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A Paradigm for Modelling Infectious Diseases

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***Prof. Egils Ginters** is Full time Professor at the Riga Technical University and Corresponding Member of the Latvian Academy of Sciences. He is fellow of the European Academy of Industrial Management and Senior member of Institute of Electrical and Electronics Engineers (IEEE). The main research directions involve sociotechnical systems modelling and simulation, digital technologies sustainability research and risks assessment. Hirsh index by Scopus is 22 (2025).*

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Actuality

- The Independent IT-Security Institute records more than ***450,000 new malware cases per day***. By the end of August 2024, the number of ***newly registered malware*** instances had reached ***73 million***. ***How to describe and forecast malware spread?***

- Is the spread of malware in the digital environment ***similar to the spread of infections in populations?*** **Yes**, but it is ***simpler*** and much more ***faster.***

- There is no need to reinvent the wheel — ***existing epidemiological models should be used.***

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Aim

- Conduct a ***comparative analysis of existing epidemiological models*** and assess their applicability in the early phases of infection spread.

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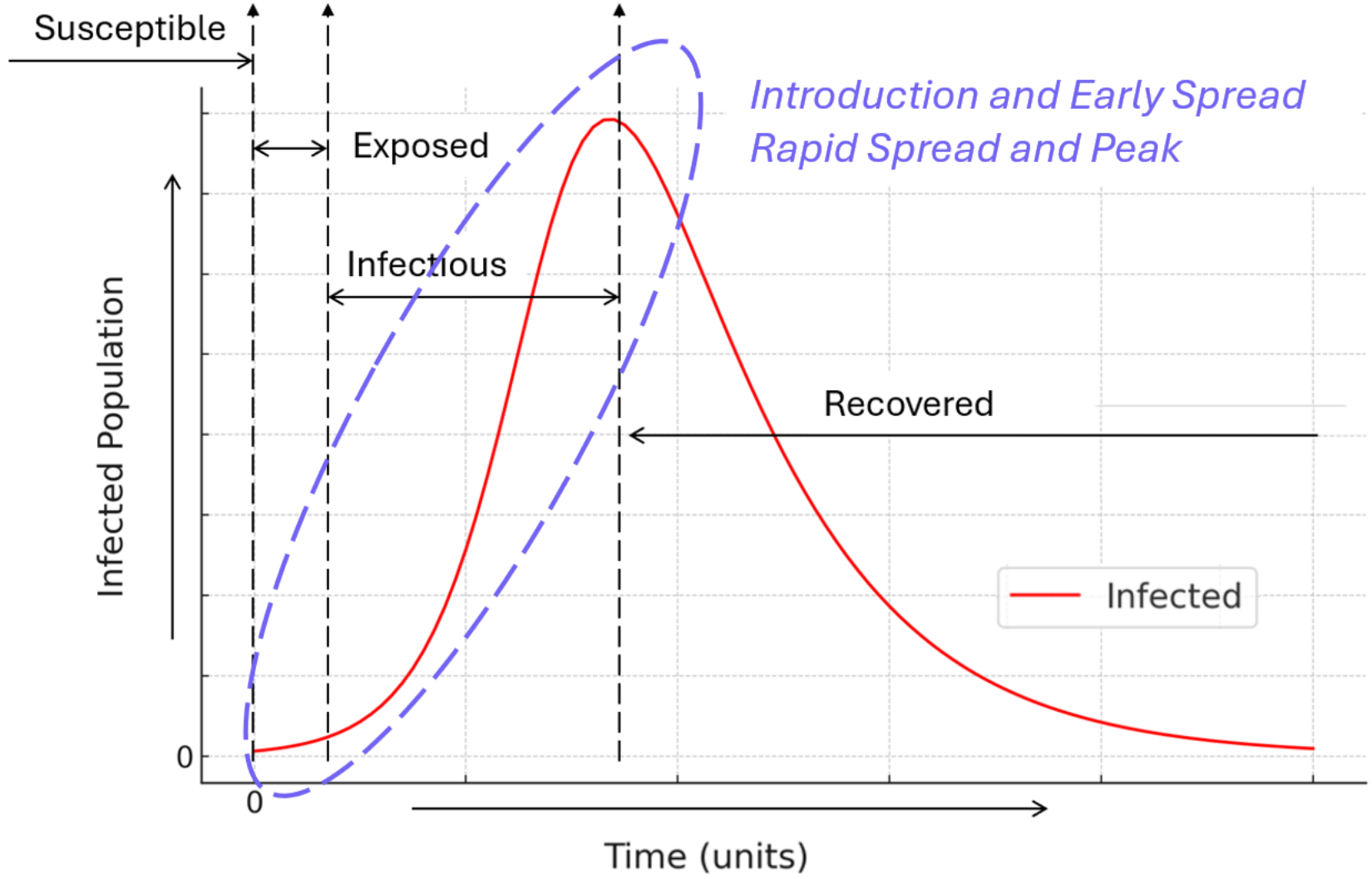
Epidemiological modelling timeline



