Introduction to Agent Based Models

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5/21/25

Schelling Segregation Model

"Dynamic Models of Segregation" by Thomas Schelling, 1971

- Models the world as a grid where each cell is a house
- Houses are occupied by blue and red agents
- Agents are "happy" or "unhappy" based on the other agents in their neighborhood: the 8 neighboring cells
  - Happy: at least ____% of neighbors are like themselves
  - Unhappy: otherwise
- Every time step, if an agent is unhappy, it moves to an unoccupied cell

Schelling Segregation Model

https://ric-colasanti.github.io/PyHASE/Schelling/Schelling.html

Change the % alike and population density sliders and run to observe model behaviors

Look for at least two combinations that produce different behavior

Emergent Model Behaviors

High Population Density

- <25%: no movement or segregation
- 30-40%: segregation in small groups
- 40-60%: segregation in large groups
- >75%: constant movement, no segregation

Low Population Density

- Similar behavior with different thresholds
- Aggregation

What are Agent Based Models?

Models based on simulating each individual unit (i.e. agent) in a system

- Examples of agents include organisms, genes, cells, consumers, cars, etc.

Explicitly represents agents in space and context

- Schelling ex: space = grid location, context = red or blue

Define rules for agent actions

- Often space- and/or context-dependent
- Typically based on local or network dependent information/interactions

What are ABMs good for?

- Modeling non-equilibrium dynamics
- Studying how individual actions and interactions lead to emergent patterns on the system level
- Exploring heterogeneity
- Spatial models
- Non-independence of individuals

What are challenges/limitations of ABMs?

Complexity: can be computationally intensive and complex to develop/validate

Assumptions: accuracy and meaning of model is dependent on assumptions

Scalability: can be difficult to scale to large/complex systems

Analysis: can be challenging to understand, classify and anlyze results from stochastic simulations

ABM Software

Covasim by

NetLogo
https://www.netlogoweb.org/
programmable modeling environment primarily used for simulating natural and social phenomena, particularly complex systems that evolve over time

PhysiCell
https://physicell.org/
physics-based multicellular simulation framework used to model complex biological systems, particularly in the context of tissue and cell behavior

Covasim
https://www.idmod.org/tool/covasim/
stochastic agent-based simulator designed to be used for COVID-19 epidemic analyses

and many more…

OR
Build your own!

SIRS Model in MatLab

Chapter 6.2 of James P. Keener's *Biology in Time and Space: A Partial Differential Equation Modeling Approach*

Susceptible – Infected – Recovered – Susceptible Disease Model

Agents are individuals in a population in state S, I, or R

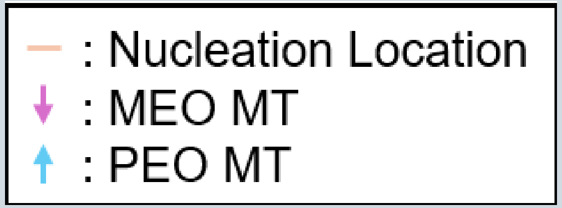
Agents are confined to a 2D domain and move over time through diffusion

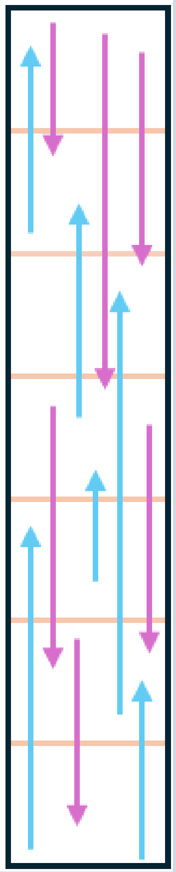
Agents transition from S to I based on local interactions with other infected agents

Agents transition from I to R or R to S based on probabilistic rates

ABMs in my research

Mechanisms of Microtubule Polarity Regulation in Neurons





Agents are microtubules (MTs)

MTs are either minus-end-out (MEO) or plus-end-out (PEO)

Separate model regulates their growth and shrinking dynamics

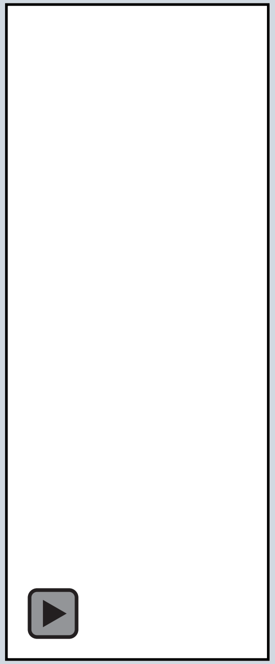
When MTs die, they are renucleated at a randomly selected nucleation location

Information from local MTs determines whether new MTs nucleate as MEO or PEO

We are interested in understanding biased polarity establishment and maintenance over time

Example Simulations

- Local mechanisms are sufficient to produce emergent global polarity behavior
- Building your own ABM allowed you to parameterize from real data and understand role of biologically observed mechanisms



Resources

Chapter 10: *Think Complexity* by Allen B. Downey

Population Health Agent-based Simulation nEtwork (PHASE) case studies

Chapter 6: *Biology in Time and Space* by James P. Keener

An Introduction to Agent-Based Modeling by Uri Wilensky and William Rand

NetLogo: https://www.netlogoweb.org/

PhysiCell: https://physicell.org/

Covasim: https://www.idmod.org/tool/covasim/

Cytosim: https://gitlab.com/f-nedelec/cytosim