



NOVEMBER 5, 2024

MODEL AGENTS: SOCIAL BEHAVIOR  
THROUGH THE FORMAL LENS

# COUGH COUGH CONTAGION MODELS

Adrian Haret  
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We want to model the spread of a disease.



PAUL E. SMALDINO

This is interesting for the obvious reasons.

But many other things behave like diseases, in terms of how they spread through a society of agents.

Smaldino, P. (2023). *Modeling Social Behavior. Mathematical and Agent-Based Models of Social Dynamics and Cultural Evolution*. Princeton University Press.



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EVERETT ROGERS

Like innovations!



From hybrid seed corn among Midwest farmers, to the adoption of ham radio among tech enthusiasts, to the adoption of new ideas among French intellectuals.

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SANDER VAN DER LINDEN

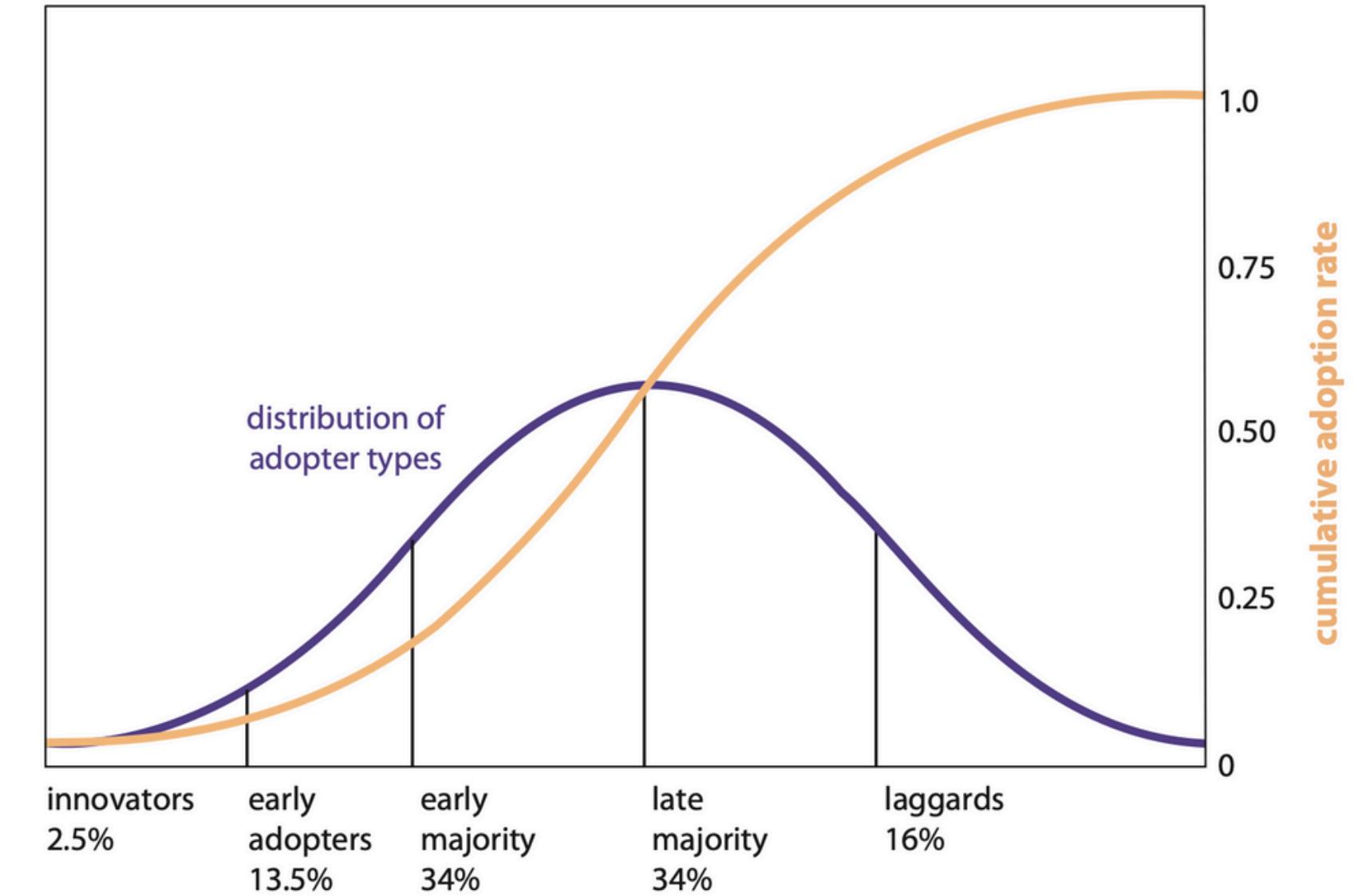
Also misinformation!

Grimes, D. R., & van der Linden, S. (2024). Misinformation really does spread like a virus, suggest mathematical models drawn from epidemiology. *The Conversation*.

If we look at the data, how *do* such things spread?

# THE S-SHAPE OF DIFFUSION

Many patterns of diffusion follow an S-shape.



Rogers, E. M. (2003). *Diffusion of Innovations*, 5th Edition (5th ed.). Free Press.



PAUL E. SMALDINO

We'll try to approximate this behavior through a series of formal models.

Sometimes called *compartmental models*, because they put agents in specific boxes.

# COMPARTMENTAL MODELS

## DESCRIPTION

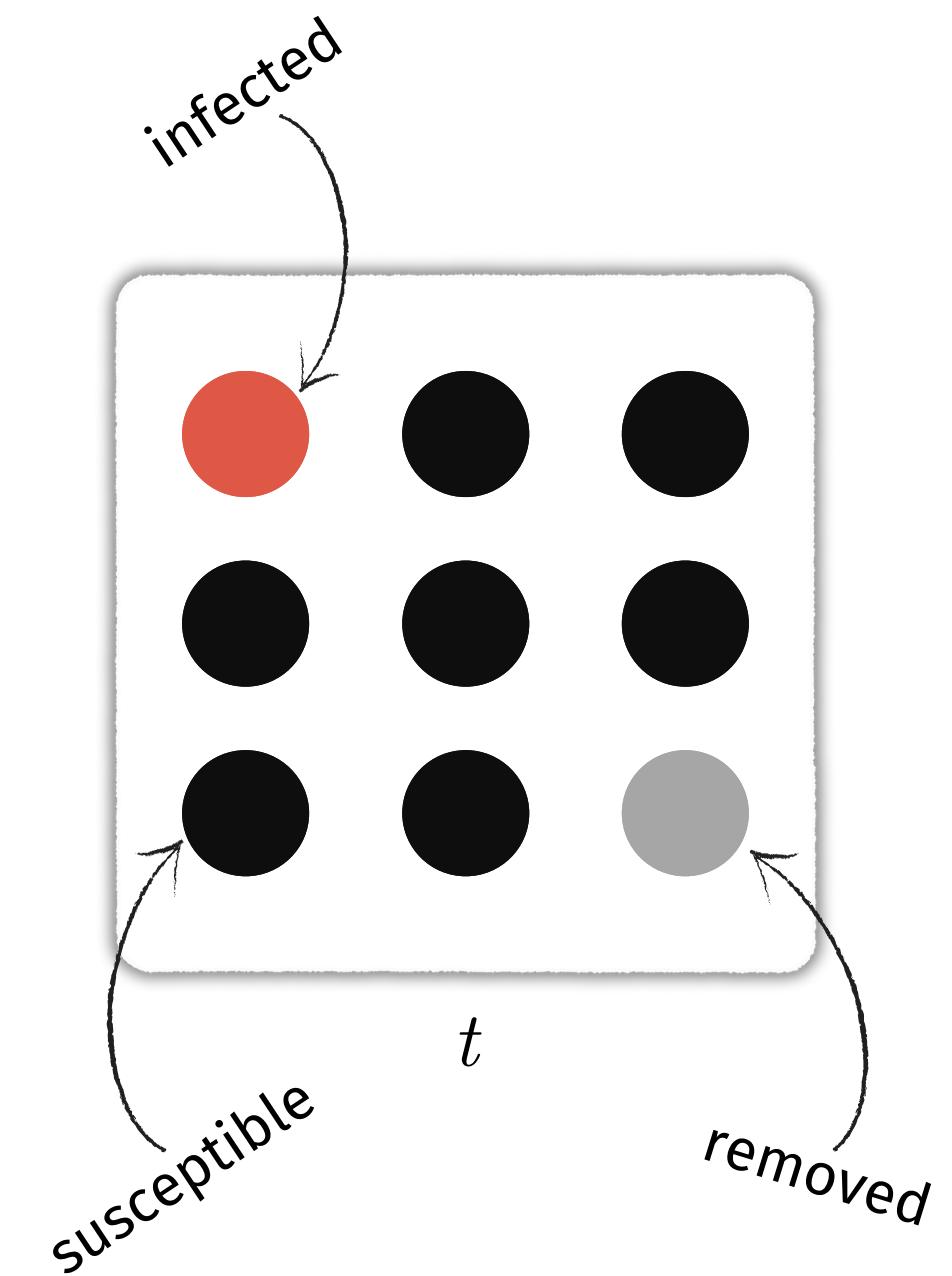
We have  $N$  agents in an environment.

At any time-step  $t$ , agents are in one of several possible states.

*Infected* agents have caught the infection. The number of infected agents at time  $t$  is  $I_t$ .

*Susceptible* agents are not infected, but they can become infected. The number of susceptible agents at time  $t$  is  $S_t$ .

*Removed*, or *recovered* agents are not infected and they cannot become infected, either because they are immune, or because they are dead. The number of removed agents at time  $t$  is  $R_t$ .



We're interested in the dynamics of  $I_t$ ,  $S_t$  and  $R_t$  over time.

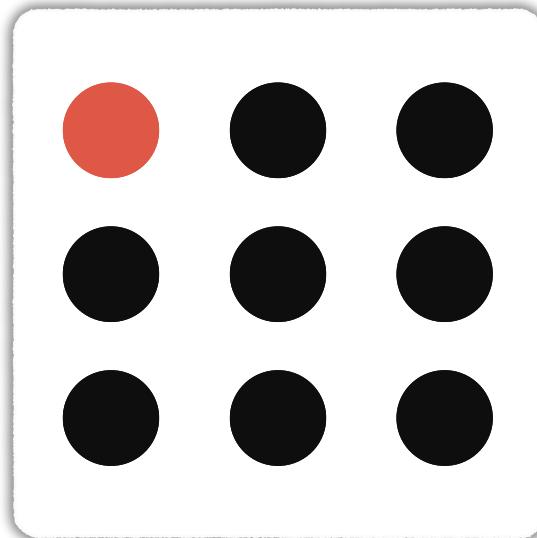
# THE SPONTANEOUS INFECTION MODEL

## DESCRIPTION

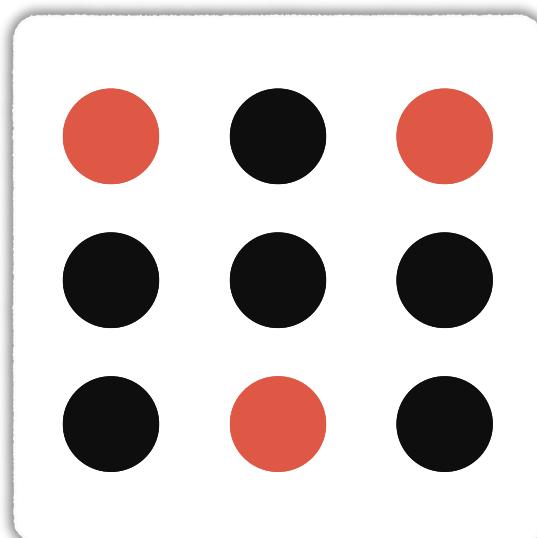
Only two possible states: susceptible and infected.

At time  $t$ , a susceptible agent becomes infected with probability  $\alpha$ .

Movement and social structure play no role.



$t = 1$



$t = 2$

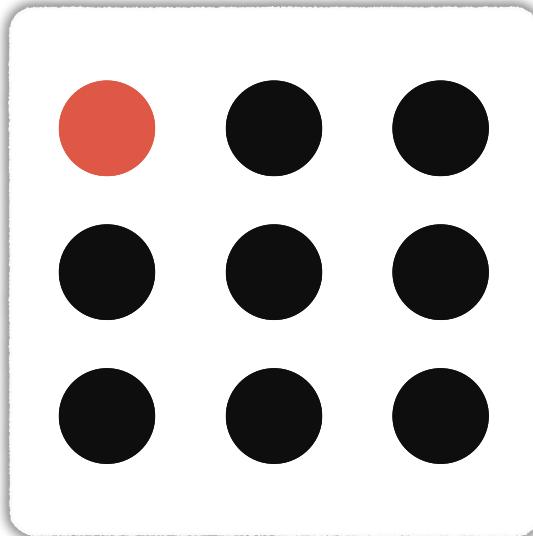
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# THE SPONTANEOUS INFECTION MODEL

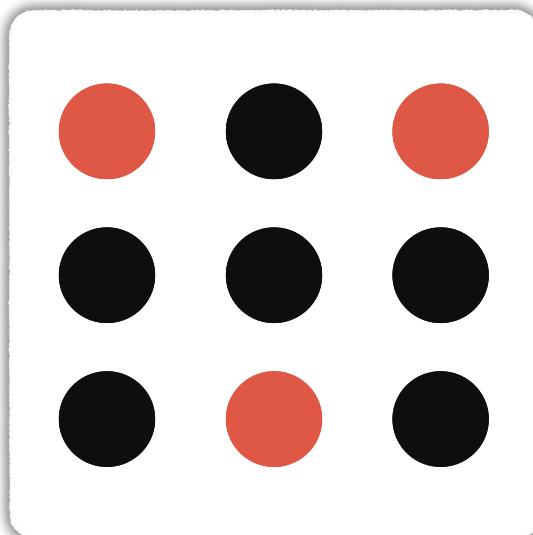
## ANALYSIS

The number of susceptibles at time  $t$  are the non-infected agents:

$$S_t = N - I_t.$$



$t = 1$



$t = 2$

...

