# **Computational Sociology**

**Agent-based modeling** 

Dr. Thomas Davidson

Rutgers University

April 26, 2021

### **Plan**

- 1. Course updates
- 2. What is agent-based modeling?
- 3. NetLogo and NetLogo Web
- 4. How to construct a simple ABM using R
- 5. The future of agent-based modeling

## **Course updates**

#### **Presentations**

- In-class presentations next Monday
- ► Link to Google Slides posted in Slack
  - Add your slides in alphabetical order
  - See example at the beginning
    - Feel free to customize your slides as much as you want

## **Course updates**

### Deadlines (according to the syllabus)

- ► Homework 4 due today at 4pm
- ▶ Preliminary analyses due next Monday, 5/3
- ► Final paper due 5/10

## **Course updates**

#### **Actual** deadlines

- ightharpoonup Ensure to have your presentation ready before class on 5/3
- ightharpoonup Submit all outstanding homework and the final paper by 5pm on 5/10

### Agent-based modeling and quantitative social science

- Most quantitative social science is variable-centered
  - e.g. We study the associations and interactions between variables in a linear regression

### Agent-based modeling and quantitative social science

- As a consequence, many sociologists think about the world in terms of what Andrew Abbott calls "general linear reality"
  - ▶ A social world composed of fixed entities with fixed attributes

### Agent-based modeling and quantitative social science

- Agent-based modeling is the study of "social life as interactions among adaptive agents who influence one another in response to the influence they receive." (Macy and Willer 2002)
  - ► Rather than interactions between variables, we consider interactions between interdependent individuals

Computational Sociology

### Agent-based modeling and quantitative social science

- Often we are interested in the emergent properties of local interactions between agents and how they aggregate into system-level processes such as diffusion, polarization, and segregation
  - ► These complex system-level patterns can emerge without any centralized coordination
- ► Like historical sociology and ethnography, agent-based modeling is a *relational* approach, focusing on the context-dependent and contingent nature of social interaction

### **Key assumptions**

- Macy and Willer 2002 outline four key assumptions that underpin many sociological agent-based models
  - Agents are autonomous
    - There is no system-wide coordination
  - Agents are interdependent
    - Agents respond to each other and to their environment
  - Agents follow simple rules
    - Simple local rules can generate global complexity
  - Agents are adaptive and backwards looking
    - Agents can alter their behavior through processes such as imitation and learning

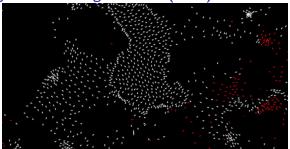
Computational Sociology

### **Advantages of ABMs**

- Virtual experiments to test causal mechanisms
  - Particularly useful where real-world experimentation is impractical
- Theory building and testing
  - Bridging between micro and macro levels of analysis
  - ► Varying the social structure *and* the agency of individuals

Computational Sociology

Craig Reynolds Flocking behavior (1987)



Reynolds, Craig W. 1987. "Flocks, Herds and Schools: A Distributed Behavioral Model." In *Proceedings of the* 14th Annual Conference on Computer Graphics and Interactive Techniques, 25–34.

### Thomas Schelling Homophily and segregation

DYNAMIC MODELS OF SEGREGATION

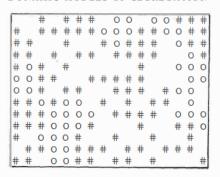
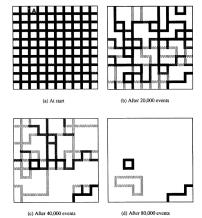


Fig. 13

Schelling, Thomas C. 1971. "Dynamic Models of Segregation." Journal of Mathematical Sociology 1: 143-86.

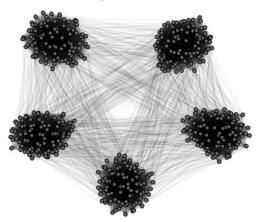
Robert Axelrod *Local convergence and global polarization* (1987)



Axelrod, Robert. 1997. "The Dissemination of Culture: A Model with Local Convergence and Global Polarization." Journal of Conflict Resolution 41 (2): 203–26.