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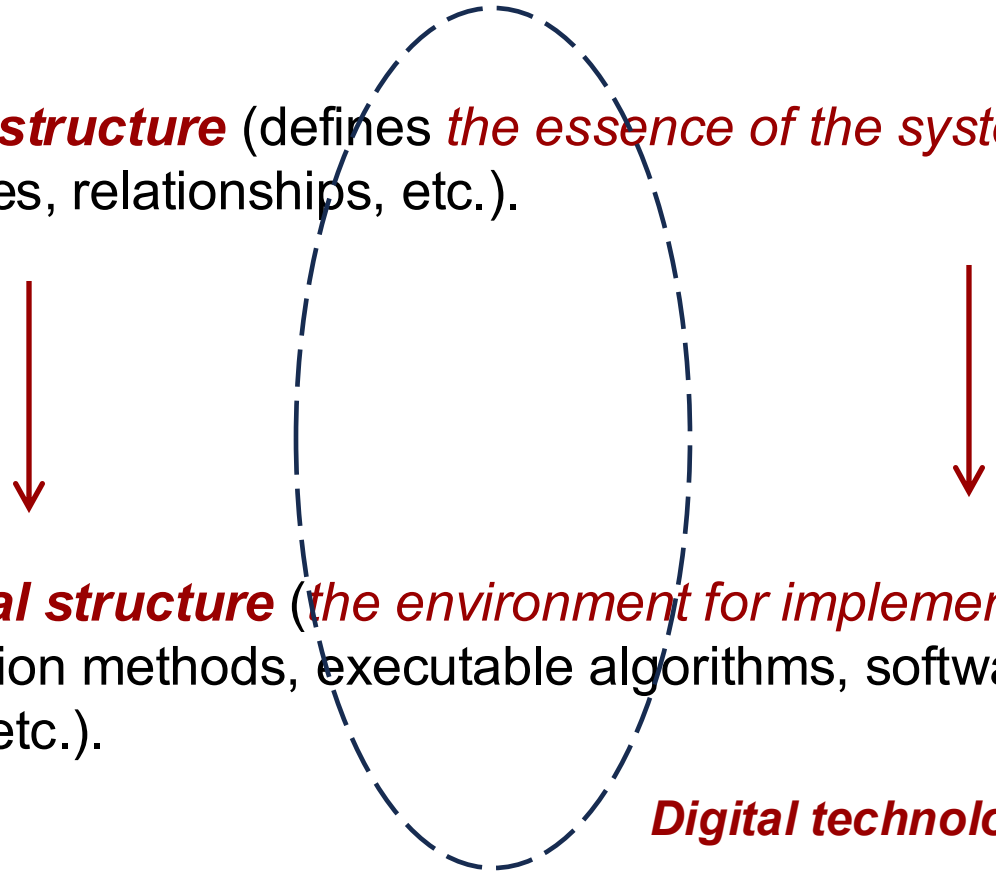
Epidemiological forecasting is an application of digital technology within a sociotechnical system

- **Soul:** ***Logical structure*** (defines *the essence of the system*: principles, laws, regularities, relationships, etc.).



- **Body:** ***Physical structure*** (*the environment for implementing the logical structure*: solution methods, executable algorithms, software, technical infrastructure, etc.).

