### **Computational Modeling of Social Behavior**

### Day 2

## **Spreading Infection**

Paul Smaldino

# Outline of the day

#### • Morning

- Review modeling challenges
- Infection Models

### · Afternoon

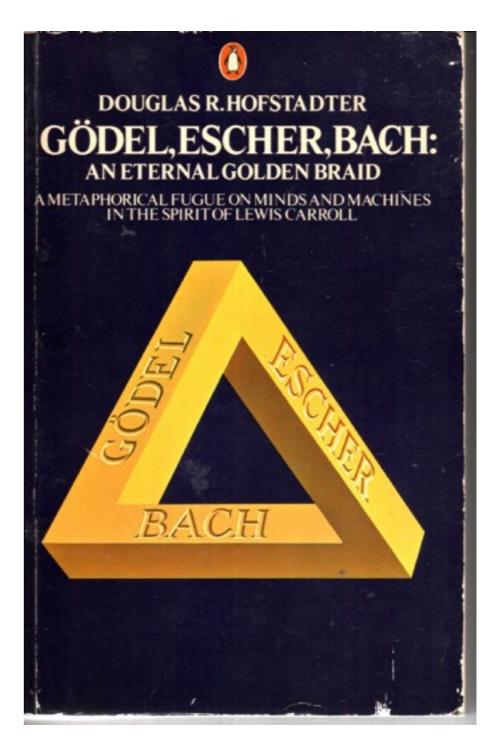
Modeling infections with collisions



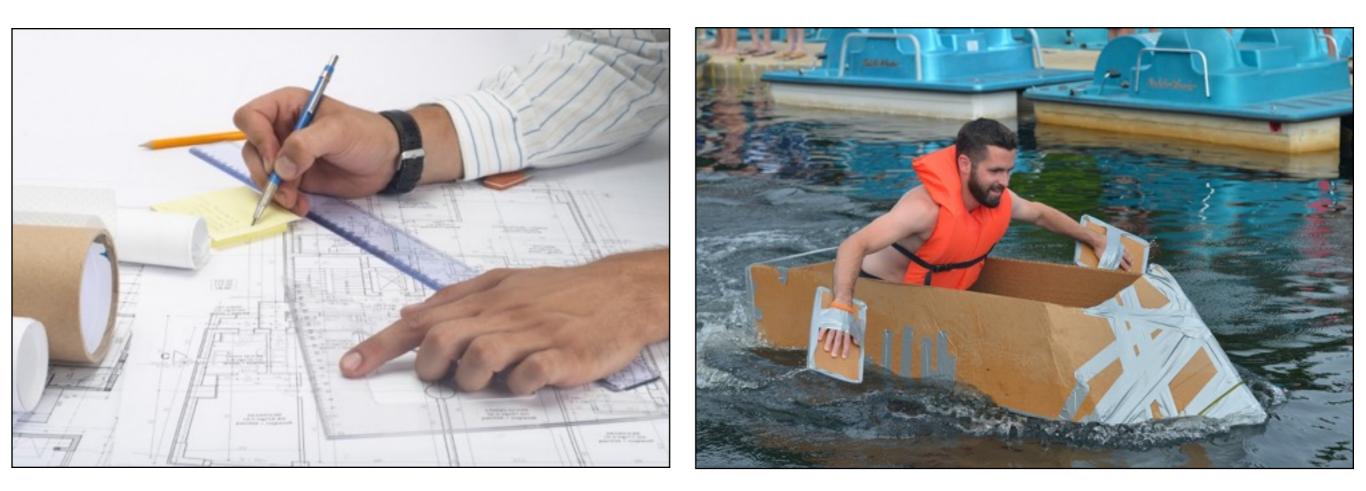
If you wish to make an apple pie from scratch, you must first invent the universe.

# Writing, planning, outlining

#### Hofstadter's Law: It always takes longer than you expect, even when you take into account Hofstadter's Law.



### Separating Design and Implementation



## The iterative process

Sometimes people ask: "How does your show get written?" Like this: performance, feedback, revision

-Baba Brinkman, The Rap Guide to Evolution

### Pseudocode

- A description of a computer programming algorithm that uses the structural conventions of programming languages, but omits detailed subroutines or language-specific syntax.
- Valuable for *stepwise refinement*

- Initialize:
  - ▶ ???

