Social Data Science

Agent-based modeling

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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

- Project workshop on Monday
- In-class presentations next Wednesday
  - Add slides to shared deck
    - Title slide
    - Data slide
    - Analysis / visualization slide
    - App screenshot and link
    - What did you learn?
  - 5-10 minutes to present

What is agent-based modeling?

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

What is agent-based modeling?

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
  - Statistical analysis consists of finding patterns of relationships between these attributes
    - e.g. We add gender, race, sex, education, income to a model and assume linear relationships between variables

What is agent-based modeling?

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

What is agent-based modeling?

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

What is agent-based modeling?

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

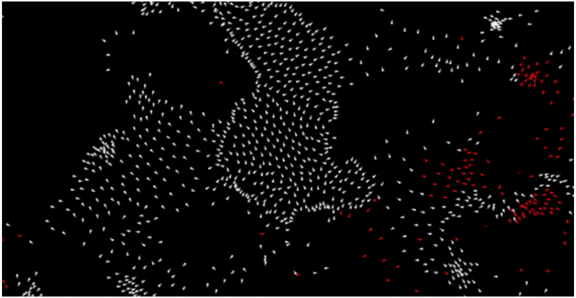
What is agent-based modeling?

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

What is agent-based modeling?

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.

What is agent-based modeling?

Thomas Schelling *Homophily and segregation*

DYNAMIC MODELS OF SEGREGATION

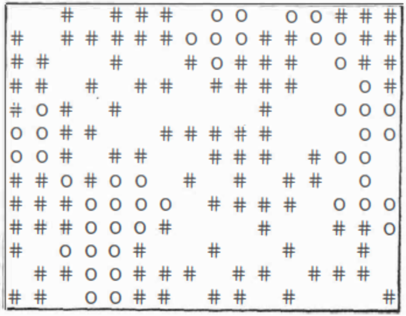
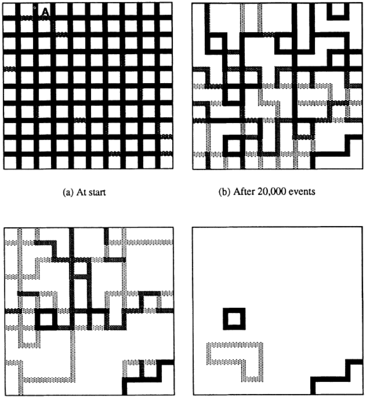


Fig. 13

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

What is agent-based modeling?

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



(a) At start (b) After 20,000 events

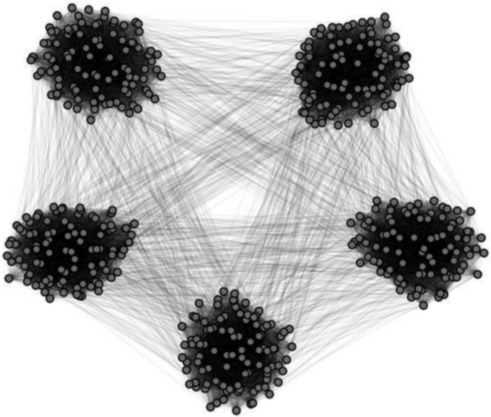
(c) After 40,000 events (d) After 80,000 events

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

What is agent-based modeling?

Testing mechanisms

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



What is agent-based modeling?

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

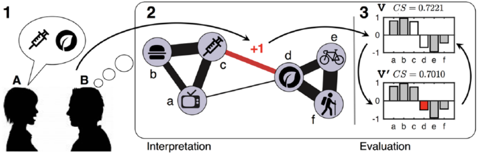


Figure 3. An Illustration of the Agent-Based Model Sequence

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, R (the edge connecting nodes c and d in the network representation of R); 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 B's preference vector V remains unchanged.

What is agent-based modeling?

Integrating real-world data

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

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 externalities	−.516**	−.536**	−.399**	−.685**	−.238**	−.611**	−.351**
General network externalities	.030**	.028**	.043**	.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^2	.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.

* $P < .05$.

** $P < .01$.

DiMaggio, Paul, and Filiz Garip. 2011. "How Network Externalities Can Exacerbate Intergroup Inequality."

What is agent-based modeling?

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

What is agent-based modeling?