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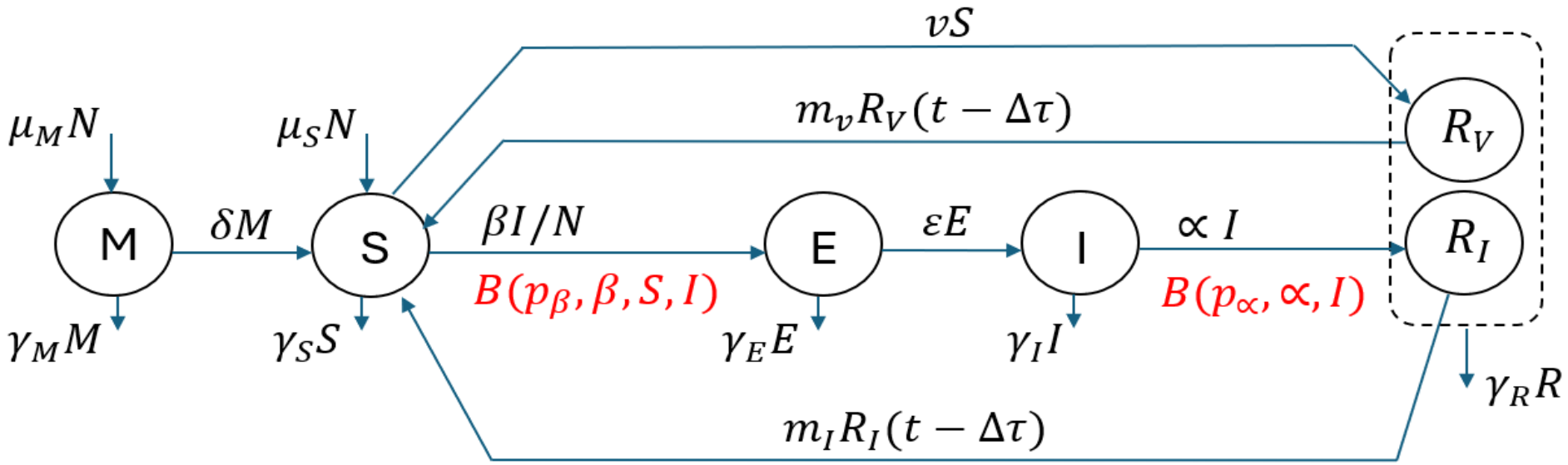
Logical structure: *pMSEIR* model



Compartments: ***M-Immune*** (w/innate or vaccination-acquired immunity), ***S-Susceptible*** (general population), ***E-Exposed*** (on the frequency of contact and the contagiousness of the infection), ***I-Infectious*** (with or w/o visible symptoms the individual becomes infectious), ***R-Recovered*** (no longer infectious)

Hethcote, H. W. (2000). The mathematics of infectious diseases. *SIAM Review, 42*(4), 599–653. https://doi.org/10.1137/S0036144500371907

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Logical structure: Basic models

- ***Classic SIR:*** Assumes a ***homogeneous*** and ***constant size*** population.
- ***SEIR:*** A classic SIR model with a ***latent period*** (E-compartment) added.
- ***SIS:*** Focuses on recurrent infection dynamics ***without a R-compartment***.

Features added:

- ***w/vital dynamics:*** respect **demographic changes** (births and deaths) and mobility.
- ***w/vaccination and mutations:*** incorporates ***limited immunity*** and the potential for recurrent infections.

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Physical structure: Implementation

- ***Planar vs Spatial***
  - The variation of a single-argument function values over time
  - *Model w/diffusion* to represent the density of compartments
  - Multi-level hierarchical and spatial representation

- ***Deterministic vs Stochastic***
  - Each subsequent result is determined by the previous one.
  - Deterministic model with added noise to introduce randomness and/or with probabilistic transitions between compartments

- ***Analytical vs Simulation***
  - Differential equations ODE or PDE
  - Graph theory and ABM simulation technologies

mathematics

MDPI

Article

A Paradigm for Modeling Infectious Diseases: Assessing Malware Spread in Early-Stage Outbreaks

Egils Ginters [1,*], Uga Dumpis [2], Laura Calvet Liñán [3], Miquel Angel Piera Eroles [3], Kawa Nazemi [4], Andrejs Matvejevs [5] and Mario Arturo Ruiz Estrada [6]

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Ginters, E., Dumpis, U., Liñán, L. C., Eroles, M. A. P., Nazemi, K., Matvejevs, A., & Estrada, M. A. R. (2025). A Paradigm for Modeling Infectious Diseases: Assessing Malware Spread in Early-Stage Outbreaks. *Mathematics*, *13*(1), 91. https://doi.org/10.3390/math13010091