- At each tick:

# Color Spreading

#### • Initialize:

- All patches are initially white
- Set center patch to blue

#### • At each tick:

- Each patch checks its neighbors to see if any of them are blue. If so, it turns blue.
- Stop if no patches are white

```
to setup
  clear-all
  ask patches [ set pcolor white] ;; set patches to white
  ask patch 0 0 [ set pcolor blue ] ;;select center patch blue
  reset-ticks
end
to go
  if not any? patches with [pcolor = white]
  [stop]
  ask patches [ spread-move ]
  tick
end
to spread-move
  if any? neighbors with [ pcolor = blue ]
  [set pcolor blue]
end
```

# Rainbow Spiral

#### Initialize:

- All patches are initially white
- Set center patch to random color
- Place invisible agent on center patch, headed east.
- stepLength = 1
- twostep = 0

#### • At each tick:

- For x from 1 to stepLength
  - Move forward 1
  - · Set patch occupied by agent to random color
- Turn left 90 degrees
- Twostep++
- If Twostep = 2
  - Twostep = 0
  - StepLength++
- Continue until no patches are white.

## Collisions

#### Initialize:

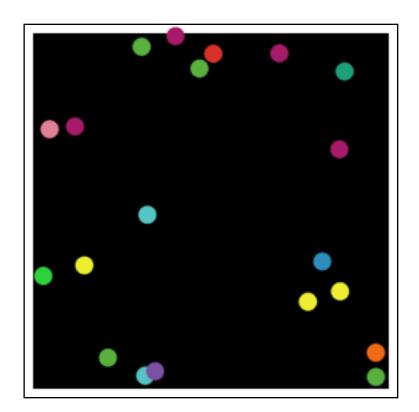
turtles are placed in random locations with random headings

#### • At each tick:

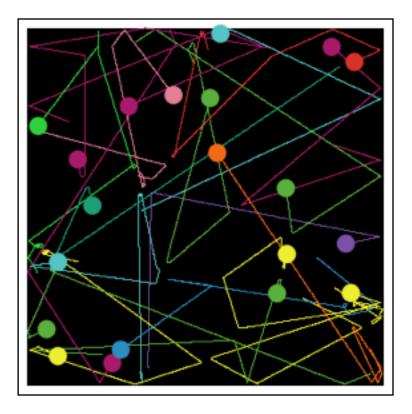
- For each turtle:
  - If a step forward would place outside grid
    - turn to "bounce" off wall
  - If another turtle is within search-radius
    - set heading to random direction, and set other turtle's heading to the opposite direction
  - move forward step-length

```
SETUP
to setup
 clear-all
 set-default-shape turtles "circle"
 draw-walls
  create-turtles n-turtles ;; create some turtles
    [ randomize ]
                         ;; place them randomly
 ask turtles [set size 2]
 reset-ticks
end
; draws the boundaries (walls) of the space
to draw-walls
  ; draw left and right walls
  ask patches with [abs pxcor = max-pxcor]
    [ set pcolor white ]
  ; draw top and bottom walls
  ask patches with [abs pycor = max-pycor]
    [ set pcolor white ]
end
: set random location
to randomize
  setxy random-xcor random-ycor
  if pcolor = white ; if it's on the wall...
    [ randomize ] ; ...try again
```

end



```
GO
to go
  ask turtles [
    ifelse leave-trace? ;; pen up or down?
      [ pen-down ]
      [ pen-up ]
    bounce
    fd move-speed
  tick
end
to bounce
  ; Hitting left or right wall? Reflect heading around x axis
  if abs [pxcor] of patch-ahead 0.4 = max-pxcor
  [ set heading (- heading) ] ;
  ; Hitting top or bottom wall? Reflect heading around y axis
  if abs [pycor] of patch-ahead 0.4 = max-pycor
  [ set heading (180 - heading) ]
  ; check if any other turtles are close enough to hit.
  if collisions? and count turtles in-radius 1.5 > 1
      let new-heading (heading + random 90)
      set heading new-heading
      fd 0.1
      ask other turtles in-radius 2 [
        set heading new-heading + 180
        fd 0.1
```