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

NetLogo and NetLogoWeb

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.r-project.org/web/packages/RNetLogo/RNetLogo.pdf)

NetLogo and NetLogoWeb

Flocking behavior in NetLogo

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

NetLogo and NetLogoWeb

Schelling's segregation model in NetLogo

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

NetLogo and NetLogoWeb

A simple voting model

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

Building an agent-based model

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

Building an agent-based model

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)
```

Building an agent-based model

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 <- 'a' # uncomment and run to produce error
```

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

Building an agent-based model

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)
}

agent.generator(4)
```

```
## [[1]]
## An object of class "agent"
## Slot "id":
## [1] 1
##
## Slot "infected":
```

Building an agent-based model

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)
}
```

Building an agent-based model

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)
}
```

Building an agent-based model

Putting together a simulation

```
simulator <- function(N, t, P, agents){
  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
      agents <- interact(agents, i, j, P) # interact
    }
    statuses <- numeric(N)
    for (i in 1:N) {statuses[[i]] <- agents[[i]]@infected}
    results[[timestep]] <- sum(statuses)/N # prop infected at timestep
    }
  return(list("results"=results,
              "agents"=agents))
}
```

Building an agent-based model

Running a single simulation

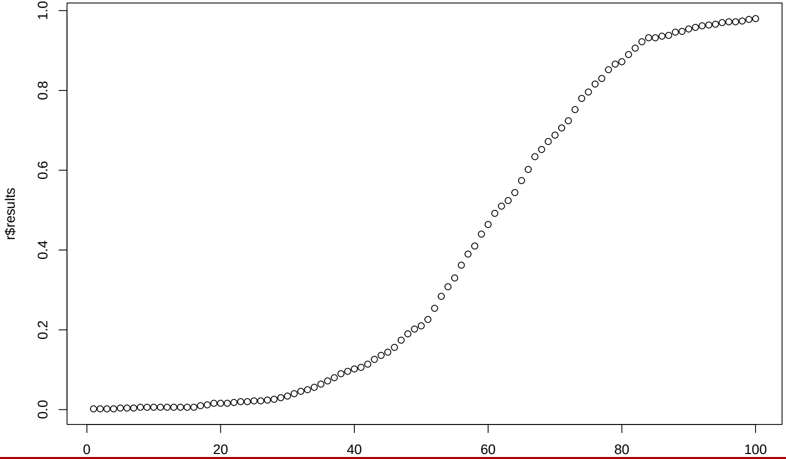
Here we define the relevant parameters, generate a set of agents, and run `simulator`.

```
N = 500 # agents
P = .05 # transmission probability
t= 100 # 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] 0.002 0.002 0.002 0.002 0.004 0.004 0.004 0.006 0.006 0.006 0.
##  [13] 0.006 0.006 0.006 0.006 0.010 0.012 0.016 0.016 0.016 0.018 0.
##  [25] 0.022 0.022 0.024 0.026 0.030 0.034 0.040 0.046 0.050 0.056 0.
##  [37] 0.080 0.090 0.096 0.102 0.106 0.114 0.126 0.136 0.144 0.156 0.
##  [49] 0.202 0.210 0.226 0.254 0.284 0.308 0.330 0.362 0.390 0.410 0.
```

Building an agent-based model

The graphic shows the proportion infected at each timestep.



Building an agent-based model

Running multiple simulations

```
K = 10 # trials
results.matrix <- matrix(nrow=K*t, ncol=3)

i <- 1 # iterator
for (k in 1:K) {
  print(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
  }