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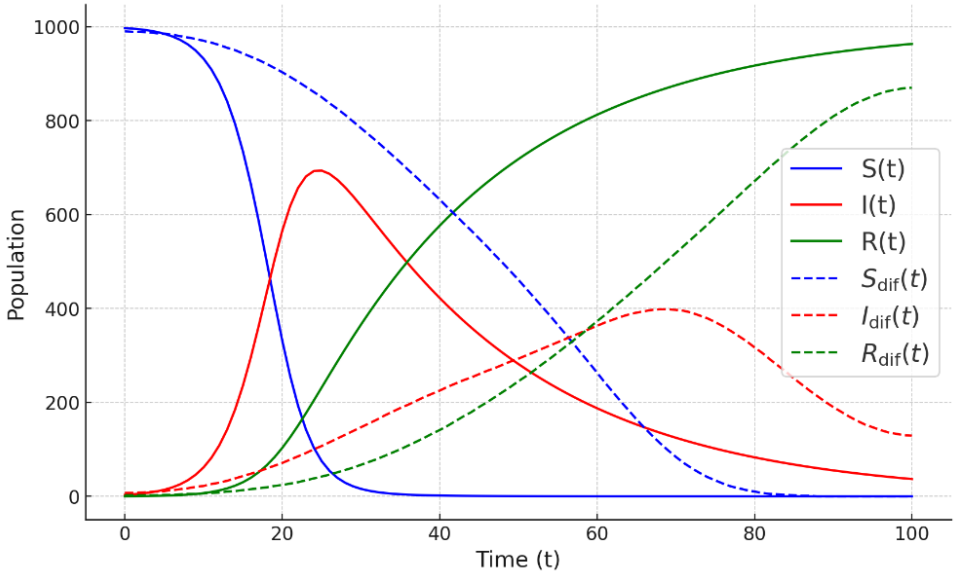
Research workflow

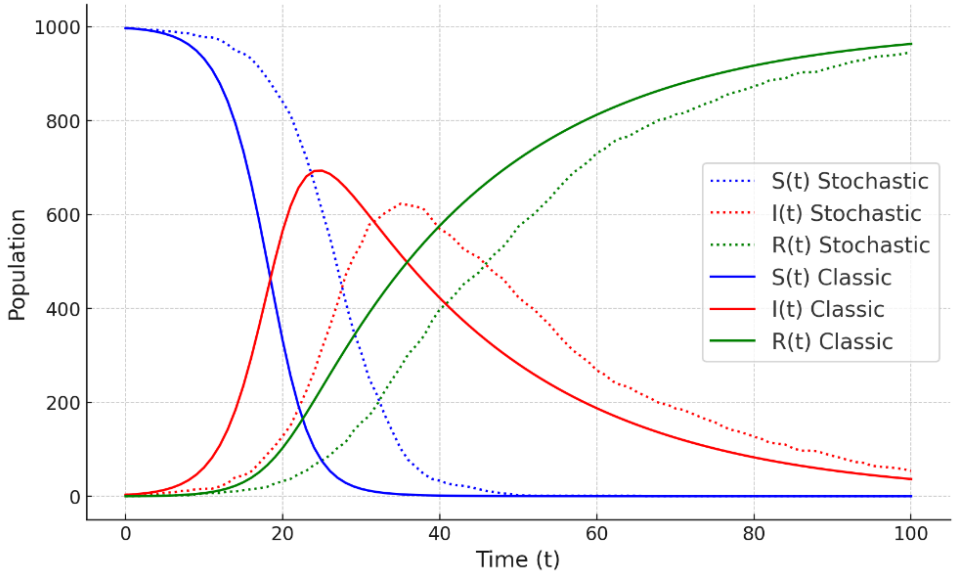
- ***The applicability*** of the above-mentioned models ***was evaluated*** based on an analysis of 100 information sources.
- To support the verifiability and comparability of calculations, a ***benchmark example*** was defined based on all available data from Wikipedia.
- Based on considerations of logical and physical structure, ***a set of the most used epidemiological models*** was identified and ***tested*** using a benchmark case.

The features assessed

- ***Scalability and Homogeneity*** - ability to specify infection spread across populations of varying scales.
- ***Robustness and Reliability*** - sensitivity to parameter changes and the volume of computational operations.
- ***Complexity and Workload*** - complexity of the algorithms, which dictates the computational resources needed and the effort required for model development.
- ***Transparency and Manageability*** - how easy the model's structure and logic can be understood, verified and adjusted; and how its results can be visualized and unambiguously interpreted.
- ***Aggregation*** - indicates whether the model describes only overall changes within each compartment or can also be used to track changes in everyone's state.