### **Testing mechanisms**

DellaPosta, Shi, and Macy (2015) suggest a mechanism to explain observed correlations between political attitudes and lifestyle choices



#### **Evaluating competing explanations**

Goldberg and Stein (2018) propose an alternative mechanism, arguing that culture does not spread like a virus, but depends on belief structures

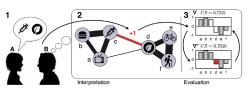


Figure 3. An Illustration of the Agent-Based Model Sequence
Note: (1) Agent B observes A express support for vaccinations and organic food (practices c and d); (2) B updates the corresponding element in his associative matrix, B (the edge connecting nodes c and din the network representation of B); and (3) randomly updates his preference for organic food (practice d, resulting in preference vector V), which is the weaker preference of the pair (c,d) in his preference
vector V. Because constraint satisfaction is reduced from .7221 to .7010, this preference update is
rejected, and Bs preference vector V remains unchanged.

### Integrating real-world data

DiMaggio and Garip (2011) construct agent with attributes based on the General Social Survey

Network Externalities, Intergroup Inequality

 ${\bf TABLE~2}$  Linear Regression of Adoption Levels on Experimental Conditions

		RACE		INCOME		Education	
	ALL	Whites	Blacks	High	Low	BA	Less than High School
No network exter-							
nalities	516**	536***	399°°	685	238°°	611**	351°°
General network ex-							
ternalities				.032***	.017**	.023**	.030**
Homophily = .25	003**	001	012**	.009**	014**	.005**	011°°
Homophily = .5	005**	002**	024**	.017**	028**	.010**	$024^{**}$
Homophily = .75	011**	006**	$040^{**}$	.024**	046**	.012**	043**
Homophily = 1	$019^{**}$	012**	061°°	.029**	067°°	.015**	$068^{**}$
Intercept	.618**	.647**	.454°°	.925**	.249°°	.788**	.392**
R <sup>2</sup>	.99	.99	.97	.99	.96	.99	.96

NOTE.—All independent variables are binary. Both dependent and independent variables are measured on the final period of simulations (t=100). Reference: homophily = 0; N=7,000.

<sup>\*</sup>P < .05.

<sup>\*\*</sup> P < .01.

#### Realism

- Bruch and Atwell (2015) distinguish between two types of realism in ABMs
  - Low-dimensional realism: simple, parsimonious models
  - ► High-dimensional realism: complex, complicated models
- ► Trade-offs:
  - ► The latter might be more realistic, but involve more parameters and may be less intelligible

#### Parameters and sensitivity

- Use theory to guide decisions regarding which parameters vary and should be fixed
- ▶ How do system-wide outcomes vary as we adjust parameters?
- Models can be extremely sensitive to small variations in parameters
  - ▶ Be careful to check for coding errors!
- ► Timing matters
  - Constant time vs. discrete-time
  - Asynchronous vs. synchronous updating

### Running agent-based models

- NetLogo is a widely used environment for constructing agent-based models, storing, and visualizing results
- NetLogoWeb is a browser version with many examples (https://www.netlogoweb.org/launch)
- ► There are various interfaces with R to run NetLogo, but I have not used them (e.g. https://cran.rproject.org/web/packages/RNetLogo/RNetLogo.pdf)

### Flocking behavior in NetLogo

```
http://www.netlogoweb.org/launch\#http://ccl.northwestern.edu/netlogo/models/models/Sample\%20Models/Biology/Flocking.nlogo
```

### Schelling's segregation model in NetLogo

http://www.netlogoweb.org/launch#http://ccl.northwestern.edu/netlogo/models/IABM%20Textbook/chapter%203/Segregation%20Extensions/Segregation%20Simple.nlogo

### A simple voting model

```
http://www.netlogoweb.org/launch\#http://www.netlogoweb.org/assets/modelslib/Sample%20Models/Social%20Science/Voting.nlogo
```

