



Epidemics



Outbreak

- An outbreak occurs when a contagious disease spreads in one community.

Epidemic

- An epidemic is an outbreak of infectious disease that spreads more rapidly than expected and affects many people, e.g. SARS in 2003

Pandemic

- A pandemic is a large version of epidemic which affects people globally, e.g. Hong Kong influenza (H3N2) killed 1 to 4 millions people in 1968.



Connections to the Diffusion of Ideas and Behaviors

- Epidemic disease ↔ The diffusion of ideas through social networks
 - Spread from person to person
 - Across similar kinds of networks that connect people
- The process of one person "infects" another
 - diffusion of ideas : social contagion
 - decision making
 - Epidemic
 - randomness

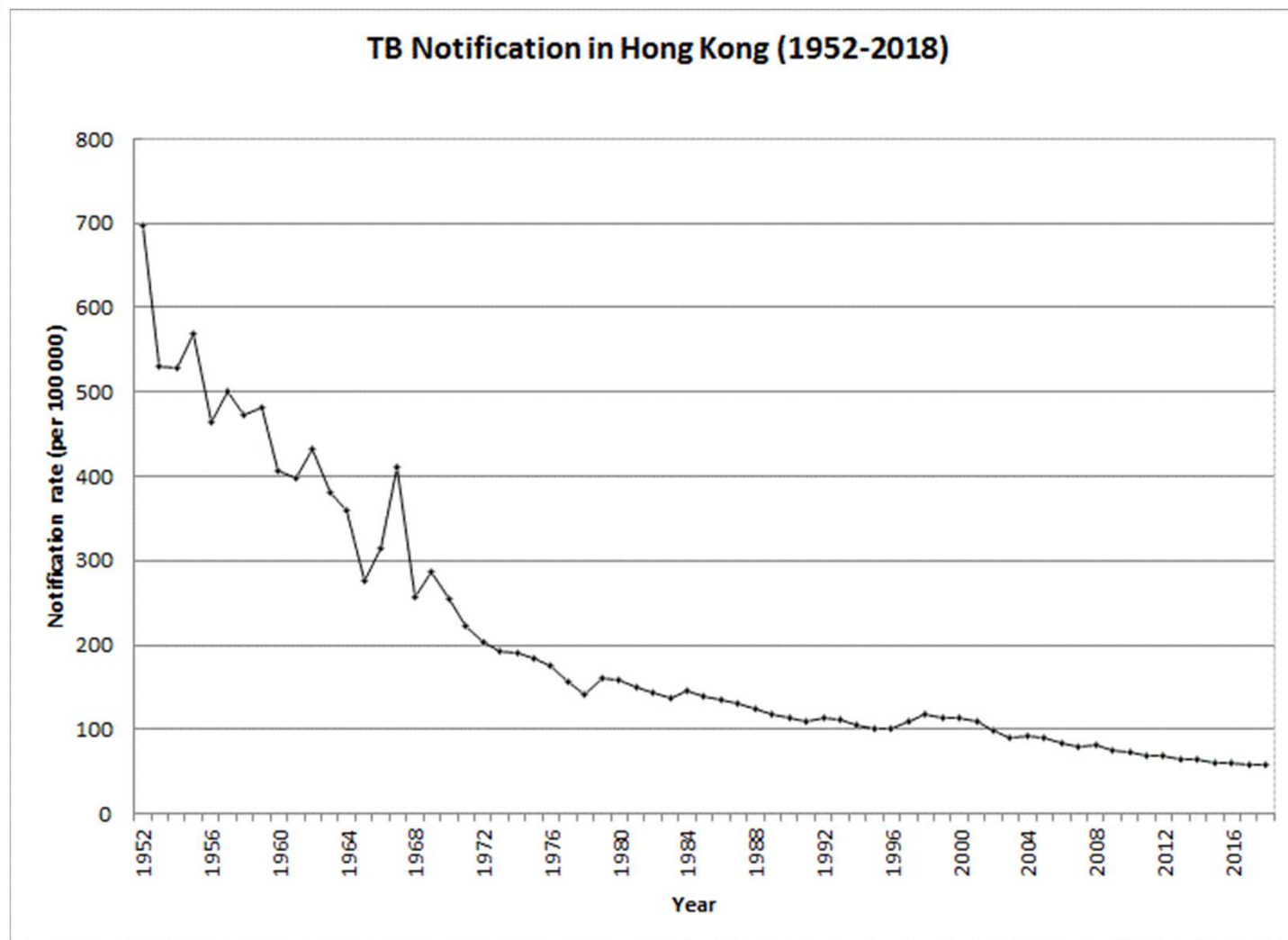


Epidemics



- The patterns by which epidemics spread through groups of people is determined by
 - the **properties** of the pathogen carrying it : including its contagiousness, the length of its infectious period, and its severity
 - by **network structures** within the population it is affecting
- **Contact network**
 - node : each person
 - edge : if two people come into contact with each other
 - Contact networks vary from one disease to another
 - Airbourne transmission
 - Droplet contact
 - Direct physical contact
 - Sexual contact







Influenza-like illness outbreak surveillance, 2015-19

In week 10, 34 ILI outbreaks occurring in schools/institutions were recorded (affecting 176 persons), as compared to 72 outbreaks recorded in the previous week (affecting 553 persons) (Figure 3). The overall number was at the low intensity level currently (Figure 4*). In the first 4 days of week 11 (Mar 10 to 13), 15 ILI outbreaks in schools/institutions were recorded (affecting 74 persons). Since the start of the 2018/19 winter influenza season in week 1, 774 outbreaks were recorded (as of Mar 13).