SIR modelling





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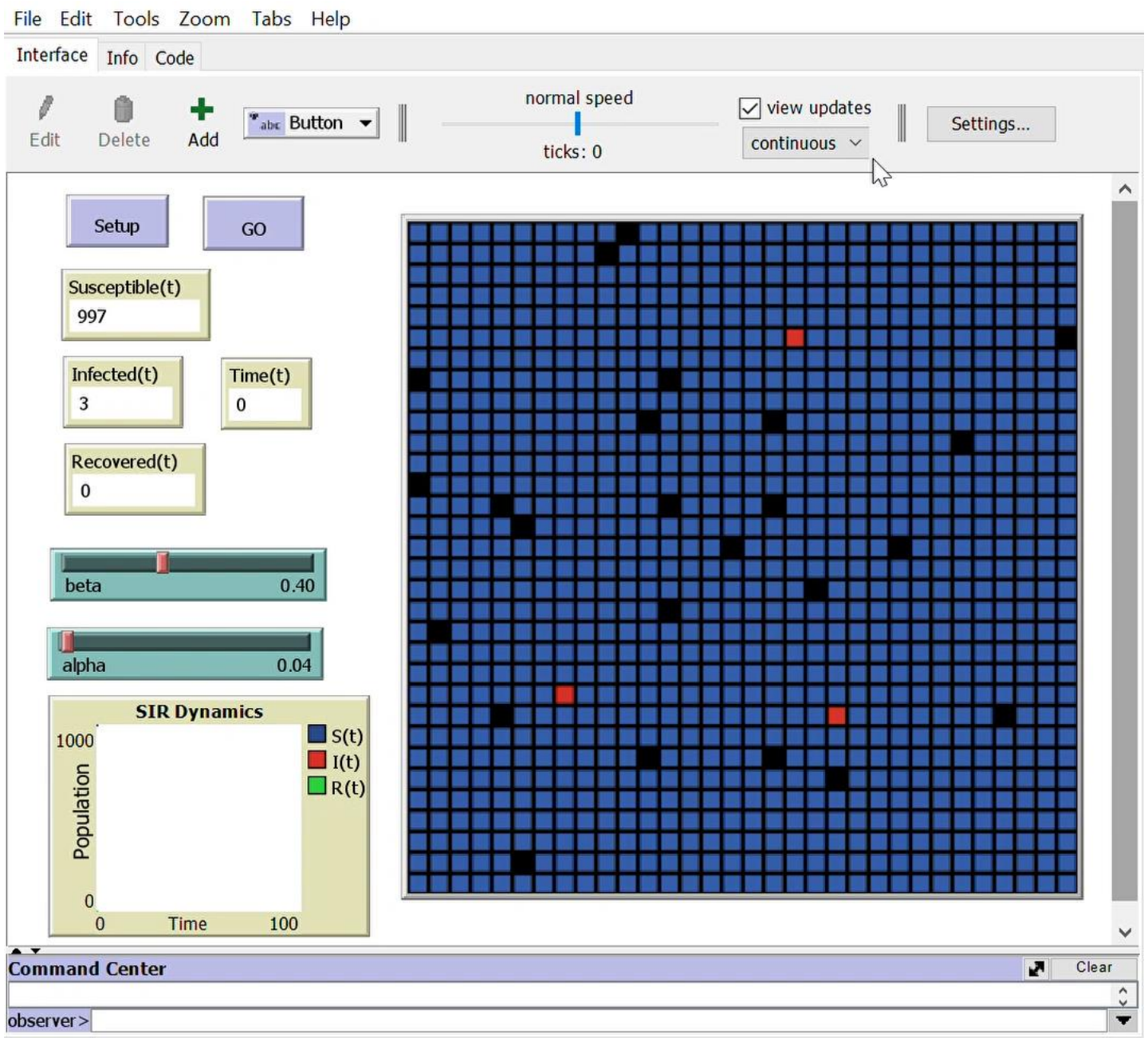
ABM SIR Model



Ginters, E. (2024). *SIR agent-based model without demographics in the NetLogo environment*. Zenodo. https://doi.org/10.5281/zenodo.13940933