### A simple contagion model in R

- Let's simulate a contagion among a population of agents
- Assumptions
  - Agents interact at random
  - Transmission probability is constant for all agents
  - No agent is immune

#### **Generating agents**

I use the setClass option to define a new class called agent with two different numeric properties, id and infected. I then use new t create two different instances of the class.

```
setClass("agent", slots=list(
   id="numeric",
   infected="numeric"
))

a <- new("agent", id=100, infected=0)
b <- new("agent", id=101, infected=1)</pre>
```

#### **Generating agents**

The agents are what are known as S4 classes in R. This means that all slots must be of the correct type. e.g. We cannot set id to be characters.

```
print(a@id)
## [1] 100
print(a@infected)
## [1] 0
```

 $\#a@id \leftarrow 'a' \# uncomment \ and \ run \ to \ produce \ error$ 

Read more about S4 classes here: http://adv-r.had.co.nz/S4.html

#### **Generating agents**

We can use a function to generate a set of N agents and store them in a list.

```
agent.generator <- function(N){
  agents <- list()
  for (i in 1:N) {
    agents[[i]] <- new("agent", id=i,infected=0)
  }
  return(agents)
}</pre>
```

Computational Sociology

#### Interaction protocols

Next we want to define how agents interact. This function takes a focal agent, indexed by i, and randomly selects another agent j, where i is not equal to j.

```
select.partner <- function(i, N){ # i is the focal agent
   ids <- c(1:N) # define list of IDs
   ids <- ids[-i] # remove ith id
   j <- sample(ids, 1) # pick j at random
   return(j)
}</pre>
```

#### Interaction protocols

The next function, interact, defines how agents i and j interact, in this case, whether the virus spreads. Parameter P denotes the probability of transmission. Note the function takes and modifies the entire list of agents.

```
interact <- function(agents, i, j, P){
  if (agents[[i]]@infected == agents[[j]]@infected) {} # no action if s
  else if (agents[[i]]@infected == 1) {
    # infect j with P
    agents[[j]]@infected <- rbinom(n=1, size=1, prob=P)
} else {
    # infect i with P
    agents[[i]]@infected <- rbinom(n=1, size=1, prob=P)
}
return(agents)
}</pre>
```

### Putting together a simulation

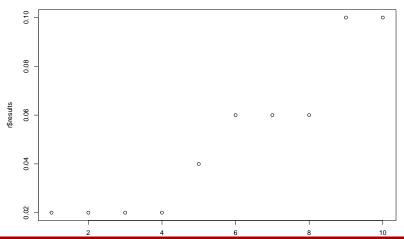
```
simulator <- function(N, t, P, agents){</pre>
  results <- numeric(t) # 0 vector of length t
  agents[[sample(1:N, 1)]]@infected <- 1 # randomly infect 1 agent
  for (timestep in 1:t) { # for each timestep
    for (i in sample(1:N)) { # for reach agent
      j <- select.partner(i, N) # selected a partner</pre>
      agents <- interact(agents, i, j, P) # interact
    statuses <- numeric(N)
    for (i in 1:N) {statuses[[i]] <- agents[[i]]@infected}</pre>
    results[[timestep]] <- sum(statuses)/N # prop infected at timestep
  return(list("results"=results,
              "agents"=agents))
```

#### Running a single simulation

Here we define the relevant parameters, generate a set of agents, and run simulator.

```
N = 50 # agents
P = .1 # transmission probability
t= 10 # timesteps
set.seed(478437) # set randomization seed
agents <- agent.generator(N) # gen N agents
r <- simulator(N, t, P, agents) # run sim
print(r$results)
## [1] 0.02 0.02 0.02 0.02 0.04 0.06 0.06 0.06 0.10 0.10</pre>
```

The graphic shows the proportion infected at each timestep.



