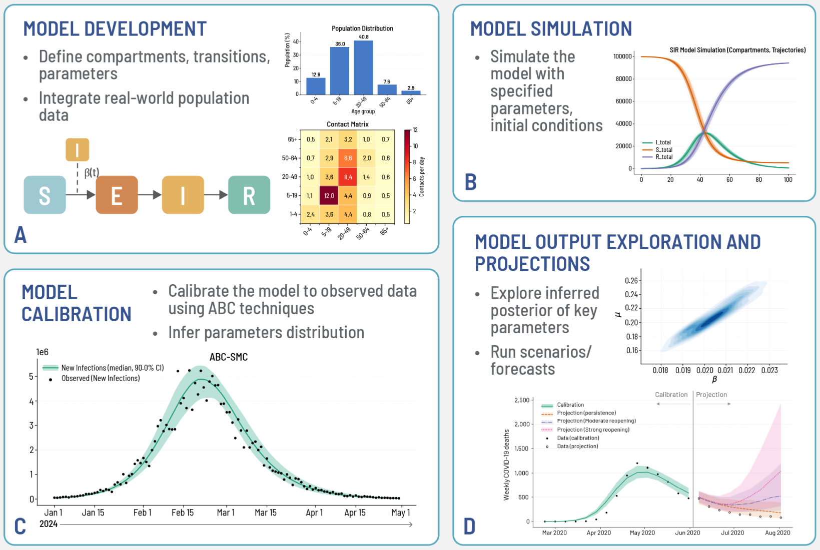
Activity in a Snapshot

Insight Net

Epydemix, the ABC of epidemics

Epydemix is designed to support users through the last mile of epidemic modeling. From model definition to calibration and scenario exploration. It allows users to build models with an arbitrary number of compartments and transitions, providing the flexibility to define custom transition rules, time-varying parameters, and the impact of interventions on both contact structures and disease parameters. The package supports classic models (e.g., SIR, SEIR) and enables custom modifications, including behavioral dynamics and intervention effects. It is built in Python and openly available, allowing the community to contribute and extend its capabilities. The project's GitHub page provides installation instructions, along with extensive documentation and a collection of tutorials to help users get started.



MODEL DEVELOPMENT

- Define compartments, transitions, parameters
- Integrate real-world population data

	0-4	5-19	20-49	50-64	65+
65+	0.5	2.1	3.2	1.0	0.7
50-64	0.7	2.9	6.6	2.0	0.6
20-49	1.0	3.6	8.4	1.4	0.6
5-19	1.1	12.0	4.4	0.9	0.5
1-4	2.4	3.6	4.4	0.8	0.5

MODEL SIMULATION

- Simulate the model with specified parameters, initial conditions

MODEL CALIBRATION

- Calibrate the model to observed data using ABC techniques
- Infer parameters distribution

MODEL OUTPUT EXPLORATION AND PROJECTIONS

- Explore inferred posterior of key parameters
- Run scenarios/ forecasts

Epydemix bridges epidemic modeling and real-world application by providing built-in ABC[2] calibration tools for fitting models to data, enabling parameter estimation, forecasting, and scenario analysis. It also supports calibration of external models with compatible structures. The platform offers built-in visualization tools to effectively communicate model dynamics and parameter estimates, supporting clearer interpretation and results sharing. As an open-source project, it is continuously developed with input from the modeling community and public health stakeholders to remain relevant and practical.

1. Gozzi N., Chinazzi M., Davis J.T., Gioannini C., Rossi L., Ajelli M., Perra N., Vespignani A., Epydemix: An open-source Python package for epidemic modeling with integrated approximate Bayesian calibration, medRxiv 2025.05.07.25327151

2. Minter A., Retkute R., Approximate Bayesian Computation for infectious disease modelling, Epidemics, Volume 29, 2019, 100368

What's new

Flexible epidemic modeling: epydemix is an open source Python package allowing users to build, simulate, and analyze stochastic compartmental epidemic models with real-world population structures and interventions.

Built-in Approximate Bayesian Computation (ABC) calibration: epydemix supports rejection, simulation-budget- constrained rejection, and Sequential Monte Carlo (ABC-SMC) for model fitting, parameter estimation, and scenario exploration.

Integration with population data: epydemix enables the use of global demographic and contact matrix datasets to create realistic epidemic simulations.

Key takeaways

- Epydemix provides a general, modular framework for simulating stochastic compartmental epidemic models.
- It supports parameter estimation and scenario analysis using Approximate Bayesian Computation (ABC).
- It integrates demographic and contact data for more realistic, data-driven simulations.
- It is open-source and reproducible, promoting transparency and methodological innovation in epidemic modeling.

Public health relevance

Epydemix supports public health decision-making by providing an accessible software tool for epidemic modeling and calibration. It enables researchers and policymakers to assess outbreak dynamics, test intervention strategies, and forecast disease spread using real-world data[1].

EPISTORM

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