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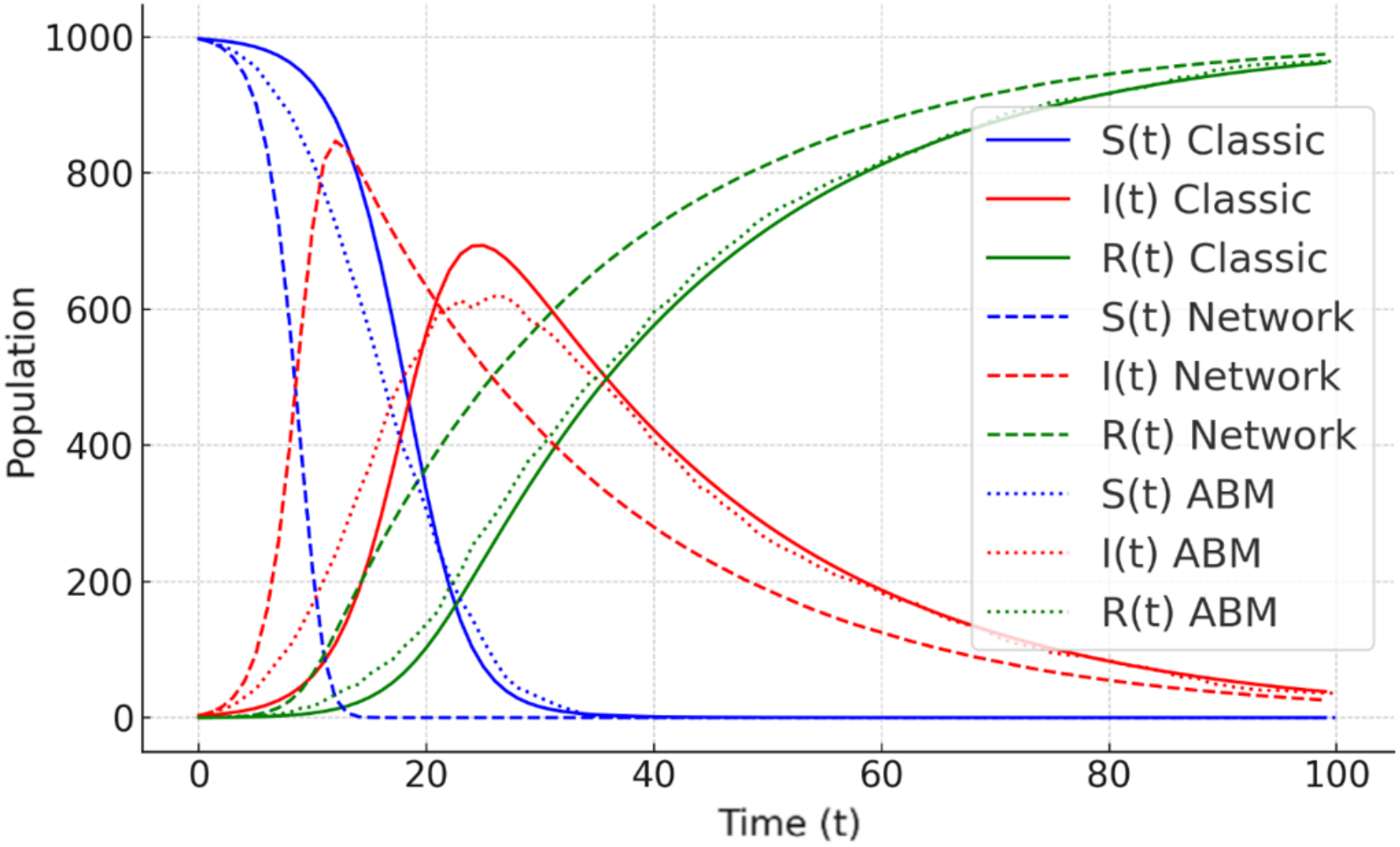
SIR modelling by ABM approach



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Conclusion

A diverse range of experience has been accumulated in infection spread modelling, and there is a ***broad spectrum of available models***. However, the conditions for applying each model are ***often insufficiently substantiated***.

In ***early outbreaks***, ***deterministic*** ODE-based ***SIR model*** offer a simple way to estimate system-wide trends with minimal computation. They support rapid assessments, which is critical when speed matters more than precision.

As more ***data becomes available***, enhanced model, such as the ***SEIR*** with vaccination and mutation extensions, offer a refined approach. These models incorporate the latent period, mutation effects, and temporary immunity.

For ***detailed analysis***, network models like ***stochastic ABM*** simulates individual agents with diverse traits, helping identify super-spreaders or critical nodes for intervention. ABMs also replace classic SIR equations with simulations, capturing both ***compartment dynamics and individual states***.

Thanks for listening — I’m happy to take any questions!