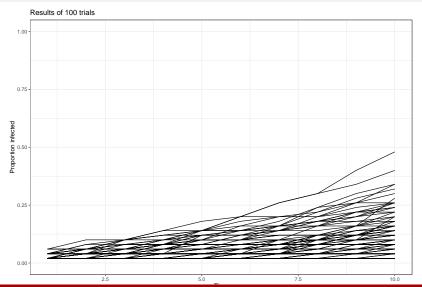
### Running multiple simulations

```
K = 100 \# trials
results.matrix <- matrix(nrow=K*t, ncol=3)
i <- 1 # i.t.era.t.or
for (k in 1:K) {
  agents <- agent.generator(N)
 results <- simulator(N, t, P, agents)
 timestep <- 1
  for (r in results$results) {
    results.matrix[i,] <- c(r,timestep,k)
    timestep <- timestep + 1
    i < -i + 1
```

### Running multiple simulations

### Running multiple simulations

```
library(ggplot2)
library(viridis)
library(tidyverse)
```



#### Varying P

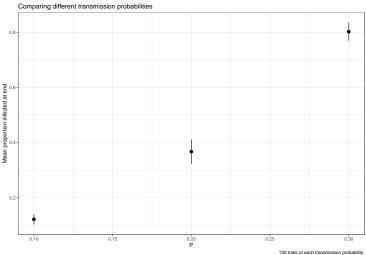
Now we want to examine how the results vary across different transmission probabilities.

```
P.vals <- c(0.1,0.2,0.3) # added three different variations of P
results.matrix <- matrix(nrow=K*t*length(P.vals), ncol=4) # Define a ne
```

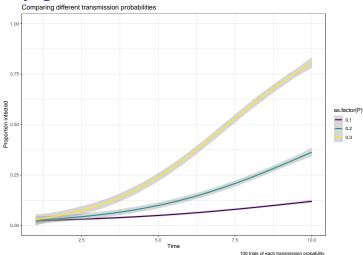
### Varying P

```
i <- 1
for (P in P.vals) {
for (k in 1:K) {
  agents <- agent.generator(N)</pre>
  results <- simulator(N, t, P, agents)
  timestep <- 1
  for (r in results$results) {
    results.matrix[i,] <- c(r,timestep,P,k)
    timestep <- timestep + 1
    i <- i + 1
```

### Varying P



### Varying P



#### Adding a parameter

```
setClass("agent", slots=list(
  id="numeric".
  infected="numeric",
  shape="character" # Adding an extra attribute
))
agent.generator <- function(N){
  agents <- list()
  for (i in 1:N) {
    agents[[i]] <- new("agent", id=i,infected=0,shape=sample(c("square"
 return(agents)
```

#### **Adding** a parameter

```
# Defining a helper function to return a list of ids of agents with a g
ids.by.shape <- function(shape, agents){
   agent.ids <- c()
   for (i in 1:length(agents)) {
      if (agents[[i]]@shape == shape)
      {
        agent.ids <- append(agent.ids, c(agents[[i]]@id))}
      else {}
   }
   return(agent.ids)
}</pre>
```

#### Updating select.partner to induce homophily

```
select.partner <- function(i, agents, H){</pre>
    i.shape <- agents[[i]]@shape # qet i shape
    agents <- agents[-i] # remove ith id
    if (i.shape == "circle") {
      alter.shape <- sample(c("square", "circle"), size=1, prob=c(1-H,H)
    else {
      alter.shape <- sample(c("square", "circle"), size=1, prob=c(H,1-H)
    ids <- ids.by.shape(alter.shape, agents)</pre>
    j <- sample(ids, 1) # pick j at random</pre>
  return(j)
```

### **Updating the simulator function**

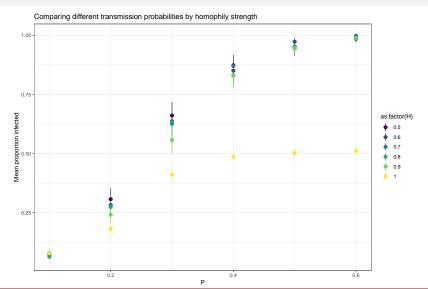
```
simulator.2 <- function(N, t, P, agents, H){</pre>
  results <- numeric(t) # 0 vector of length t
  agents[[sample(1:N, 1)]]@infected <- 1 # randomly infect 1 agent
  for (timestep in 1:t) { # for each timestep
    for (i in sample(1:N)) { # for reach agent
      j <- select.partner(i, agents, H) # selected a partner</pre>
      agents <- interact(agents, i, j, P) # interact
    statuses <- numeric(N) # get prop infected at t
    for (i in 1:N) {statuses[[i]] <- agents[[i]]@infected}</pre>
    results[[timestep]] <- sum(statuses)/N
  return(list("results"=results,
              "agents"=agents))
```