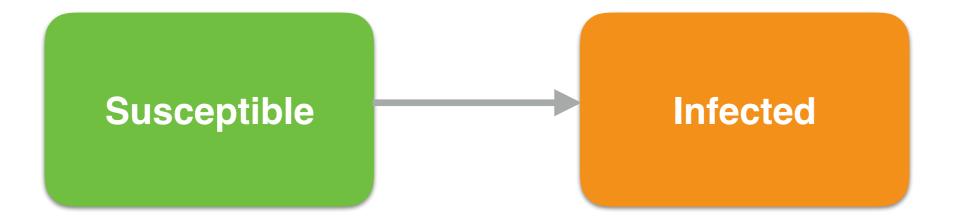


# Contagion





# Simple diffusion model



N: population size
I: # of infected
τ: transmissibility
c: contact rate

100

Time

#### Probability a meeting leads to infection

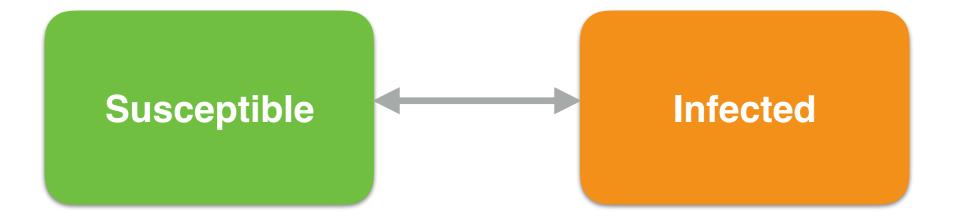
$$\tau \frac{I}{N} \left( \frac{N-I}{N} \right)$$
Pr(meeting -> infection) Pr(susceptible meets infected)

Trajectory of infected population

$$\begin{split} I_{t+1} &= I_t + \underbrace{Nc\tau \frac{I_t}{N} \left(\frac{N-I_t}{N}\right)}_{\text{\# of meetings}} \quad \text{$^{\text{populous}}_{\text{Homoson}}} \end{split}$$

0

### SIS Model



$$I_{t+1} = I_t + c\tau I_t \left(1 - \frac{I_t}{N}\right) - \gamma I_t$$
  
# new infections  
# recovered  
# recovered

#### Equilibrium infection rate

$$c\tau I \left(1 - \frac{I}{N}\right) = \gamma I$$

$$1 - \frac{I}{N} = \frac{\gamma}{c\tau}$$

$$\frac{I}{N} = 1 - \frac{\gamma}{c\tau}$$

$$0$$

$$\frac{1}{100}$$

Will the infection spread?

$$I_{t+1} = I_t + c\tau I_t \left(1 - \frac{I_t}{N}\right) - \gamma I_t$$

N: population size
I: # of infected
τ: transmissibility
c: contact rate
γ: recovery rate

close to 1 when infection is new

$$I_{t+1} \approx I_t + I_t (c\tau - \gamma)$$

Infection spreads if:  $\ c au > \gamma$ 

$$R_0 = \frac{c\tau}{\gamma} > 1$$

"basic reproduction number"

Rewrite equilibrium frequency:

$$\frac{I}{N} = 1 - \frac{1}{R_0}$$

Vaccinate a proportion V of the population

$$\Delta I = c\tau \left(1 - \frac{I}{N}\right) \left(1 - V\right)I - \gamma I$$

N: population size
I: # of infected
τ: transmissibility
c: contact rate
γ: recovery rate

Pr(encounter a susceptible and transmit)

Pr(the susceptible isn't vaccinated)

When infection is new

$$\Delta I \approx I \left( c \tau (1 - V) - \gamma \right)$$

Infection spreads if:

$$\frac{c\tau}{\gamma}(1-V) > 1$$

 $(1 - V)R_0 = r_0$  effective basic reproduction number

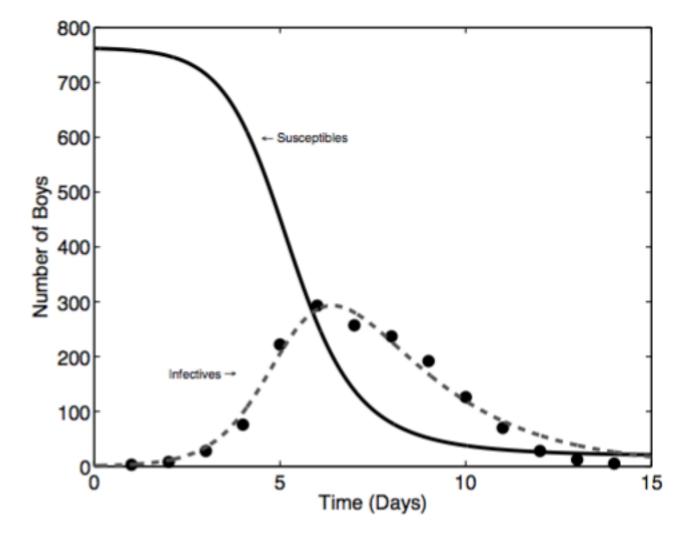
 $(1-V)R_0 = r_0$  $(1-V)R_0 \le 1$  $R_0 - R_0 V < 1$  $R_0 - 1 < R_0 V$  $\frac{1}{R_{\cap}} \le V$ 

threshold for herd immunity

V\* = 14/15  $\approx$  .93Estimated R\_0:V\* = 4/5  $\approx$  .93Measles  $\approx$  15V\* = 4/5 = .80Mumps  $\approx$  5V\* = 2/3  $\approx$  .67Influenza  $\approx$  3

### Do these models reflect reality?

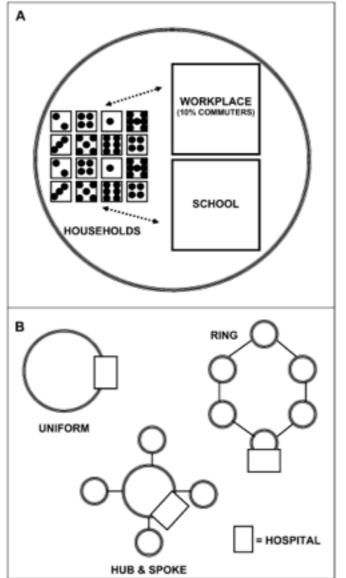


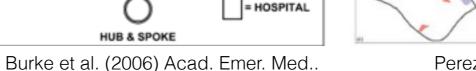


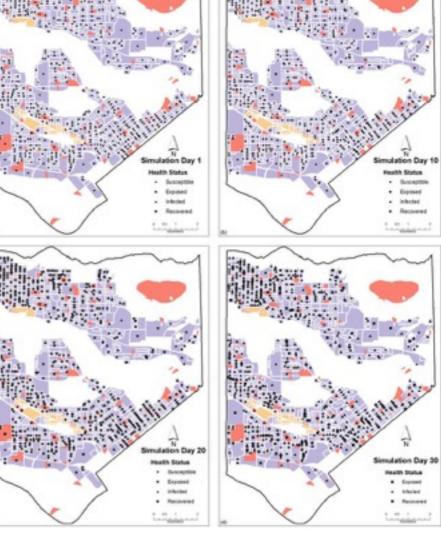
Flu outbreak English boarding school 1978

# Why use ABMs?

- Nano-sheep problem
- Allows for greater complexity
- Builds intuition







Perez & Dragicevic (2009) Int J. Health Geo.

### Relevance to social science?

#### Complex Contagions and the Weakness of Long Ties<sup>1</sup>

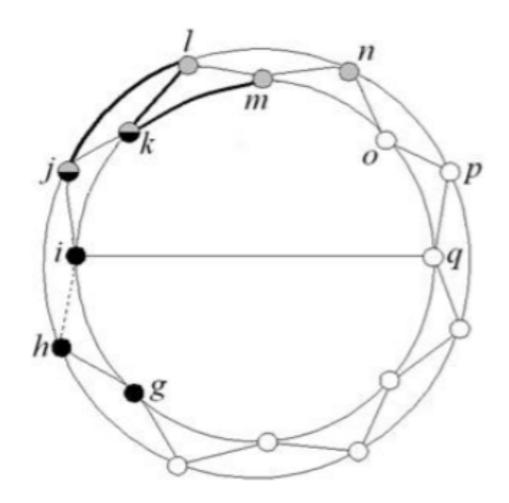
Damon Centola Harvard University

Michael Macy Cornell University

> The strength of weak ties is that they tend to be long—they connect socially distant locations, allowing information to diffuse rapidly. The authors test whether this "strength of weak ties" generalizes from simple to complex contagions. Complex contagions require social affirmation from multiple sources. Examples include the spread of high-risk social movements, avant garde fashions, and unproven technologies. Results show that as adoption thresholds increase, long ties can impede diffusion. Complex contagions depend primarily on the width of the bridges across a network, not just their length. Wide bridges are a characteristic feature of many spatial networks, which may account in part for the widely observed tendency for social movements to diffuse spatially.