# THE SPONTANEOUS INFECTION MODEL

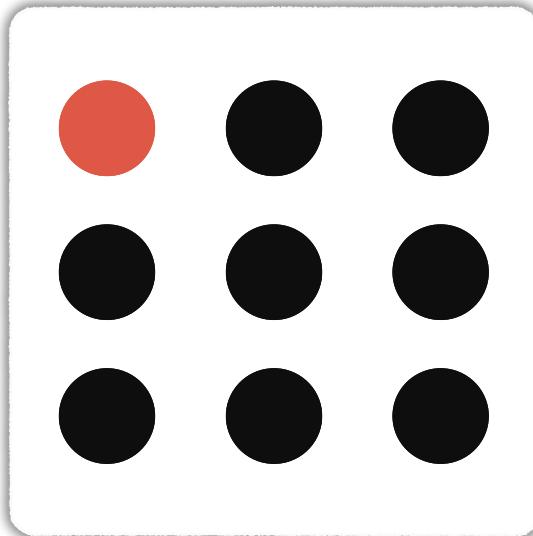
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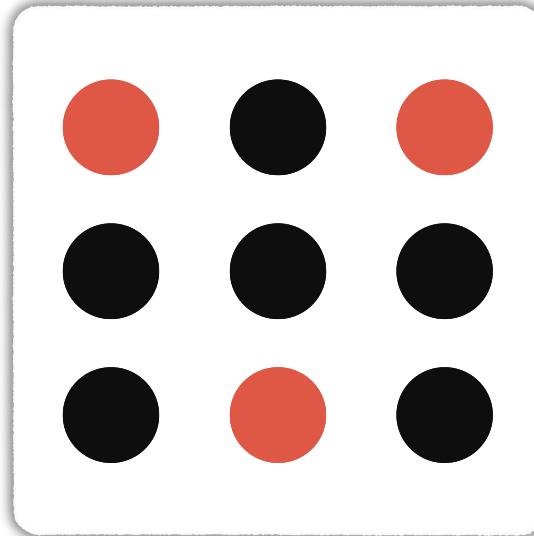
$$S_t = N - I_t.$$

The average number of newly infected at time  $t$  is  $\alpha S_t$ , or:

$$\alpha(N - I_t).$$



$t = 1$



$t = 2$

...

# THE SPONTANEOUS INFECTION MODEL

## ANALYSIS

The number of susceptibles at time  $t$  are the non-infected agents:

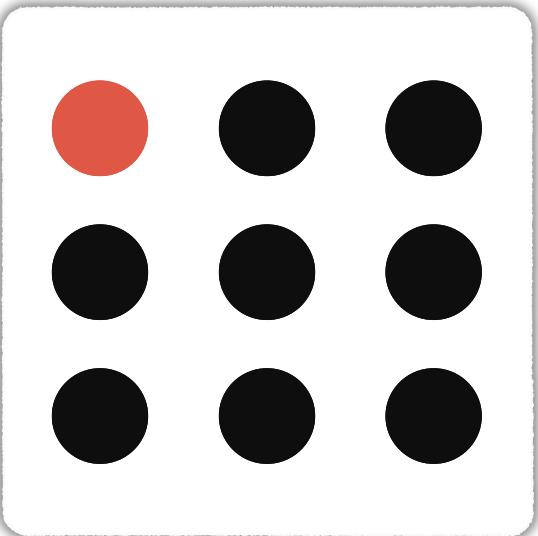
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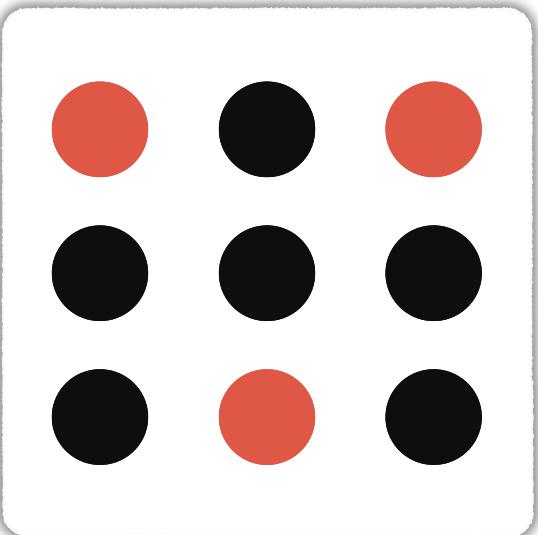
$$\alpha(N - I_t).$$

Thus, the number of infected at time  $t + 1$  is given by the recursion:

$$I_{t+1} = I_t + \alpha(N - I_t),$$



$t = 1$



$t = 2$

...

# THE SPONTANEOUS INFECTION MODEL

## ANALYSIS

The number of susceptibles at time  $t$  are the non-infected agents:

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The average number of newly infected at time  $t$  is  $\alpha S_t$ , or:

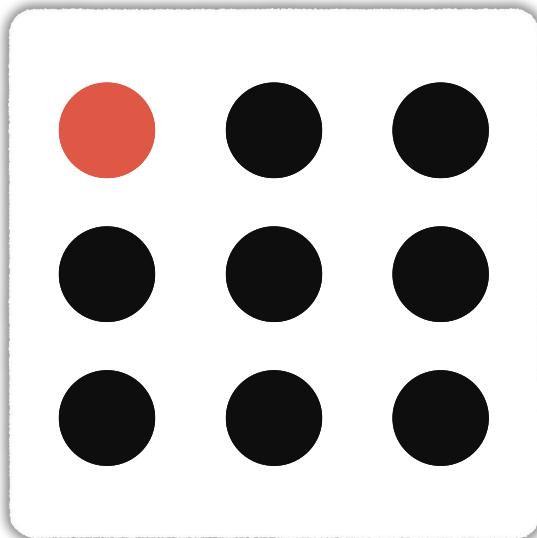
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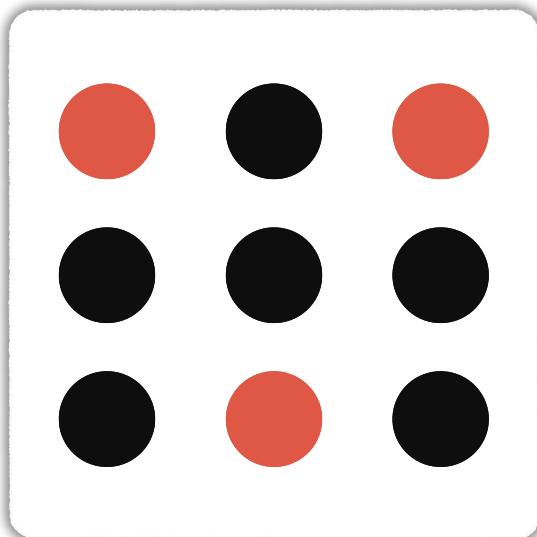
$$I_{t+1} = I_t + \alpha(N - I_t),$$

which, written as a *difference equation*, gives:

$$\begin{aligned}\Delta I &= I_{t+1} - I_t \\ &= \alpha(N - I_t).\end{aligned}$$



$t = 1$



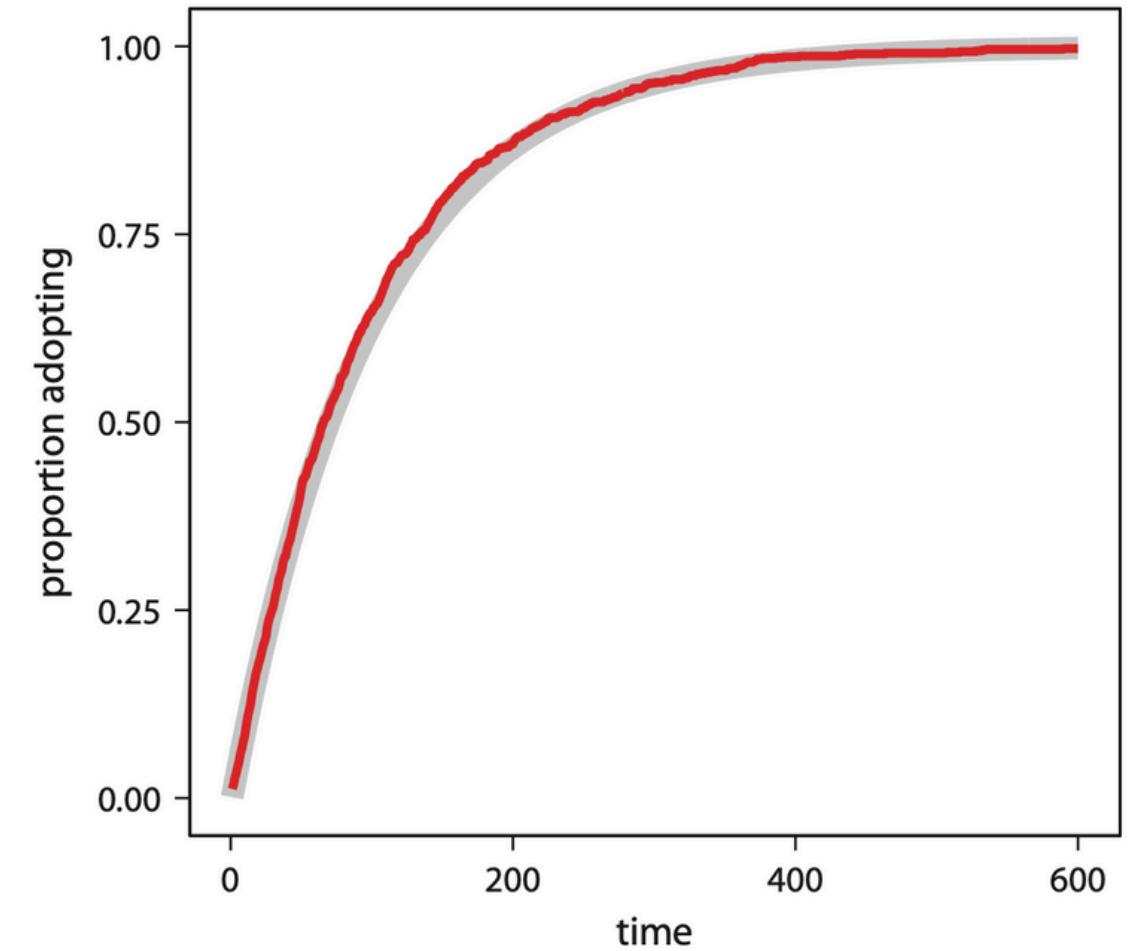
$t = 2$

...

# THE SPONTANEOUS INFECTION MODEL

## BEHAVIOR

When we plot the proportion of infected agents over time, we do not see the S-shape we are looking for.



We have to keep looking.

# THE SI (SUSCEPTIBLE-INFECTED) MODEL

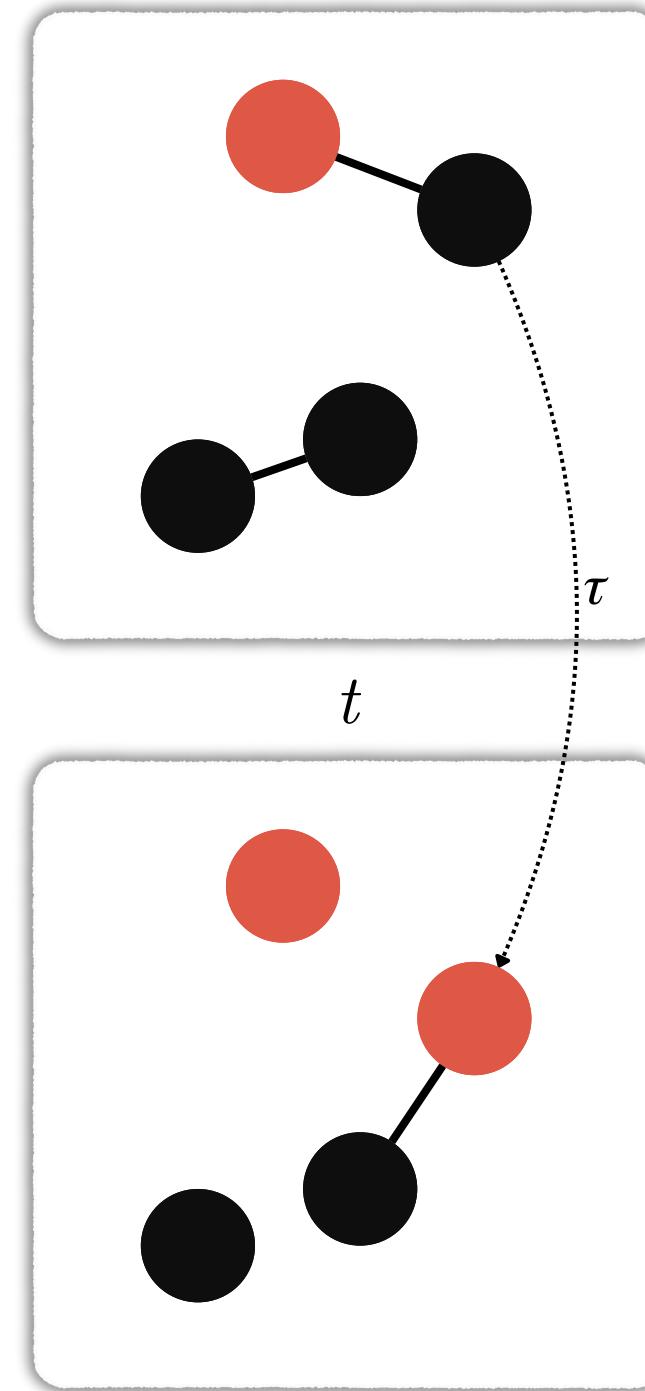
## DESCRIPTION

Only two possible states: susceptible and infected.