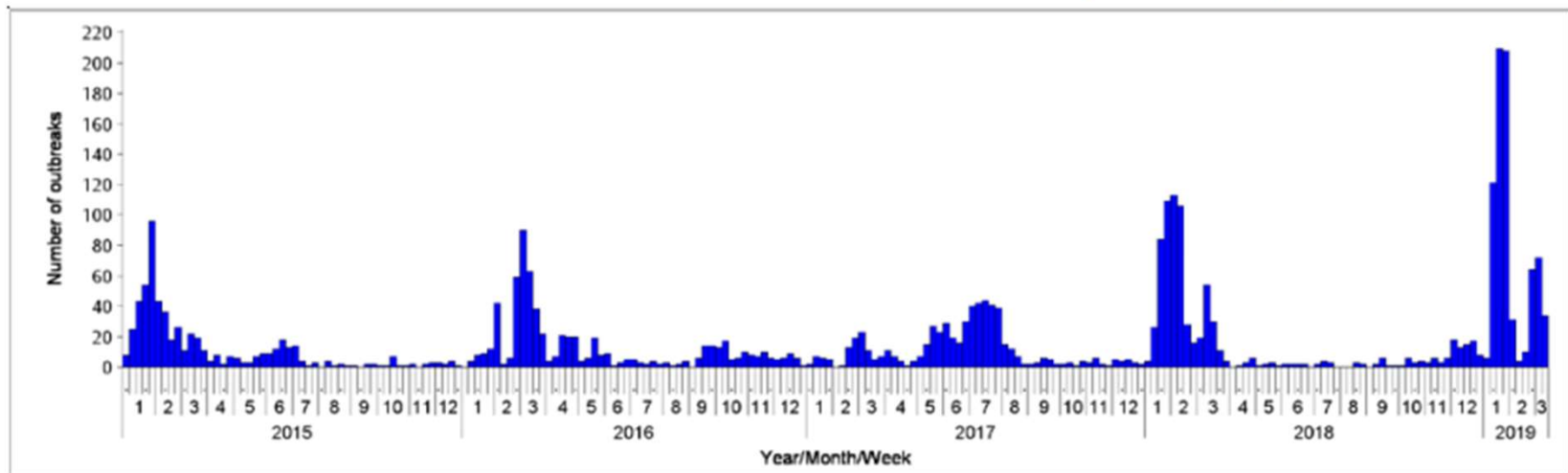


Figure 3 ILI outbreaks in schools/institutions, 2015-19

Source : Centre for Health Protection,
Department of Health, HKSAR



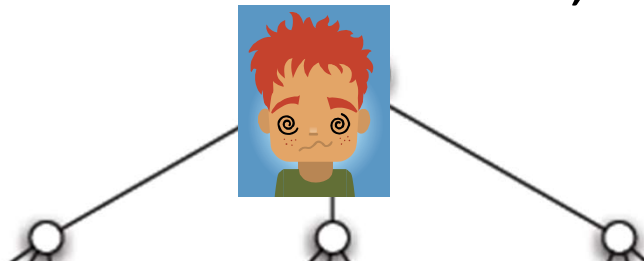
Outline

- Most basic probabilistic **models** for epidemics in networks
- How these models provide insight into some basic qualitative issues in the **spread** of disease, including synchronization, timing, and concurrency in transmission
- How some of the models developed here are related to similar issues in **genetic inheritance**, where a kind of randomized propagation takes place through genealogical networks



Branching Processes

- First wave