Most collective behaviors spread through social contact. From the emergence of social norms (Centola, Willer, and Macy 2005), to the adoption of technological innovations (Coleman, Katz, and Menzel 1966), to the growth of social movements (Marwell and Oliver 1993; Gould 1991, 1993; Zhao 1998; Chwe 1999), social networks are the pathways along which these "social contagions" propagate. Studies of diffusion dynamics have demonstrated that the structure (or topology) of a social network can have

<sup>1</sup> The authors wish to express their gratitude to the National Science Foundation for support of this research through Human and Social Dynamics grant SES-0432917 and through an IGERT fellowship for the first author. We also thank the Robert Wood Johnson Foundation for support of the first author. We thank Duncan Watts, Steve Strogatz, Jon Kleinberg, Vlad Barash, Chris Cameron, and Stephen Moseley for useful comments and suggestions. Direct correspondence to Damon Centola, Institute for Quantitative Social Science. 1230 Cambridge Street, Harvard University Cambridge

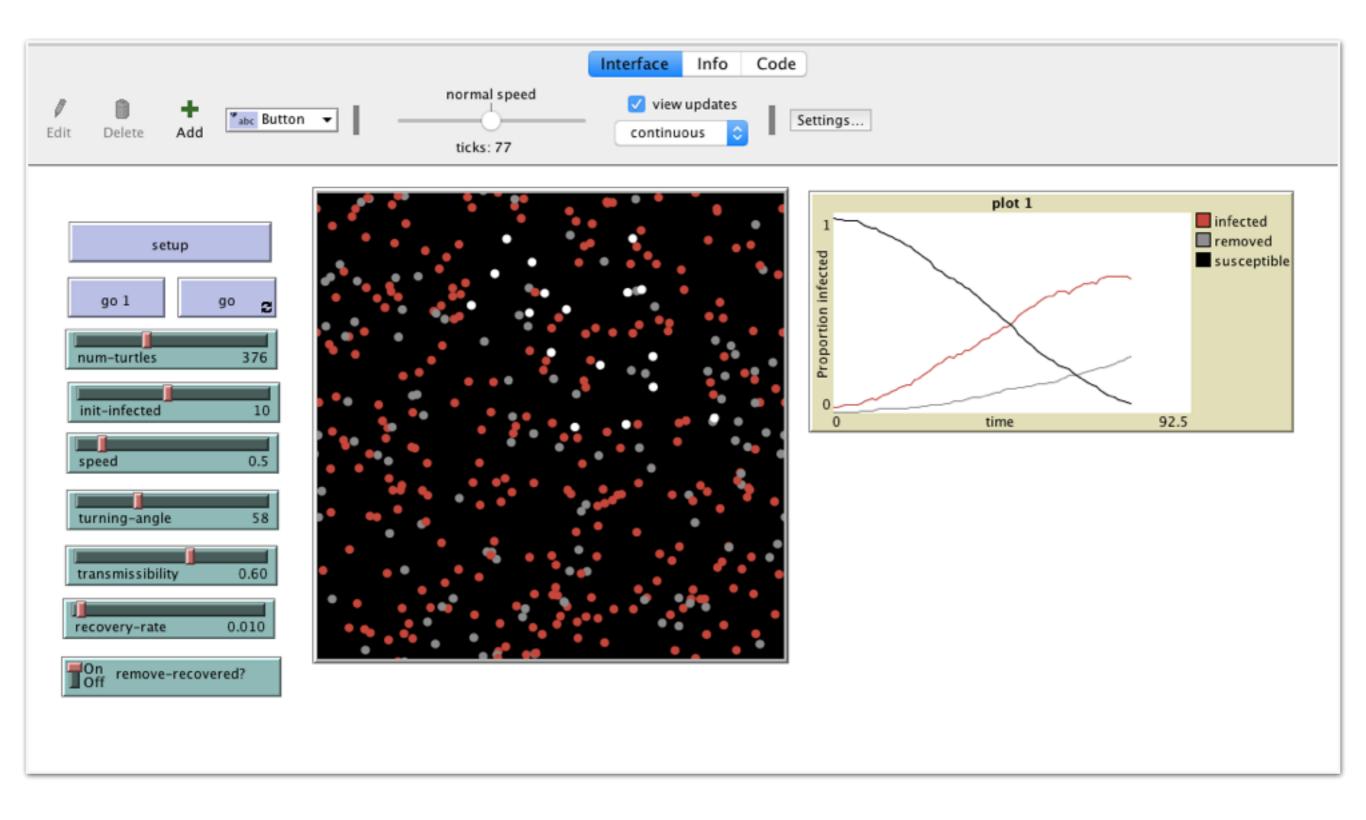


### Models as scaffolds





### Some questions for a simple model



```
turtles-own [
  infected?
  removed?
]
to setup
  clear-all
  setup-turtles
  setup-infected
  reset-ticks
end
to setup-turtles
  create-turtles num-turtles [
    set shape "circle"
    set color white
    set infected? false
    set removed? false
    setxy random-xcor random-ycor
end
to setup-infected
  if init-infected > num-turtles
  [set init-infected 1]
  ask n-of init-infected turtles [
    set infected? true
    set color red
end
```

to go

```
to go
  if (count turtles with [infected?]) = num-turtles or
    (count turtles with [infected?]) = 0
  [ stop ]
```

```
to go
if (count turtles with [infected?]) = num-turtles or
   (count turtles with [infected?]) = 0
[ stop ]
ask turtles [ ;; S -> I
```

]

```
to go
if (count turtles with [infected?]) = num-turtles or
  (count turtles with [infected?]) = 0
[ stop ]
ask turtles [ ;; S -> I
  if not removed? and
     (any? turtles with [color = red] in-radius 1) and
     (random-float 1 < transmissibility)
  [set infected? true]
]
ask turtles with [infected? and color = red] ;; I -> S or R
```

```
end
```

1

```
to go
  if (count turtles with [infected?]) = num-turtles or
