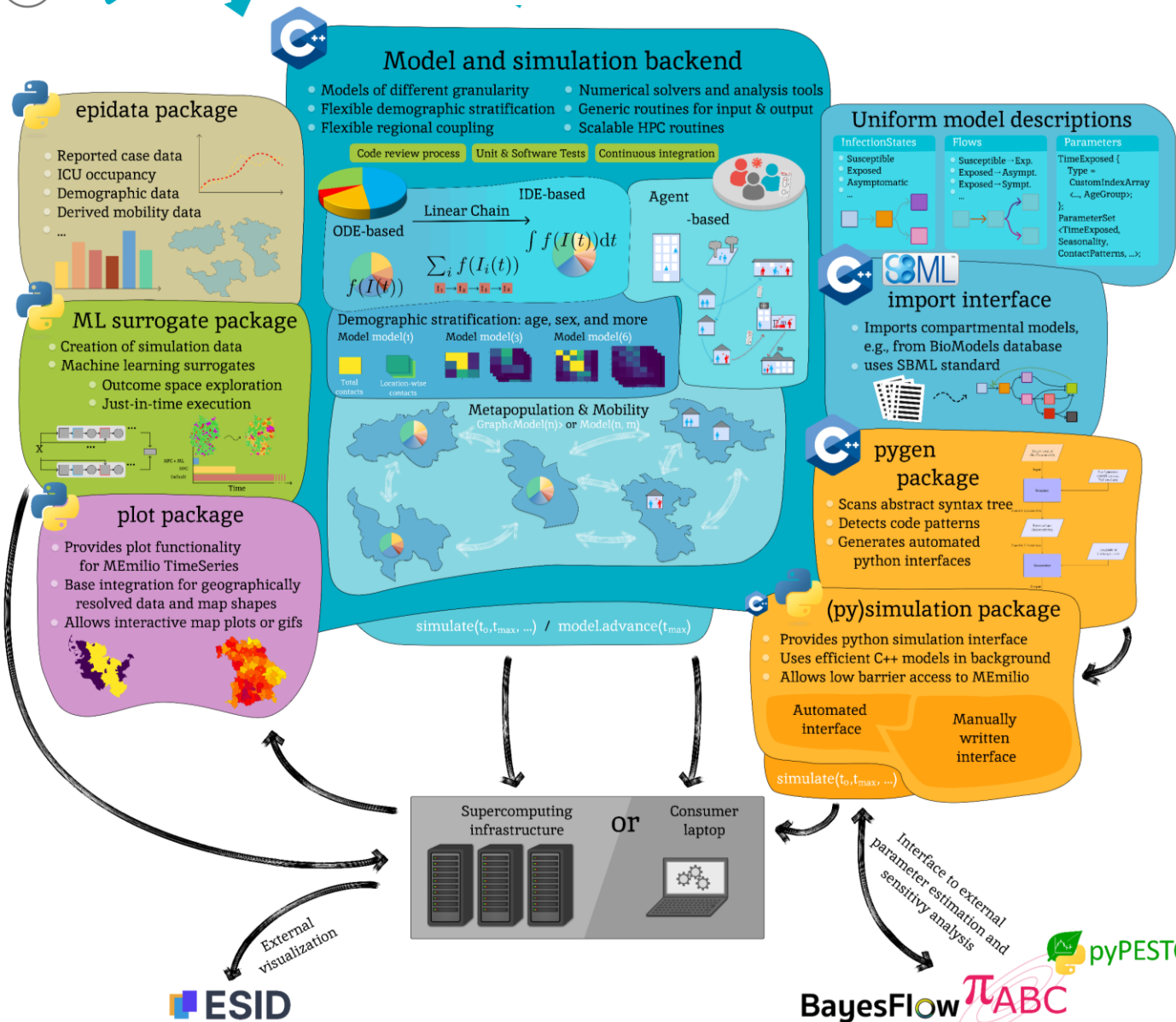


- Higher epidemic peak in IDE model
 - Different timings of peak
 - Same final size for both models
- Difference in required hospital and ICU capacities

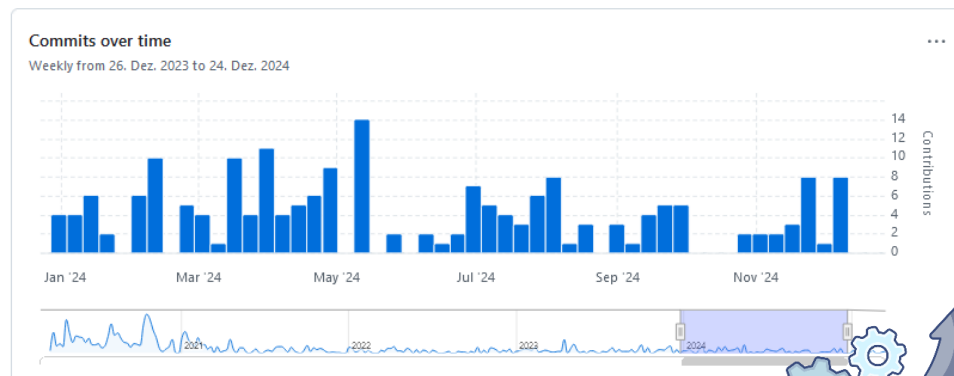
Conclusion



- Using IDE model allows flexible choice of transition distributions
- Extended solver that preserves important biological properties
- Choice of distributions has significant impact on disease dynamics, showing relevance of realistic assumptions



CI passing codecov 97%



Contributors

- 2024: 20
- Overall: 40

Activity (on main) August 2025

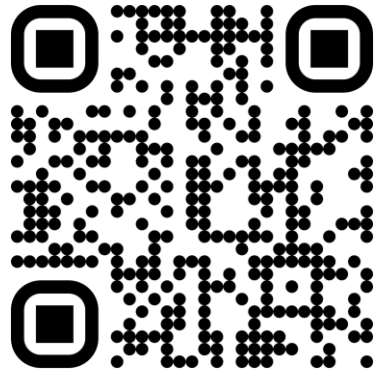
- 20 active pull requests (12 merged)
- 31 active issues (22 closed)
- 18 active authors

Software & Unit Tests

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



Paper



MEmilio



Thank you for your attention!