 - a person carries a new disease enters a population
 - he transmits it to each person he meets independently with a probability of p
 - the first wave of the epidemic refers to the k people he meets while he is contagious
 - some of the people in the first wave may get infected with the disease, while others may not





- Second wave

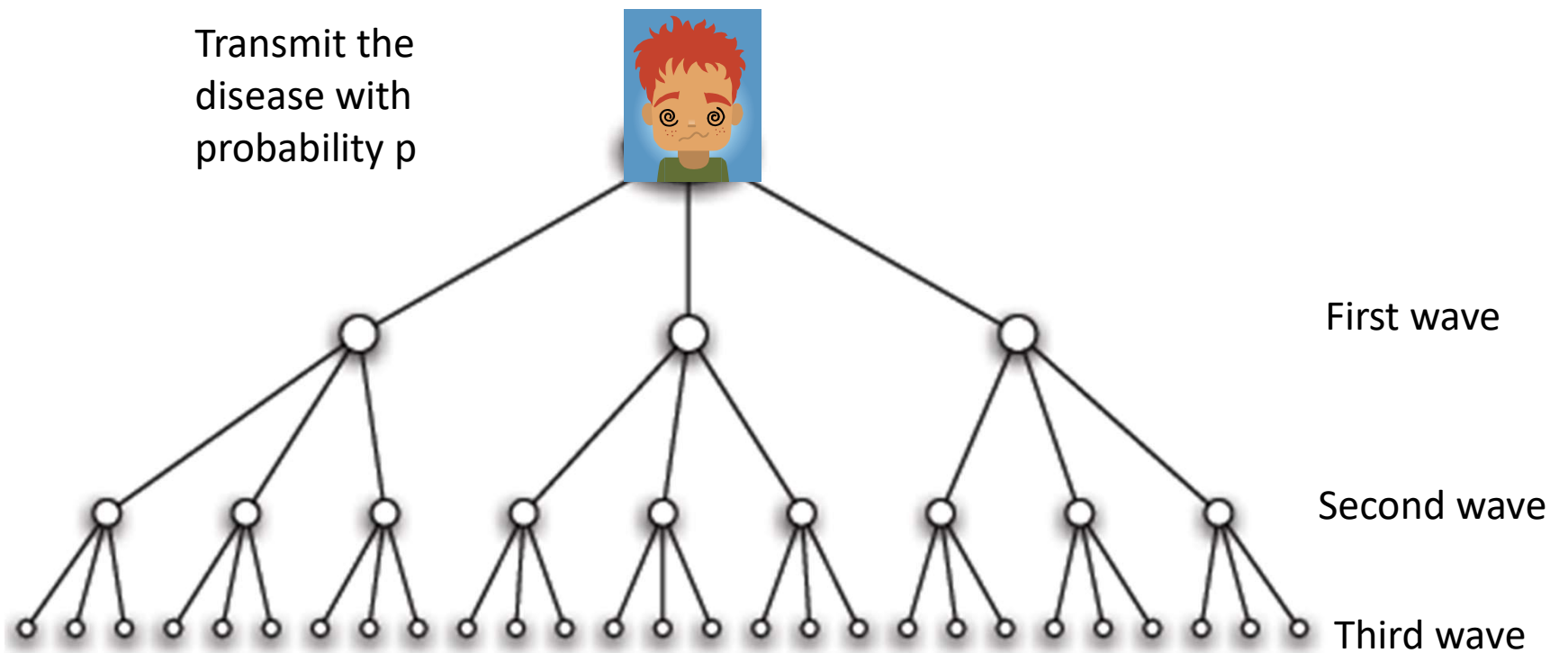
- Now, each person in the first wave goes out into the population and meets k different people, resulting in a second wave of $k \times k = k^2$ people. Each infected person in the first wave passes the disease independently to each of the k second-wave people they meet, again independently with probability p .