     (count turtles with [infected?]) = 0
  [ stop ]
  ask turtles [ ;; S -> I
    if not removed? and
       (any? turtles with [color = red] in-radius 1) and
       (random-float 1 < transmissibility)</pre>
    [set infected? true]
  ask turtles with [infected? and color = red] ;; I -> S or R
    if random-float 1 < recovery-rate [</pre>
      set infected? false
      ifelse remove-recovered?
        [set color gray
          set removed? true
        1
      [ set color white ]
  ask turtles [ ;;move
    if infected? [set color red]
    left random turning-angle
    right random turning-angle
    fd speed
  tick
end
```

### Batch Runs

#### BehaviorSpace

Experiment

Experiment name experiment

Vary variables as follows (note brackets and quotation marks):

["num-turtles" 100 500 1000]
["transmissibility" 0.3 0.6]
["recovery-rate" 0]
["init-infected" 5]
["speed" 0.5 1]

Either list values to use, for example: ["my-slider" 1 2 7 8] or specify start, increment, and end, for example: ["my-slider" [0 1 10]] (note additional brackets) to go from 0, 1 at a time, to 10. You may also vary max-pxcor, min-pxcor, max-pycor, min-pycor, random-seed.

Repetitions 10

run each combination this many times

Run combinations in sequential order

For example, having ["var" 1 2 3] with 2 repetitions, the experiments' "var" values will be: sequential order: 1, 1, 2, 2, 3, 3 alternating order: 1, 2, 3, 1, 2, 3

Measure runs using these reporters:

count turtles

one reporter per line; you may not split a reporter across multiple lines

	Measure	runs	at	every	step
_				,	

if unchecked, runs are measured only when they are over

Setup com	mands:	Go commands:				
setup		go				
Stop con the run stops in	ndition: f this reporter becomes true	Final commands:				
Time limit	0					
stop after this r	many steps (0 = no limit)					
		Cancel	ОК			

### Statistical tests for simulation data

- Statistical tests are important for comparing model results to empirical results.
- However, statistical tests are rarely appropriate for identifying an effect within the model itself.
  - A statistical test creates a model of the data generation process
  - However, you already have such a model! The solution is to run enough simulations to obtain limiting distributions.

- Remainder of today:
  - Modeling Challenge #2
- Tomorrow:
  - Modeling cooperation and social evolution