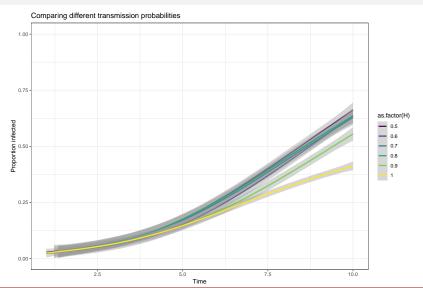
#### **Defining new parameters**

```
H.vals <- c(0.5, 0.6, 0.7, 0.8, 0.9, 1.0)
P.vals <- c(0.1,0.2,0.3,0.4,0.5,0.6)
results.matrix <- matrix(nrow=K*t*length(H.vals)*length(P.vals), ncol=5</pre>
```

### Running the new simulations

```
i <- 1
for (H in H.vals) {
  for (P in P.vals) {
    for (k in 1:K) {
      agents <- agent.generator(N)</pre>
      results <- simulator.2(N, t, P, agents, H)
      timestep <- 1
      for (r in results$results) {
        results.matrix[i,] <- c(r,timestep,P,H,k)
        timestep <- timestep + 1
        i <- i + 1
```





#### **Back to our assumptions**

➤ So far this model is very simple. What are some of the assumptions it makes?

### **Back to our assumptions**

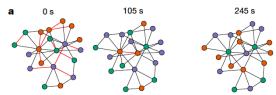
- So far this model is very simple. What are some of the assumptions I make?
  - Only groups, square and circles
    - ► Each group has the same tendency towards homophily
    - Each group is the same size
  - ► Homophily and transmission probability are constant
  - Within-group, interactions are random
    - All relationships are possible, there are no structural holes
  - No agent is immune / non-compliant

#### **Back to our assumptions**

- ► The main challenge when constructing an ABM is to determine which parameters are theoretically relevant and how to operationalize them
- ► For example, if we considered this as a model of cultural transmission it is important to recognize that culture does not spread like a virus (Goldberg and Stein 2018)
  - ▶ But how does culture diffuse? The onus is on the modeler to develop a parsimonious mechanism and implement it in code
- This is difficult, but it forces us to think carefully about our theories and our assumptions

### The future of agent-based modeling

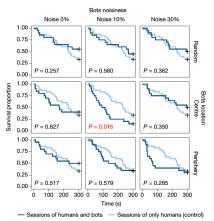
### **Human-agent interactions**



Shirado, Hirokazu, and Nicholas A. Christakis. 2017. "Locally Noisy Autonomous Agents Improve Global Human Coordination in Network Experiments." *Nature* 545 (7654): 370–74.

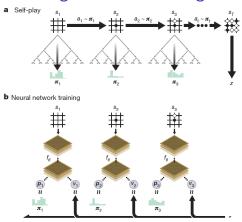
# The future of agent-based modeling

### **Human-agent interactions**



## The future of agent-based modeling

#### Reinforcement learning and autonomous agents



Silver, David et al. 2017. "Mastering the Game of Go without Human Knowledge." Nature 550 (7676): 354-59.

## **Summary**

- Agent-based modeling allows us to simulate complex social systems
  - ► Interdependent, emergent, relational
- ► The technique has been used by sociologists to study a range of different processes and to develop and test theories
  - But there are difficult trade-offs between parsimony (low-dimensional realism) and complexity (high-dimensional realism)
- NetLogo provides a suite of tools for agent-based modeling
- R's object-oriented functionality can be used to create models