

DEMOCRATIZING DESIGN AND IMPLEMENTATION OF AGENT-BASED MODELING IN BIOMEDICINE

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In biomedicine, we find many examples of complex systems characterized by a large number of interacting components without central coordination. These systems exhibit emergent properties and adaptation over time, giving rise to complex behavior.

Agent-based models (ABMs) are one of the most powerful approaches for studying complex systems, represented as a collection of individual agents with well-defined behaviors and rules of interactions.

Implementing an ABM typically requires proficiency in programming languages, which can be a significant barrier for researchers without formal programming experience. Since the role of domain experts is critical in the development of ABM, a possible solution to facilitate the creation of ABMs is to provide a platform that enables domain experts such as biomedical researchers to construct their own models.

To study how ABMs are developed and used in biomedicine, we conducted a literature review and built two novel ABMs in NetLogo: one for viral propagation and another for adaptive cancer therapy. Finally, we developed **BOAST-ABM**, a platform that enables model creation by specifying agents and their behaviors in structured YAML-based specification documents that are then translated into executable Python code using abstract syntax

trees (ASTs). Both NetLogo models—viral propagation and adaptive therapy—were reimplemented in **BOAST-ABM**, yielding the same large-scale trends as the original simulations and demonstrating the platform’s viability.

Collectively, this dissertation lays the foundation for democratizing the design and implementation of ABMs in biomedicine. The primary outcome is a platform that enables the generation of ABMs directly from structured specifications. In addition, the specifications proposed in this study can serve as a standard to facilitate the exchange, transparency, and reproducibility of ABMs.