At time  $t$  agents form pairs.

This can be approximated by agents moving around and getting close to each other. Social structure now plays a role!

An infected agent transmits the disease to a nearby susceptible agent with probability  $\tau$ .



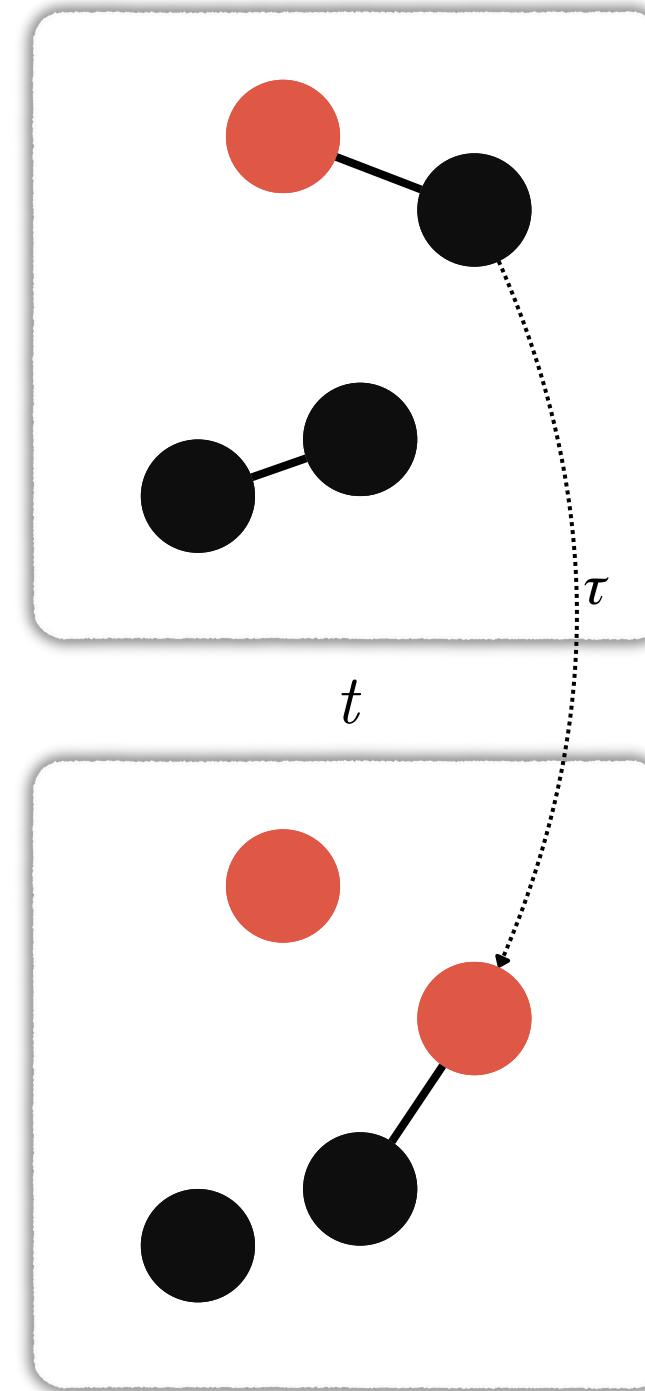
How does the number of infected agents change from one time-step to another?

# THE SI (SUSCEPTIBLE-INFECTED) MODEL

## ANALYSIS

Imagine a random variable  $X_i$  that keeps track of whether agent  $i$  gets infected at time  $t$ :

$$X_i = \begin{cases} 1, & \text{if } i \text{ gets infected,} \\ 0, & \text{otherwise.} \end{cases}$$



$t + 1$

# THE SI (SUSCEPTIBLE-INFECTED) MODEL

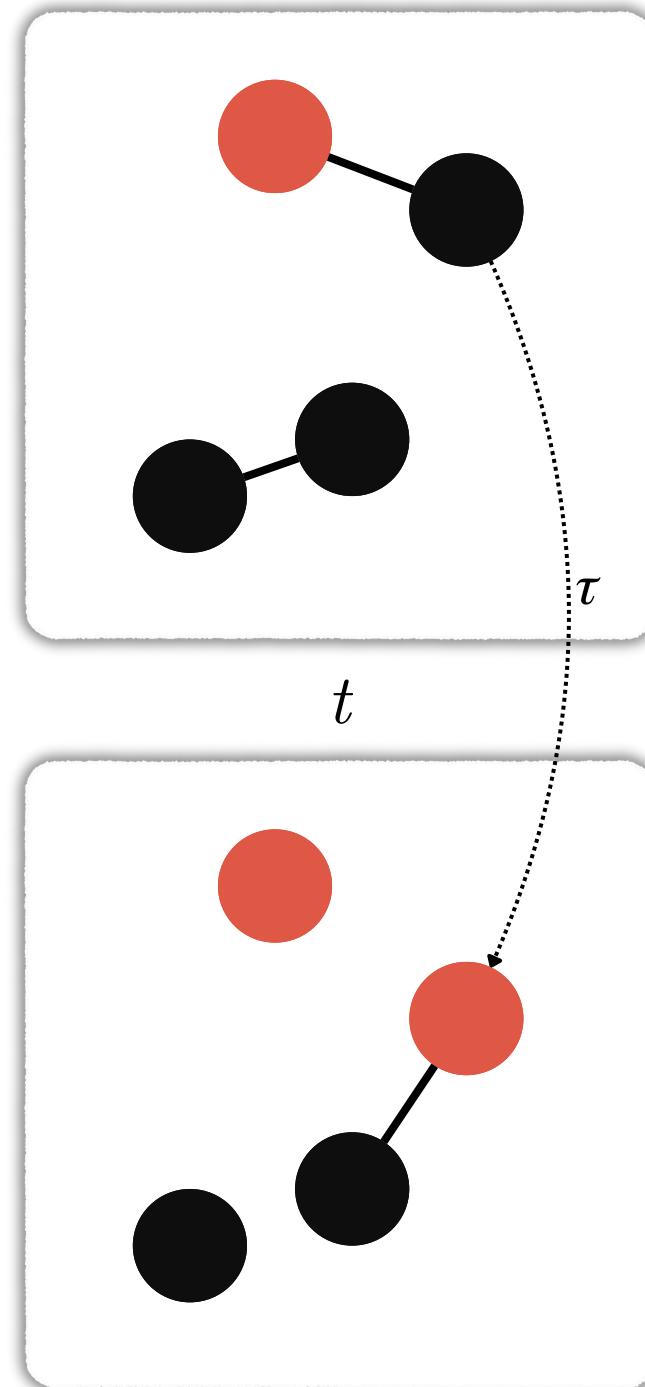
## ANALYSIS

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$$X_i = \begin{cases} 1, & \text{if } i \text{ gets infected,} \\ 0, & \text{otherwise.} \end{cases}$$

The probability of agent  $i$  getting infected at time  $t$ , assuming that  $i$  bumps into another agent  $j$ , is:

$$\begin{aligned} \Pr[X_i = 1] &= \Pr[i \text{ is susceptible, } j \text{ is infected, } j \text{ passes on the infection}] \\ &= \Pr[i \text{ is susceptible}] \cdot \Pr[j \text{ is infected}] \cdot \Pr[j \text{ passes on the infection}] \\ &= \frac{N - I_t}{N} \cdot \frac{I_t}{N} \cdot \tau. \end{aligned}$$



$t + 1$

# THE SI (SUSCEPTIBLE-INFECTED) MODEL

## ANALYSIS

Imagine a random variable  $X_i$  that keeps track of whether agent  $i$  gets infected at time  $t$ :

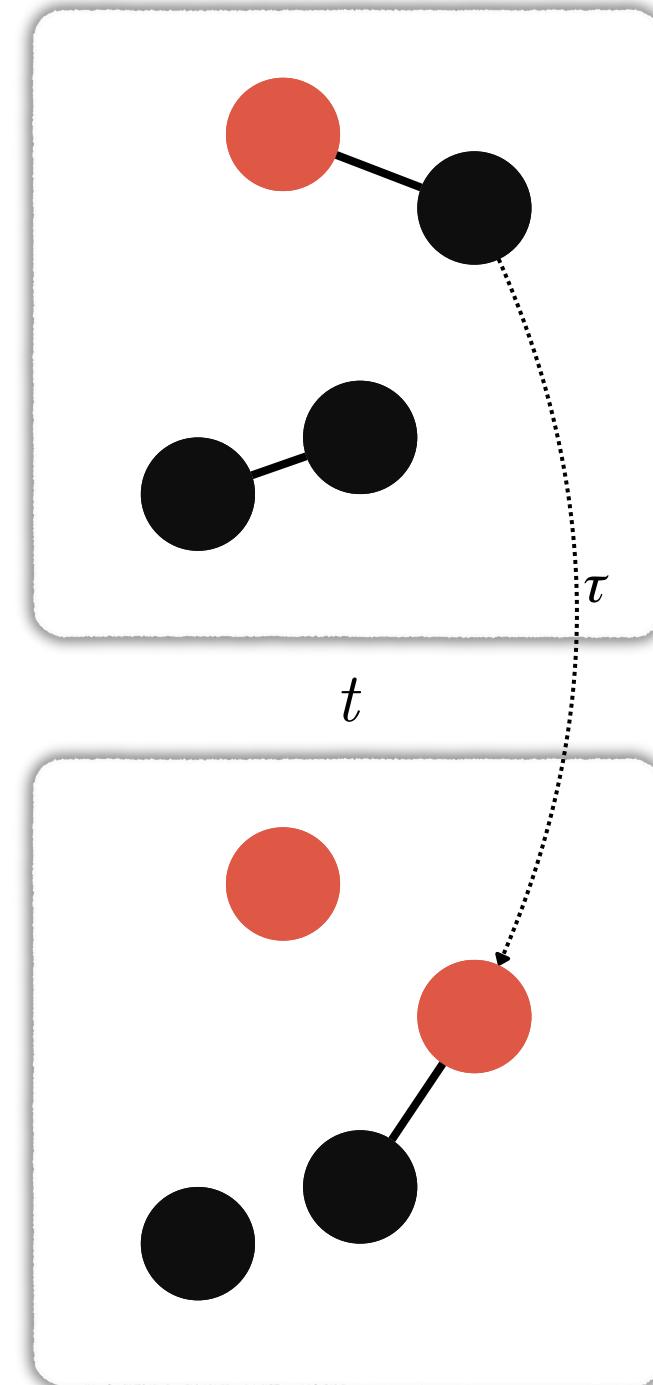
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The average number of agents becoming infected at time  $t$  is, then:

$$\begin{aligned} \mathbb{E} \left[ \sum_1^N X_i \right] &= \mathbb{E}[X_1] + \cdots + \mathbb{E}[X_N] \\ &= N \cdot \frac{N - I_t}{N} \cdot \frac{I_t}{N} \cdot \tau \\ &= \tau I_t \left( 1 - \frac{I_t}{N} \right). \end{aligned}$$