}
```

```
## [1] 1
```

Building an agent-based model

Running multiple simulations

```
df <- data.frame(results.matrix)
colnames(df) <- c("prop", "time", "id")
print(head(df))
```

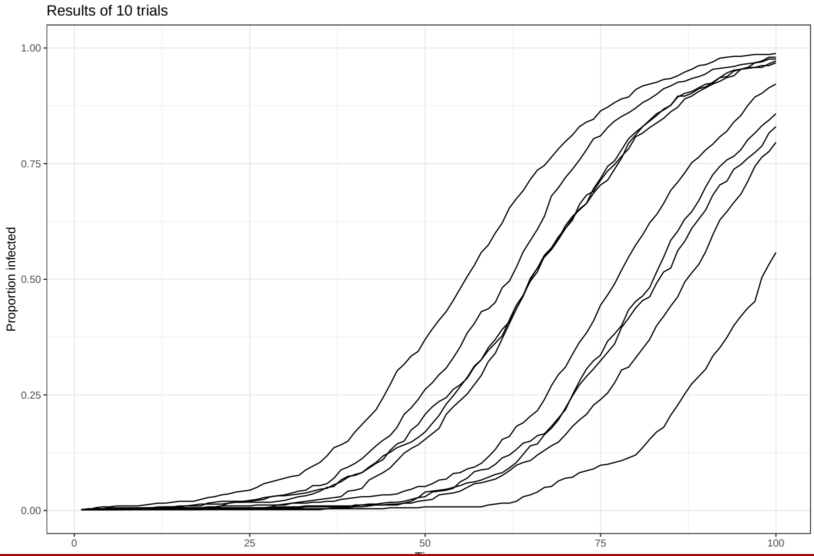
```
##    prop time id
## 1 0.002    1  1
## 2 0.002    2  1
## 3 0.002    3  1
## 4 0.002    4  1
## 5 0.002    5  1
## 6 0.002    6  1
```

Building an agent-based model

Running multiple simulations

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

Building an agent-based model



Building an agent-based model

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
```

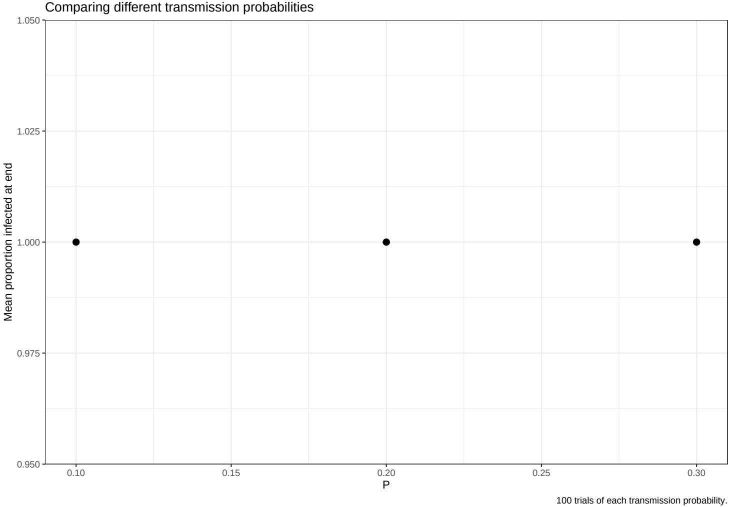
Building an agent-based model

Varying P

```
i <- 1
for (P in P.vals) {
    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,P,k)
        timestep <- timestep + 1
        i <- i + 1
      }
    }
}
```

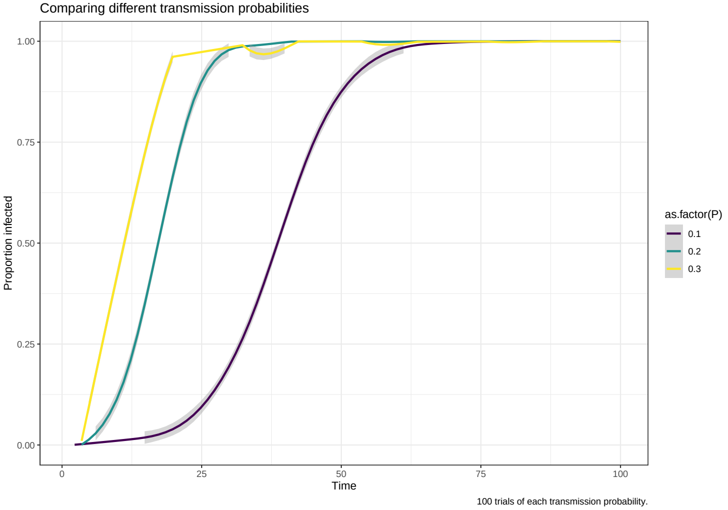
Building an agent-based model

Varying P



Building an agent-based model

Varying P



Building an agent-based model

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)
}
```

Building an agent-based model

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)
}
```

Building an agent-based model

Updating `select.partner` to induce homophily

```
select.partner <- function(i, agents, H){
    i.shape <- agents[[i]]@shape # get 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)
    j <- sample(ids, 1) # pick j at random
  return(j)
}
```