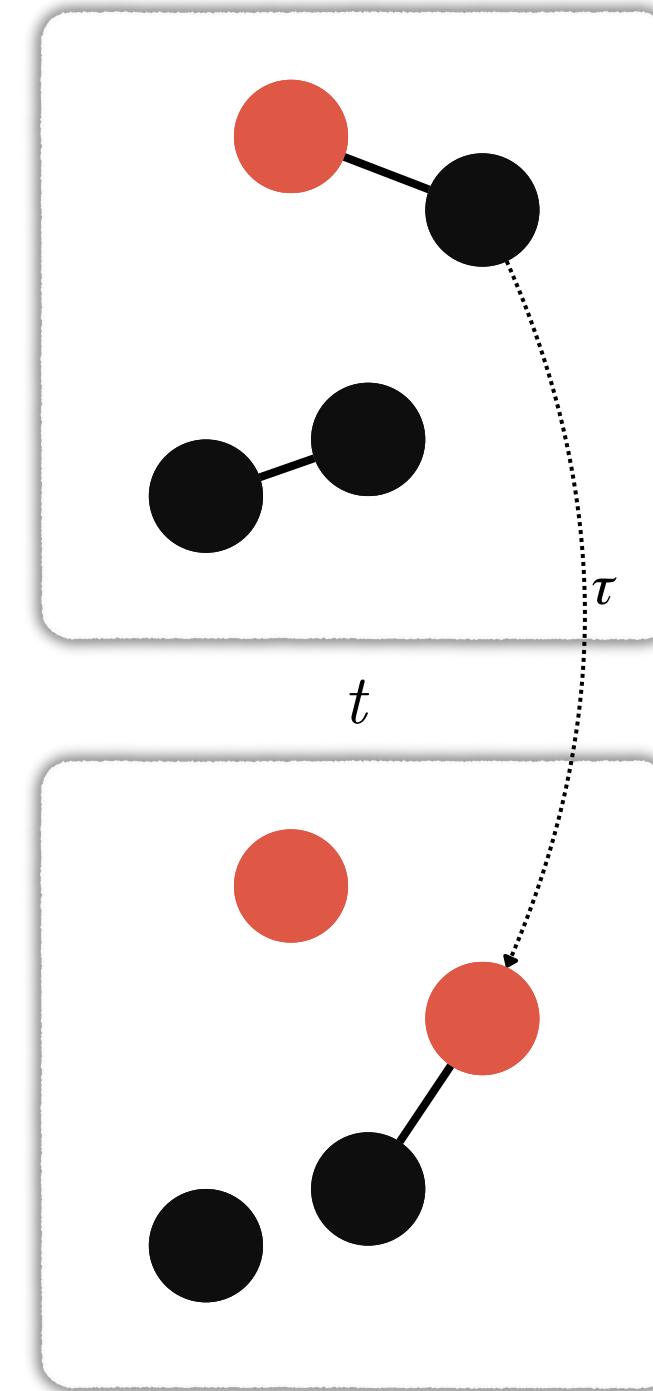


# THE SI (SUSCEPTIBLE-INFECTED) MODEL

## ANALYSIS

Hence, the recursion relation for the number of infectious agents at time  $t + 1$  is:

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

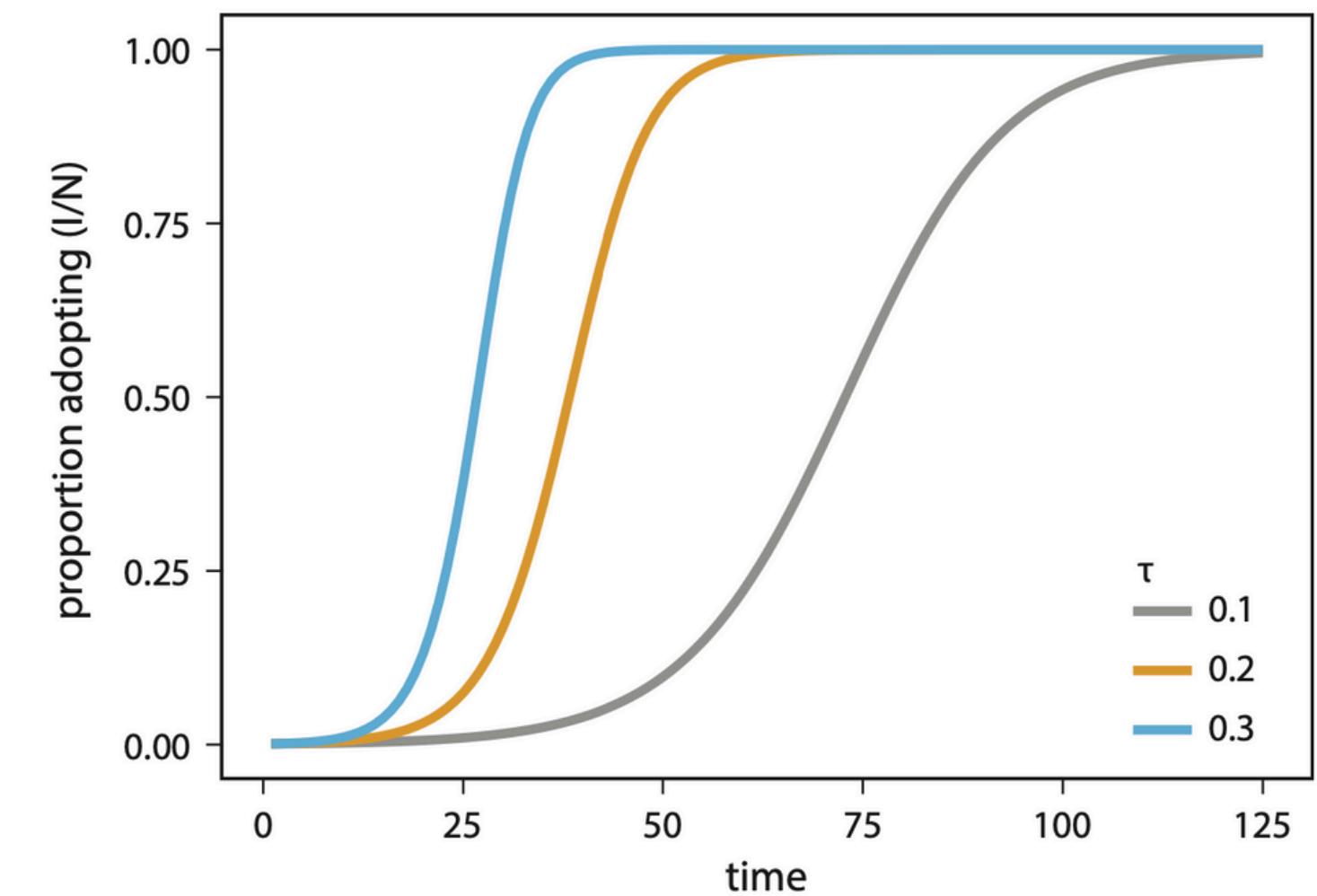


$t + 1$

# THE SI (SUSCEPTIBLE-INFECTED) MODEL

## BEHAVIOR

We see the desired S-shape. Social influence has done the trick!



We can do better though!

# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL

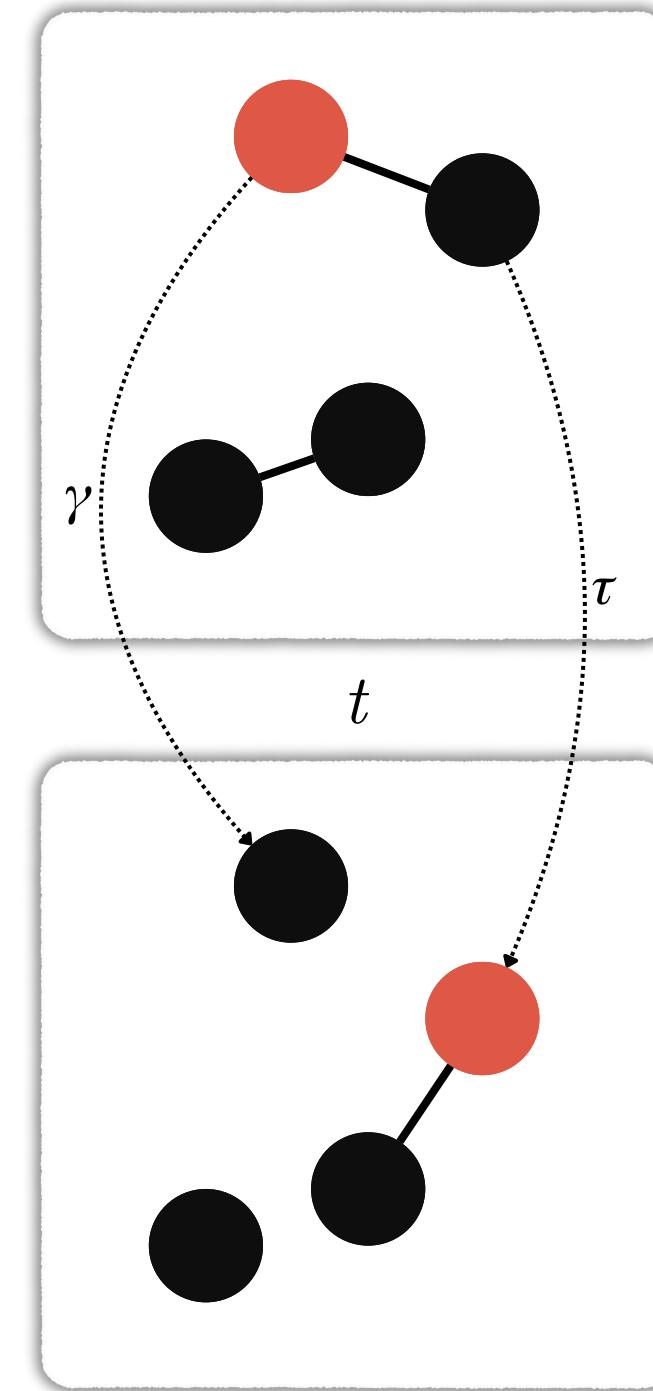
## DESCRIPTION

Only two possible states: susceptible and infected.

At time  $t$  agents form pairs, as if from getting close to each other.

An infected agent transmits the disease to a nearby susceptible agent with probability  $\tau$ .

An infected agent becomes susceptible again with probability  $\gamma$ .



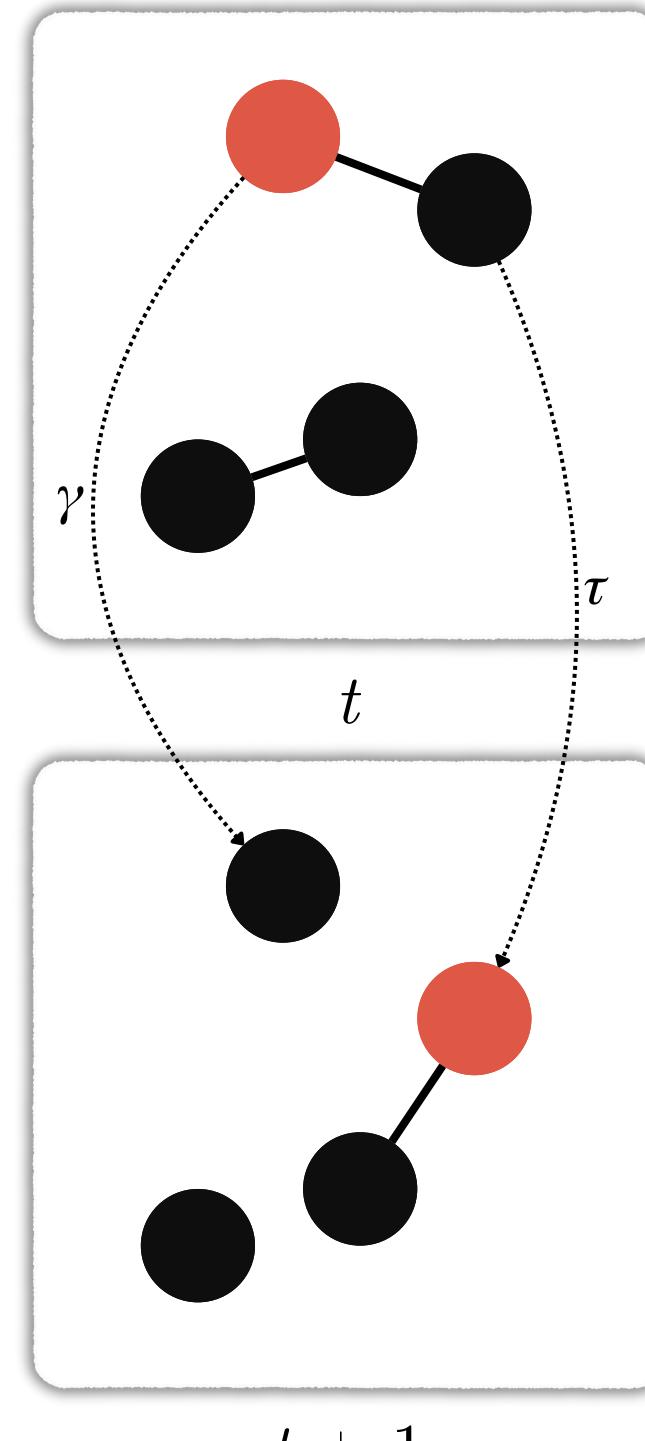
# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL

## ANALYSIS

Apart from the susceptibles that catch the infection, an average of:

$$\gamma I_t$$

infected agents become susceptible again at time  $t$ .



# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL ANALYSIS

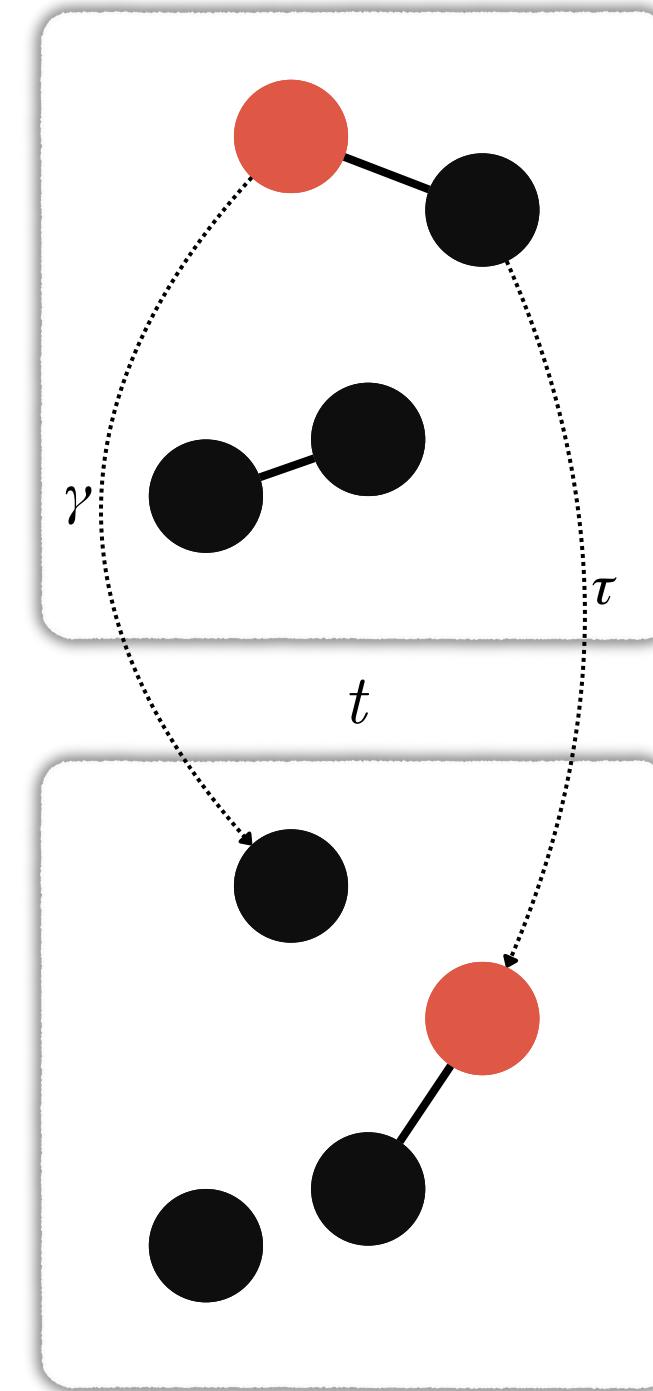
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infected agents become susceptible again at time  $t$ .

Thus, the recurrence relation becomes:

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



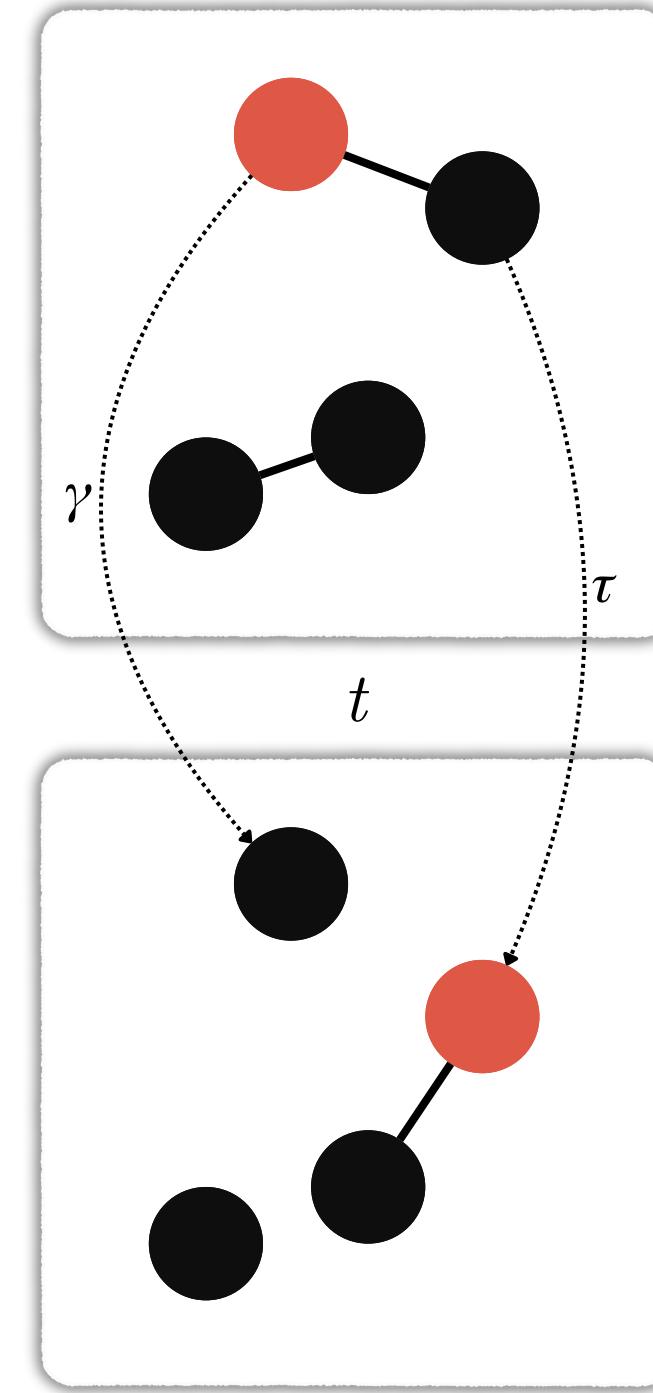
A *dynamic equilibrium* occurs when the number of infected agents stabilizes.

# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL

## DYNAMIC EQUILIBRIUM

The dynamic equilibrium is obtained by setting  $I_{t+1} = I_t = I$ ,  
and plugging this into the recurrence relation to get:

$$I = I + \tau I \left(1 - \frac{I}{N}\right) - \gamma I \quad \text{iff} \quad \tau \left(1 - \frac{I}{N}\right) = \gamma \\ \text{iff} \quad \frac{I}{N} = 1 - \frac{\gamma}{\tau}.$$

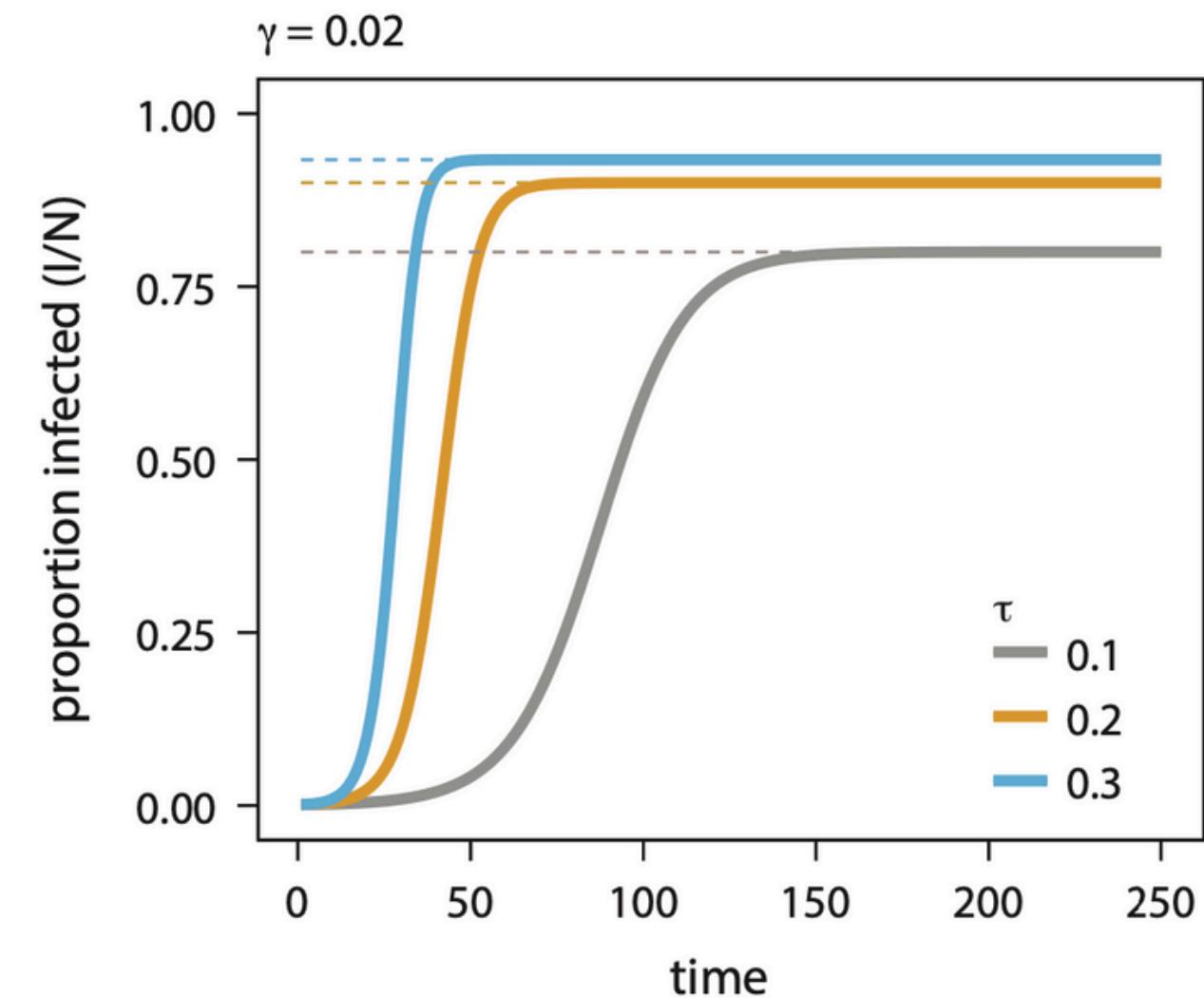


$t + 1$

# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL

## DYNAMIC EQUILIBRIUM

At equilibrium, the number of infections stabilizes.

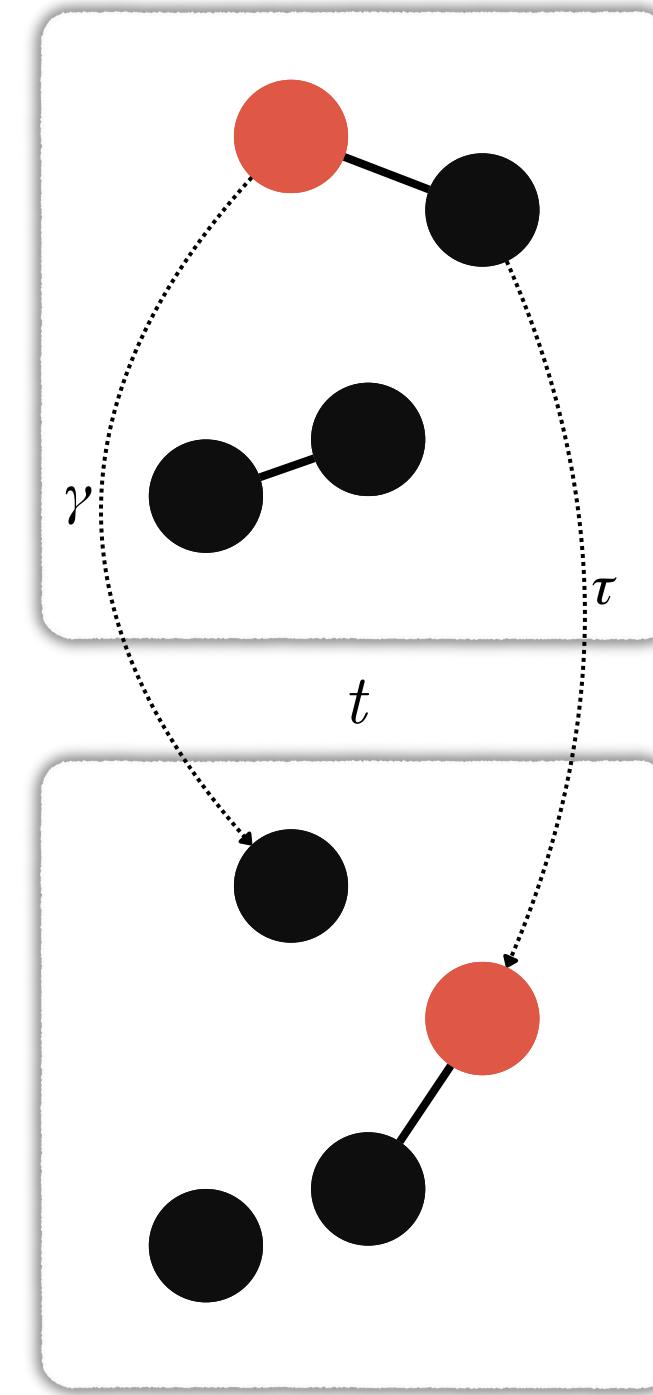


# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL

## CONTROLLING THE SPREAD

At the beginning of an infection, the number  $I_t$  of infected agents is close to 0, hence:

$$1 - \frac{I_t}{N} \approx 1.$$



# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL

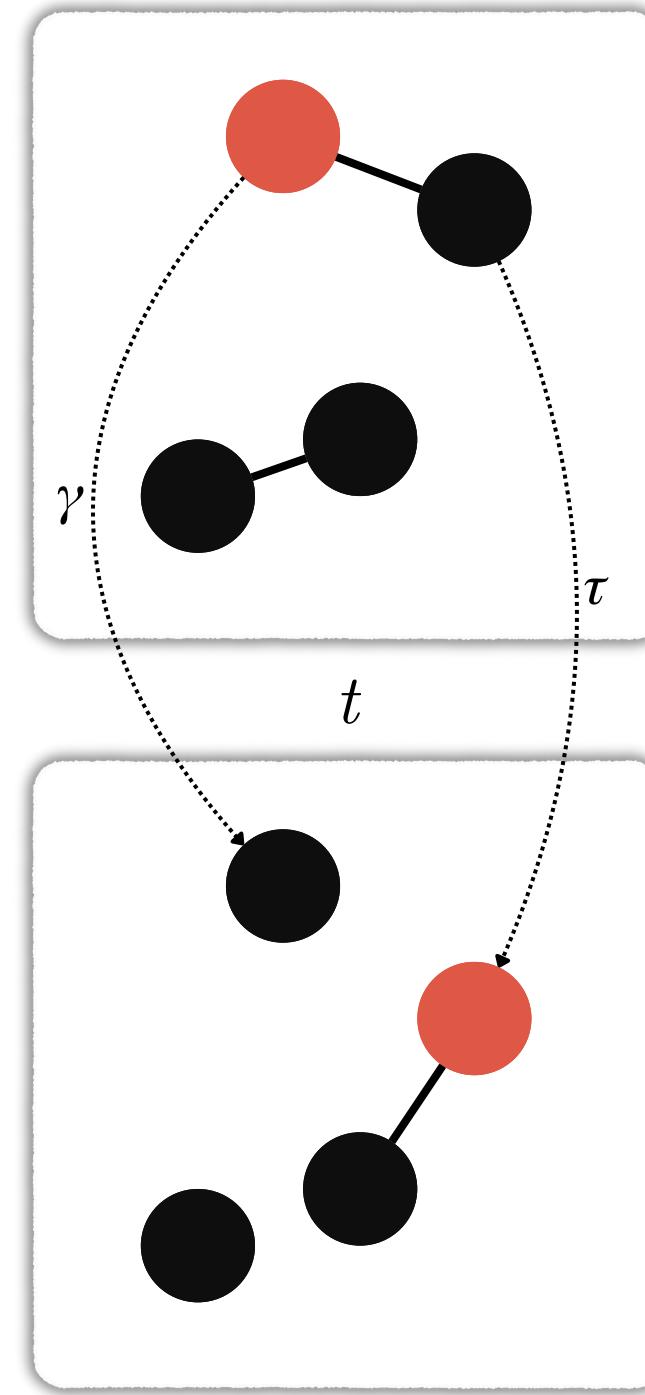
## CONTROLLING THE SPREAD

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$$1 - \frac{I_t}{N} \approx 1.$$

Plugging this into the recurrence relation, we have:

$$\begin{aligned} I_{t+1} &= I_t + \tau I_t \left(1 - \frac{I_t}{N}\right) - \gamma I_t. \\ &\approx I_t + \tau \cdot I_t - \gamma \cdot I_t \\ &= I_t + (\tau - \gamma) I_t. \end{aligned}$$



$t + 1$

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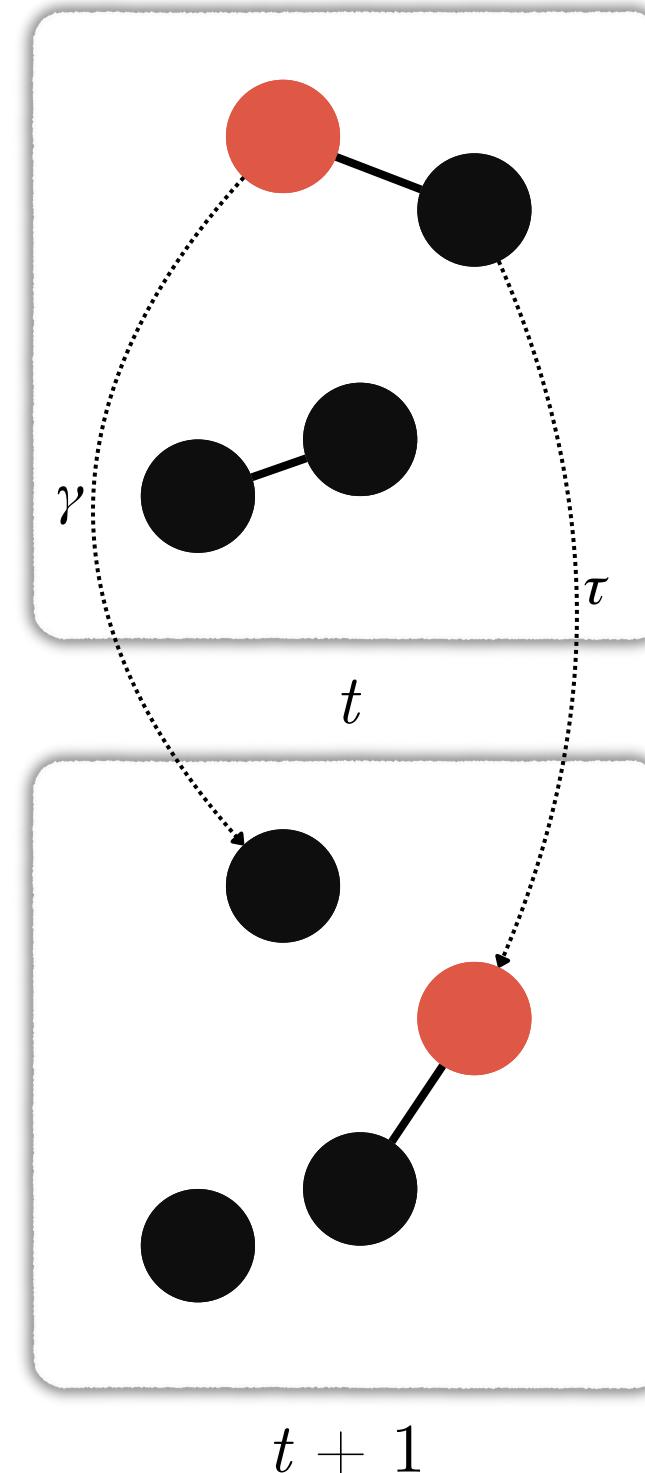
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The condition for the infection spreading becomes:

$$\tau - \gamma > 0 \quad \text{iff} \quad \frac{\tau}{\gamma} > 1.$$



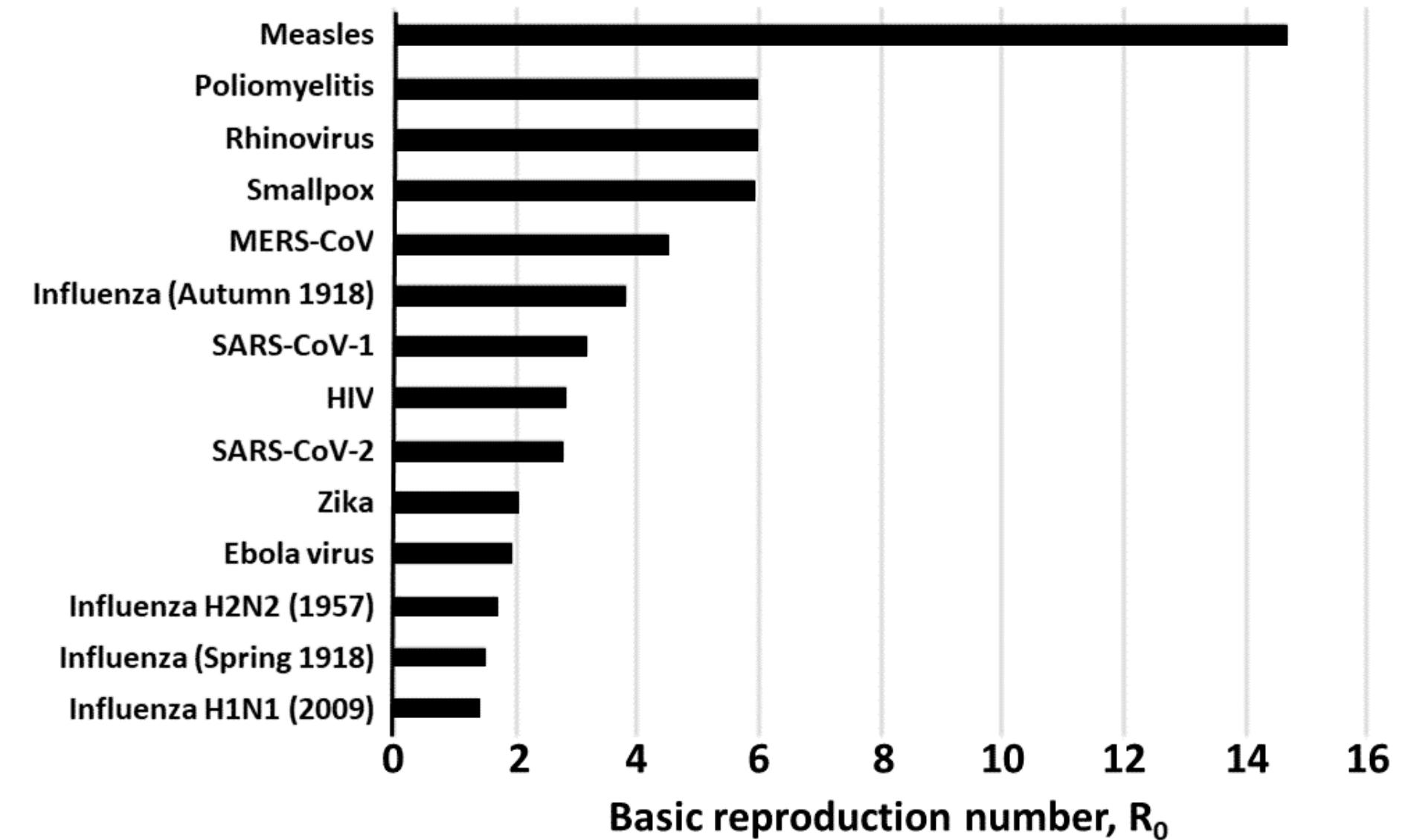
The *basic reproduction number* is defined as:

$$R_0 = \frac{\tau}{\gamma}.$$

We have just shown that, under the assumptions of the basic SIS model, infection spreads just in case  $R_0 > 1$ .

# THE REPRODUCTION NUMBER FOR VARIOUS DISEASES

The basic reproduction number predicts how many individuals, on average, an infected agent will pass the disease to.



What about vaccination?

# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL WITH VACCINATION

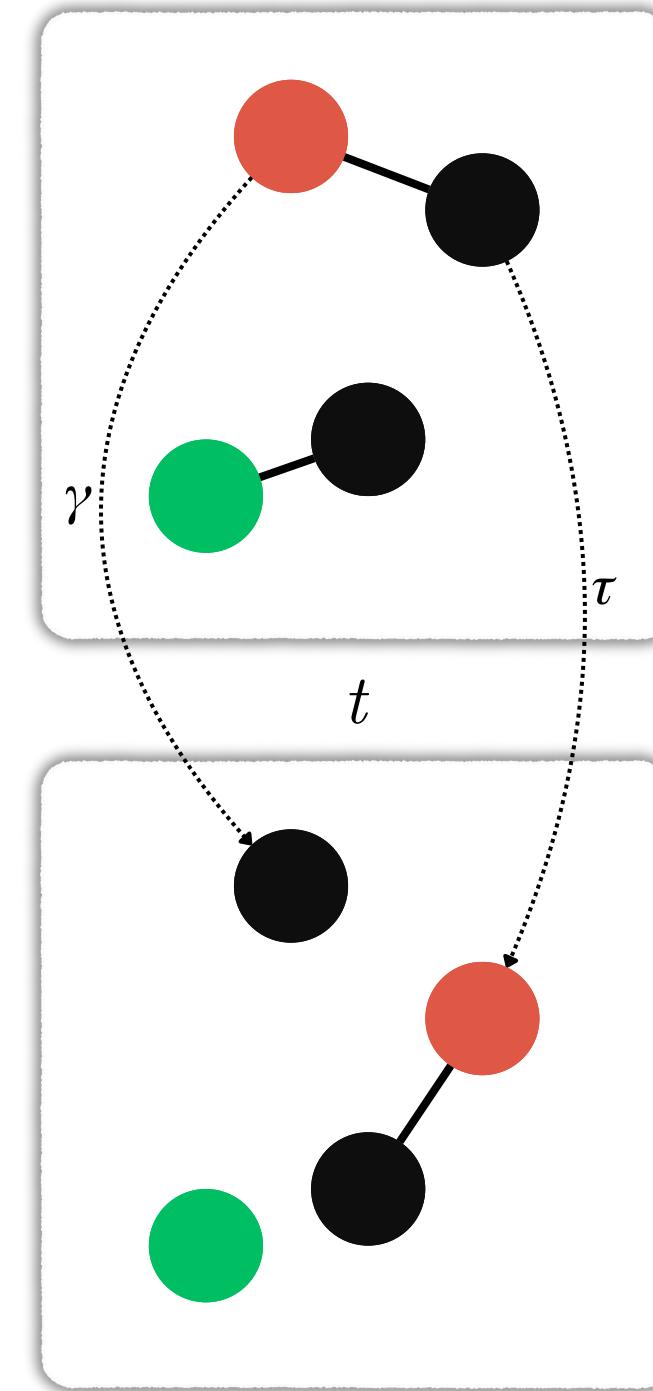
Only two possible states: susceptible and infected.

! A proportion  $V$  of the population starts out vaccinated, which means they are immune.

At time  $t$  agents form pairs, as if from getting close to each other.

An infected agent transmits the disease to a nearby susceptible agent with probability  $\tau$ .

An infected agent becomes susceptible again with probability  $\gamma$ .

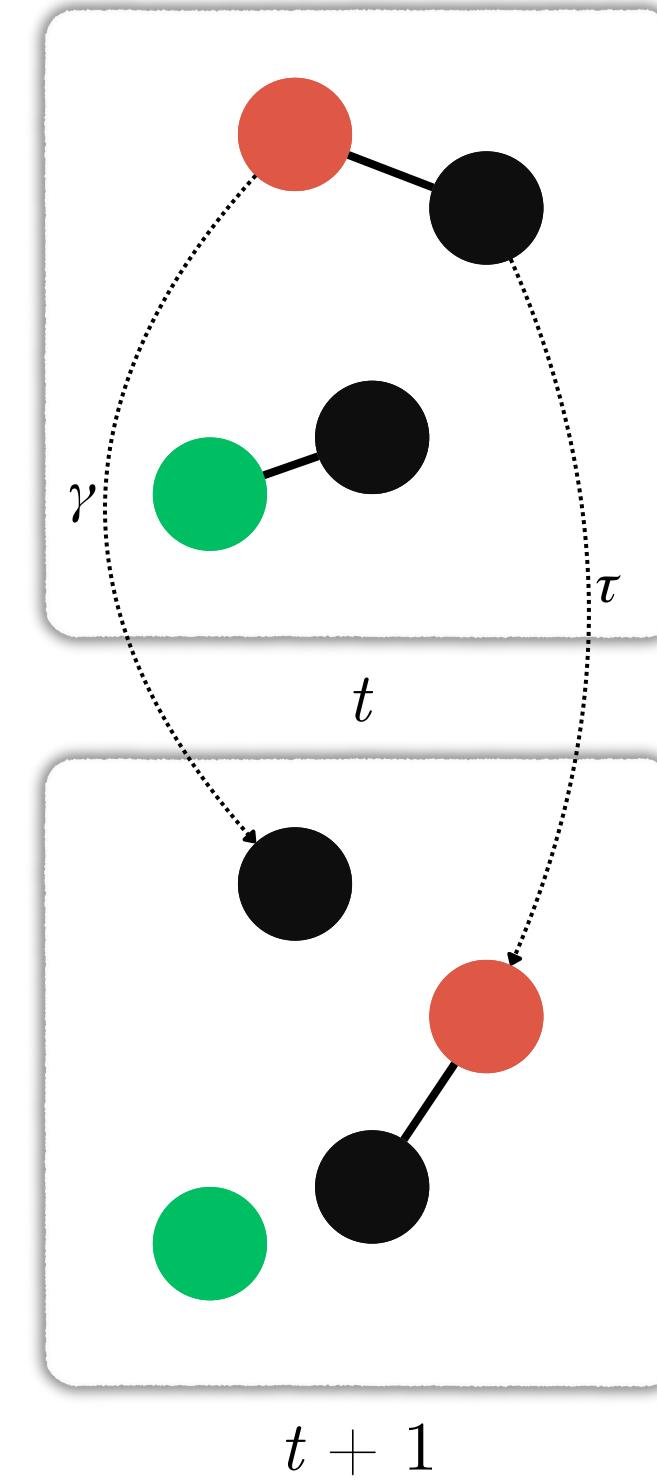


$t + 1$

# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL WITH VACCINATION: ANALYSIS

Recall how we keep track of infected agents:

$$X_i = \begin{cases} 1, & \text{if } i \text{ gets infected,} \\ 0, & \text{otherwise.} \end{cases}$$



# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL WITH VACCINATION: ANALYSIS

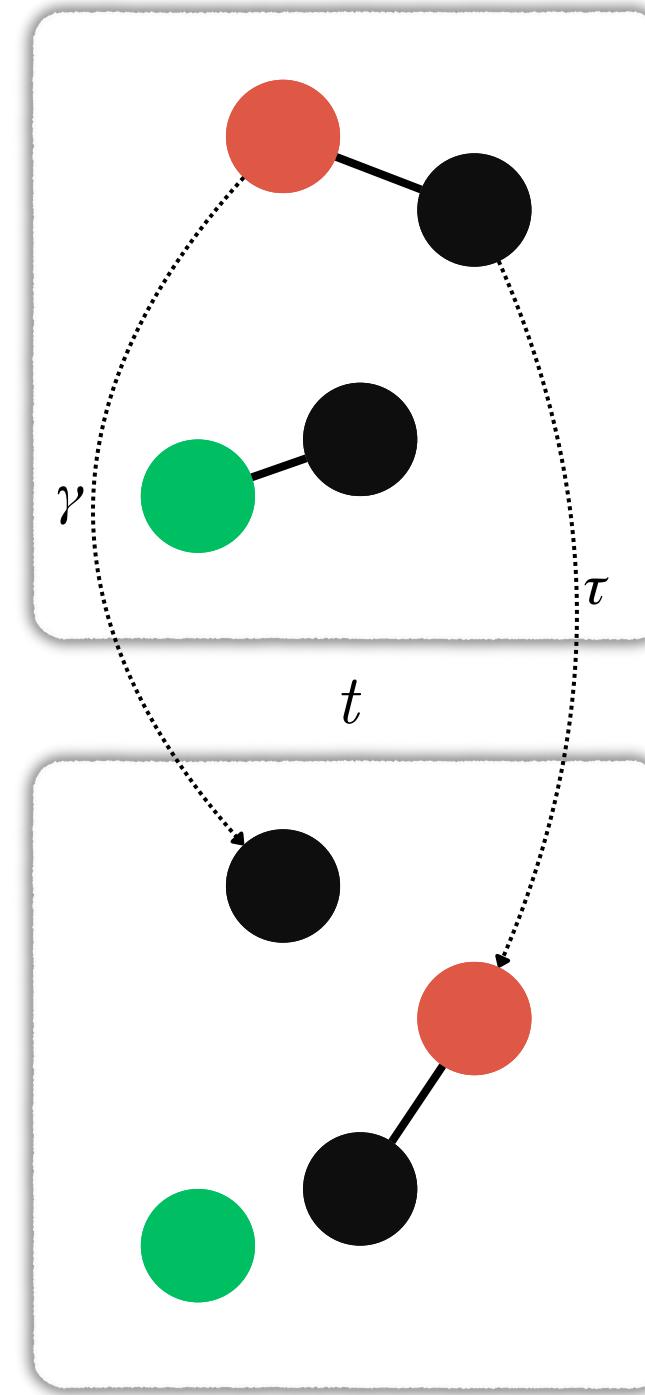
Recall how we keep track of infected agents:

$$X_i = \begin{cases} 1, & \text{if } i \text{ gets infected,} \\ 0, & \text{otherwise.} \end{cases}$$

With vaccination, the probability of agent  $i$  getting infected by  $j$  at time  $t$  depends on  $i$  being unvaccinated:

$\Pr[X_i = 1] = \Pr[i \text{ is susceptible, } i \text{ is unvaccinated, } j \text{ is infected,}$   
 $\quad \quad \quad j \text{ passes on the infection}]$

$$= \frac{N - I_t}{N} \cdot (1 - V) \cdot \frac{I_t}{N} \cdot \tau.$$



$t + 1$

# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL WITH VACCINATION: ANALYSIS

Recall how we keep track of infected agents:

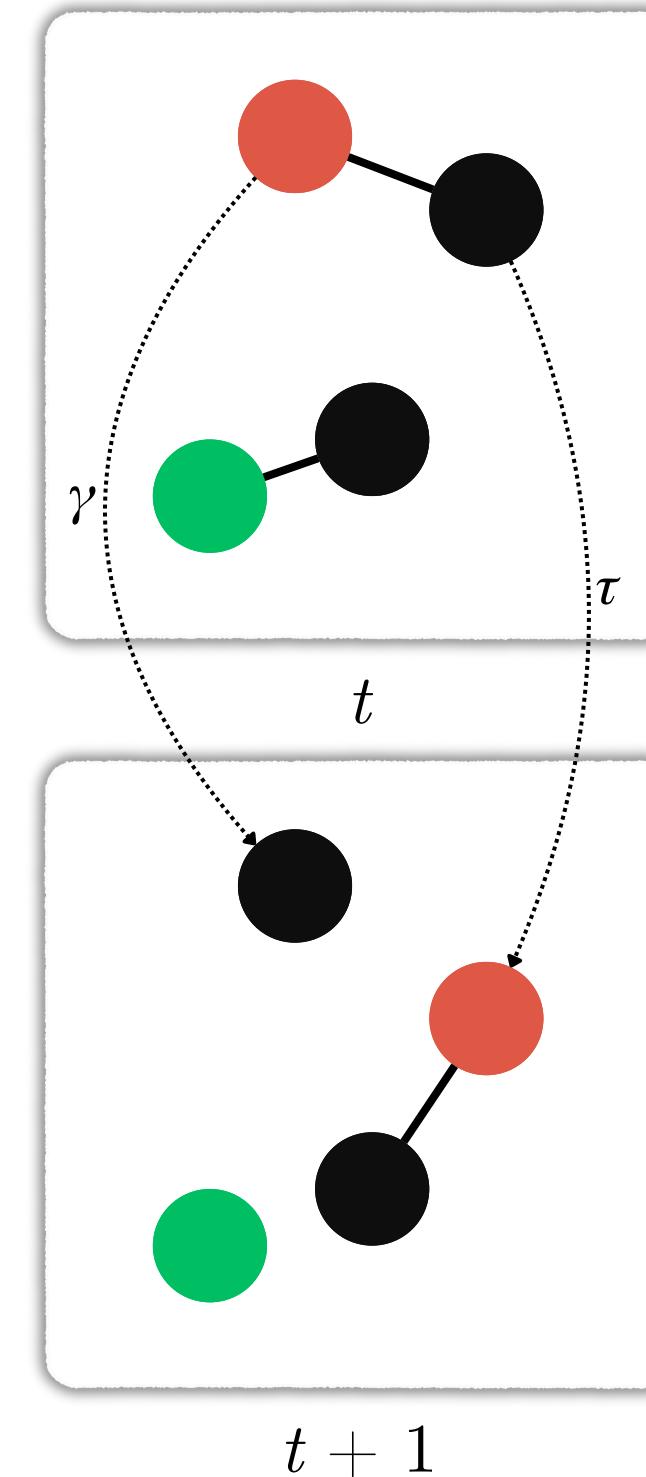
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With vaccination, the probability of agent  $i$  getting infected by  $j$  at time  $t$  depends on  $i$  being unvaccinated:

$$\begin{aligned} \Pr[X_i = 1] &= \Pr[i \text{ is susceptible, } i \text{ is unvaccinated, } j \text{ is infected,} \\ &\quad j \text{ passes on the infection}] \\ &= \frac{N - I_t}{N} \cdot (1 - V) \cdot \frac{I_t}{N} \cdot \tau. \end{aligned}$$