Building an agent-based model

Updating the simulator function

```
simulator.2 <- function(N, t, P, agents, H){
  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
      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}
    results[[timestep]] <- sum(statuses)/N
    }
  return(list("results"=results,
              "agents"=agents))
}
```

Building an agent-based model

Defining new parameters

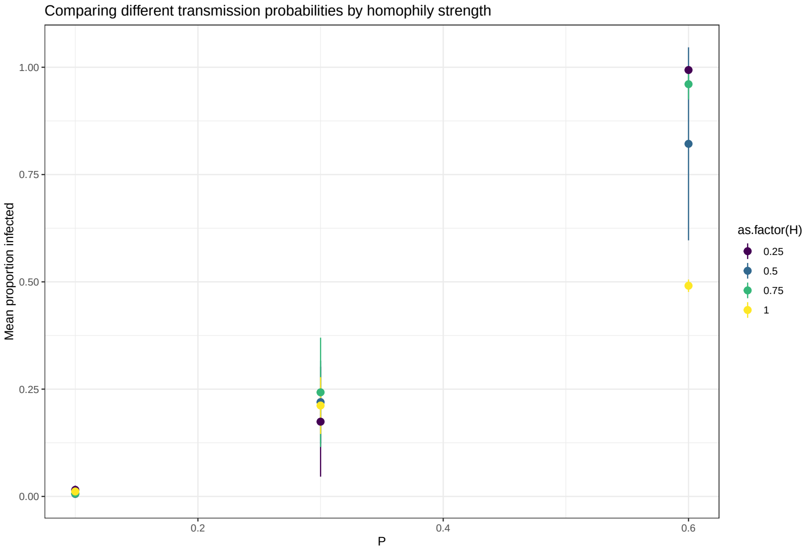
```
K <- 10
t <- 10
H.vals <- c(0.25, 0.5, 0.75,1.0)
P.vals <- c(0.1,0.3,0.6)

results.matrix <- matrix(nrow=K*t*length(H.vals)*length(P.vals), ncol=5
```

Building an agent-based model

Running the new simulations

```
i <- 1
for (H in H.vals) {
    print(H)
  for (P in P.vals) {
      print(P)
    for (k in 1:K) {
      agents <- agent.generator(N)
      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
      }
    }
  }
}
```

Building an agent-based model



Building an agent-based model

Back to our assumptions

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

Building an agent-based model

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

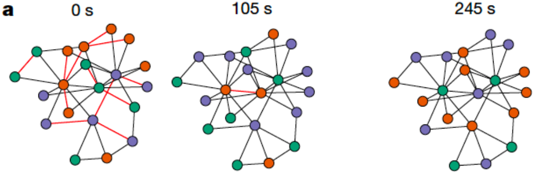
Building an agent-based model

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

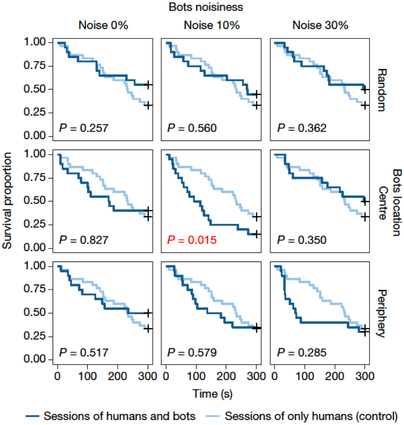
Human-agent interactions



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

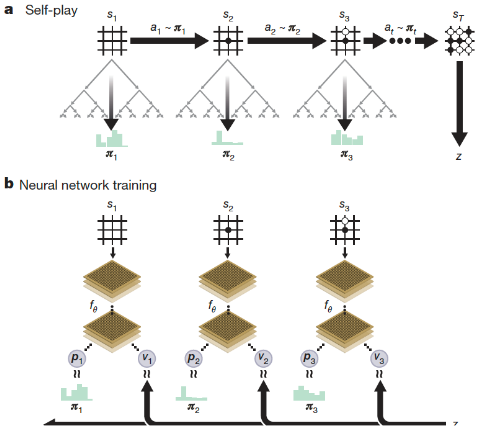
The future of agent-based modeling

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