Thus, the average number of newly infected agents at  $t$  is:

$$\tau \left(1 - \frac{I_t}{N}\right) (1 - V) I_t$$



# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL

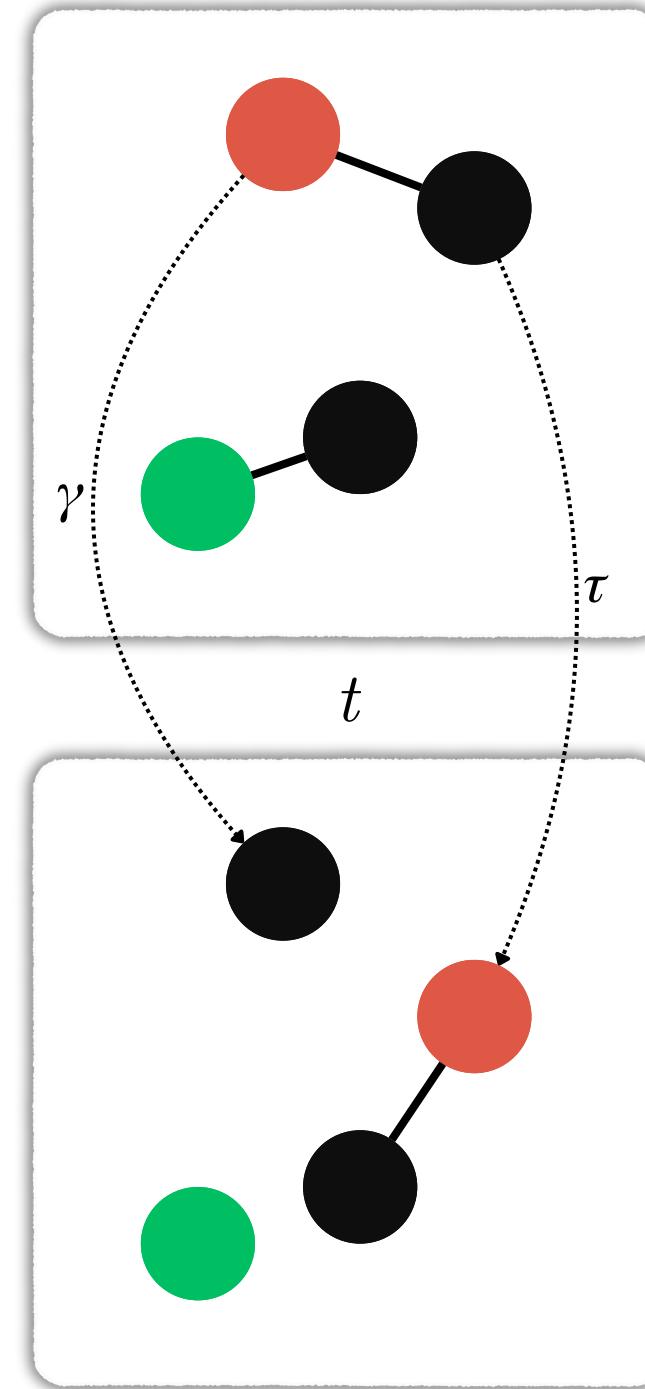
## WITH VACCINATION: WHEN DOES IT SPREAD?

With vaccinated agents, the recurrence relation for the change in infected agents is:

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

Approximating  $1 - I_t/N$  with 1 again, the condition for the infection spreading is:

$$\begin{aligned} \tau(1 - V) - \gamma > 0 &\quad \text{iff} \quad \frac{\tau}{\gamma}(1 - V) > 1 \\ &\quad \text{iff} \quad R_0(1 - V) > 1. \end{aligned}$$



The *effective basic reproductive number* is:

$$\begin{aligned} r_0 &= R_0(1 - V) \\ &= \frac{\tau}{\gamma}(1 - V). \end{aligned}$$

We have just shown that the infection spreads just in case  $r_0 > 1$ .

# THE SIS (SUSCEPTIBLE-INFECTED-SUSCEPTIBLE) MODEL

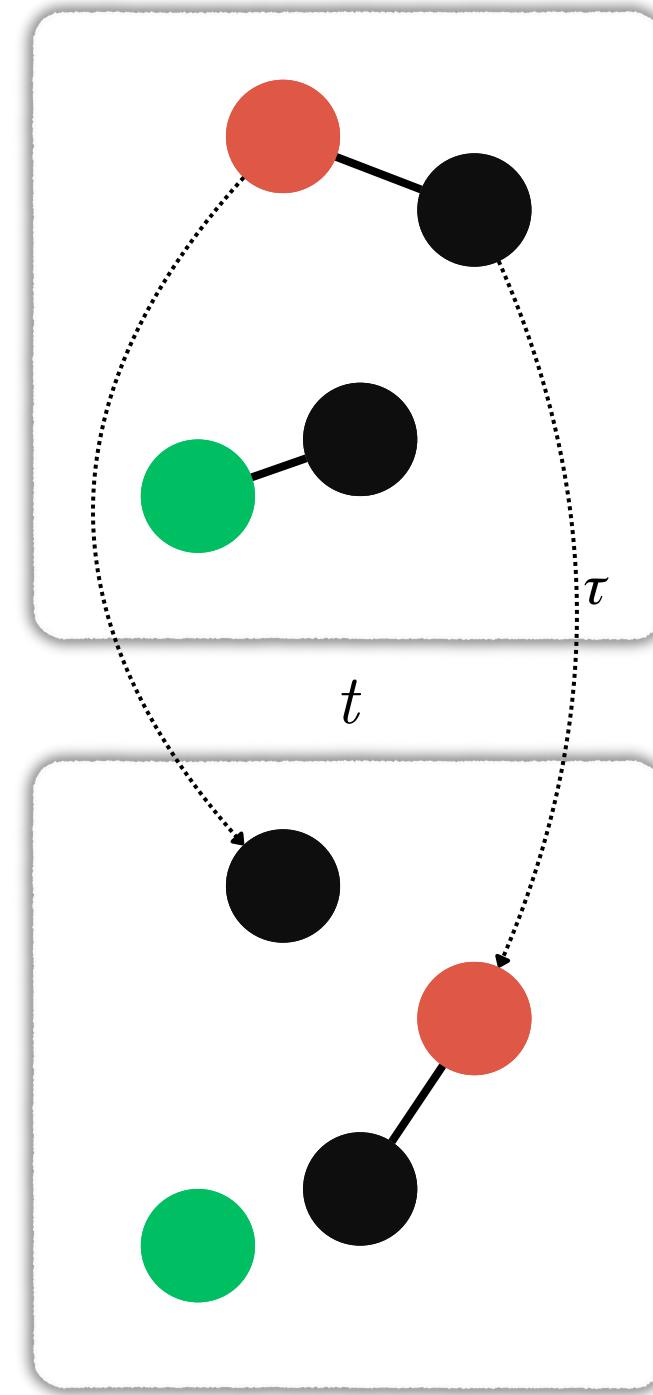
## WITH VACCINATION: CONTROLLING THE SPREAD

The infection does *not* spread just in case:

$$R_0(1 - V) \leq 1 \quad \text{iff} \quad 1 - V \leq \frac{1}{R_0}$$
$$\quad \text{iff} \quad V \geq 1 - \frac{1}{R_0}.$$

The smallest value for which the infection does not spread, called the *threshold vaccination rate for herd immunity*, is:

$$V^* = 1 - \frac{1}{R_0}.$$



# THE SIR (SUSCEPTIBLE-INFECTED-RECOVERED) MODEL

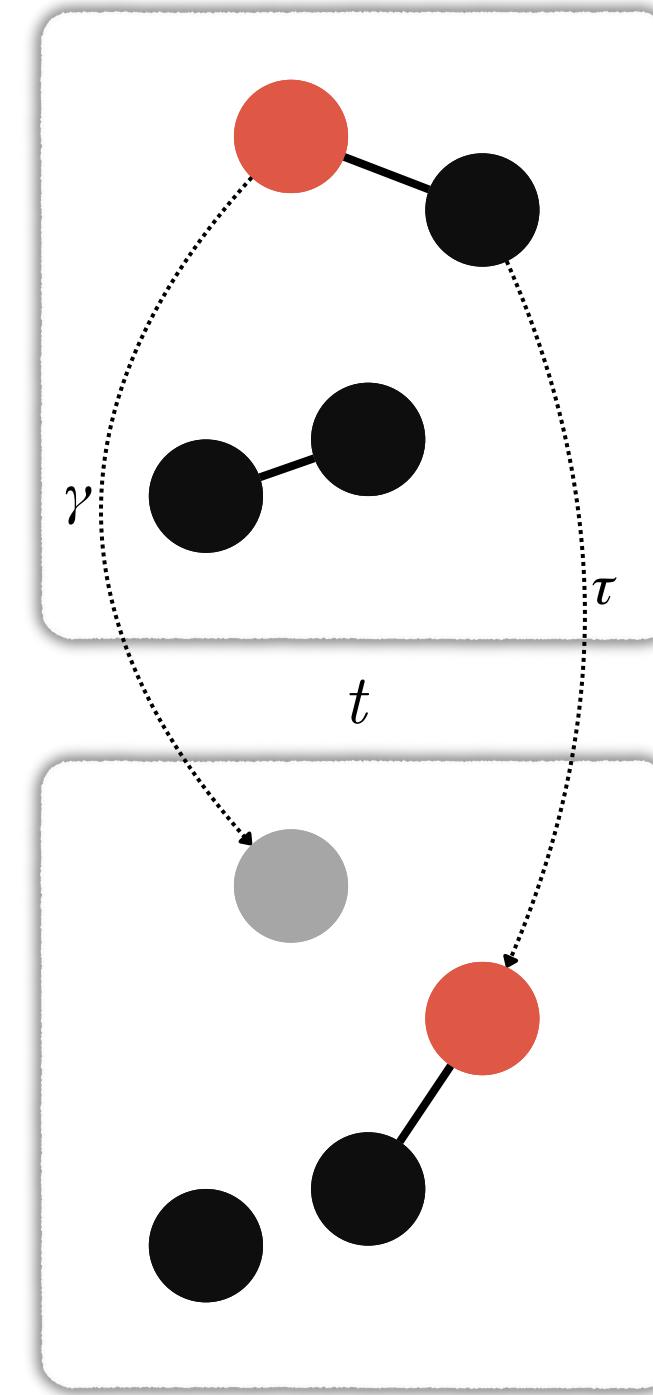
## DESCRIPTION

Three possible states: susceptible, infected and removed

At time  $t$  agents form pairs, as if from getting close to each other.

An infected agent transmits the disease to a nearby susceptible agent with probability  $\tau$ .

An infected agent becomes removed with probability  $\gamma$ .



# THE SIR (SUSCEPTIBLE-INFECTED-RECOVERED) MODEL

## ANALYSIS

The dynamics are given by the following recurrence relations:

$$S_{t+1} = S_t - \tau S_t \frac{I_t}{N},$$

$$I_{t+1} = I_t + \tau S_t \frac{I_t}{N} - \gamma I_t,$$

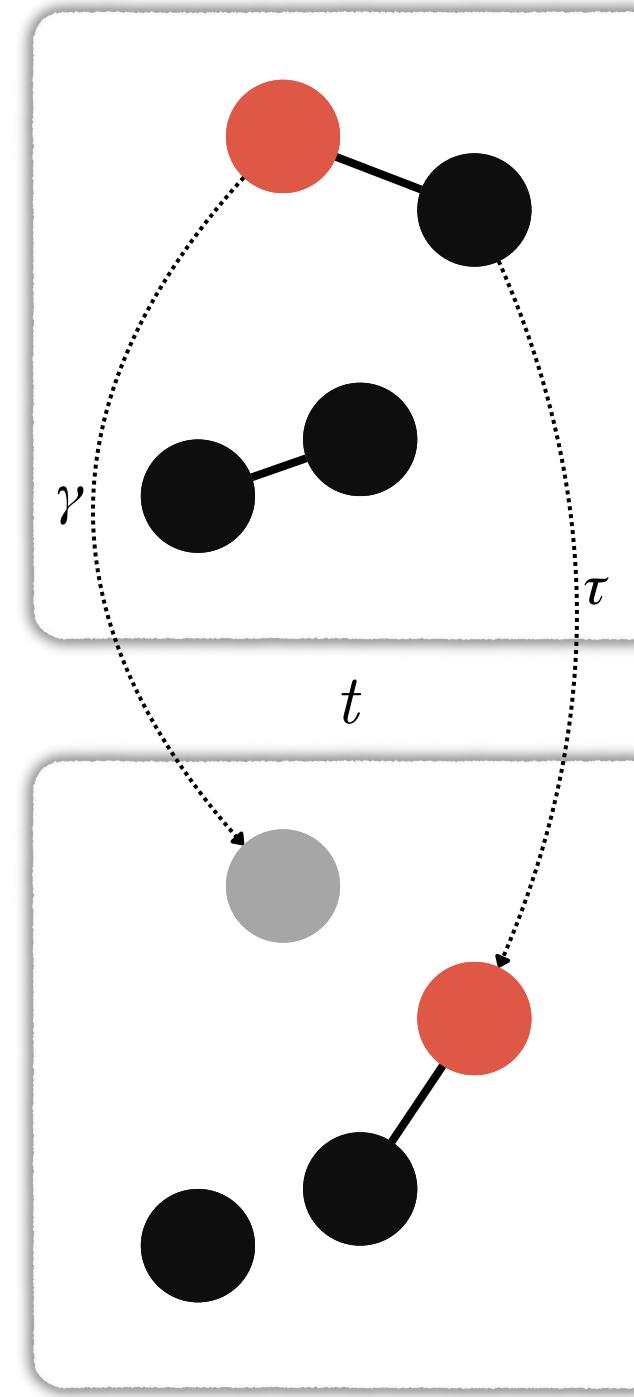
$$R_{t+1} = R_t + \gamma I_t.$$

Written as difference equations:

$$\Delta S = -\tau S_t \frac{I_t}{N},$$

$$\Delta I = \tau S_t \frac{I_t}{N} - \gamma I_t,$$

$$\Delta R = \gamma I_t.$$



$t + 1$

# THE SIR (SUSCEPTIBLE-INFECTED-RECOVERED) MODEL

## BEHAVIOR

The SIR model approximates the dynamics of real epidemics.