- Subsequent waves
 - Further waves are formed in the same way, by having each person in the current wave meet k new people, passing the disease to each independently with probability p .

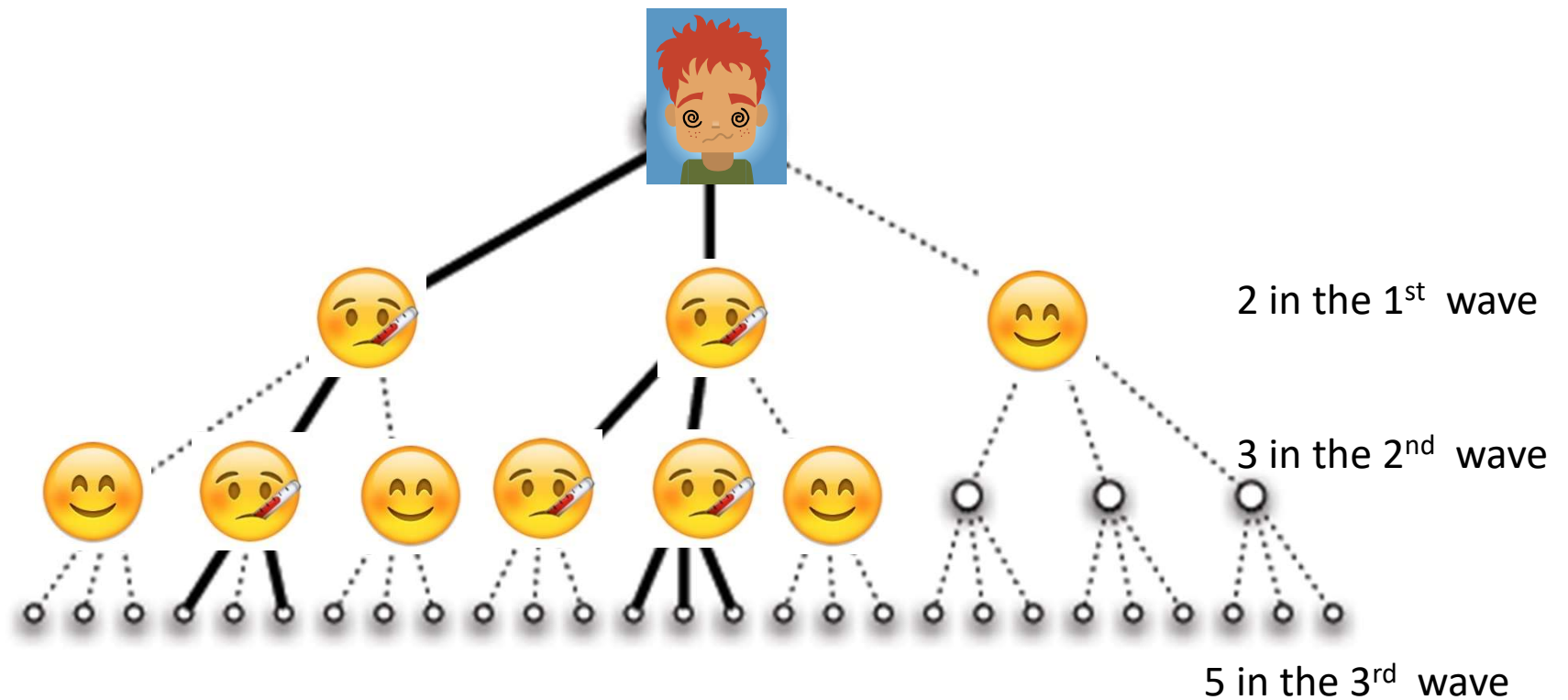


Contact network



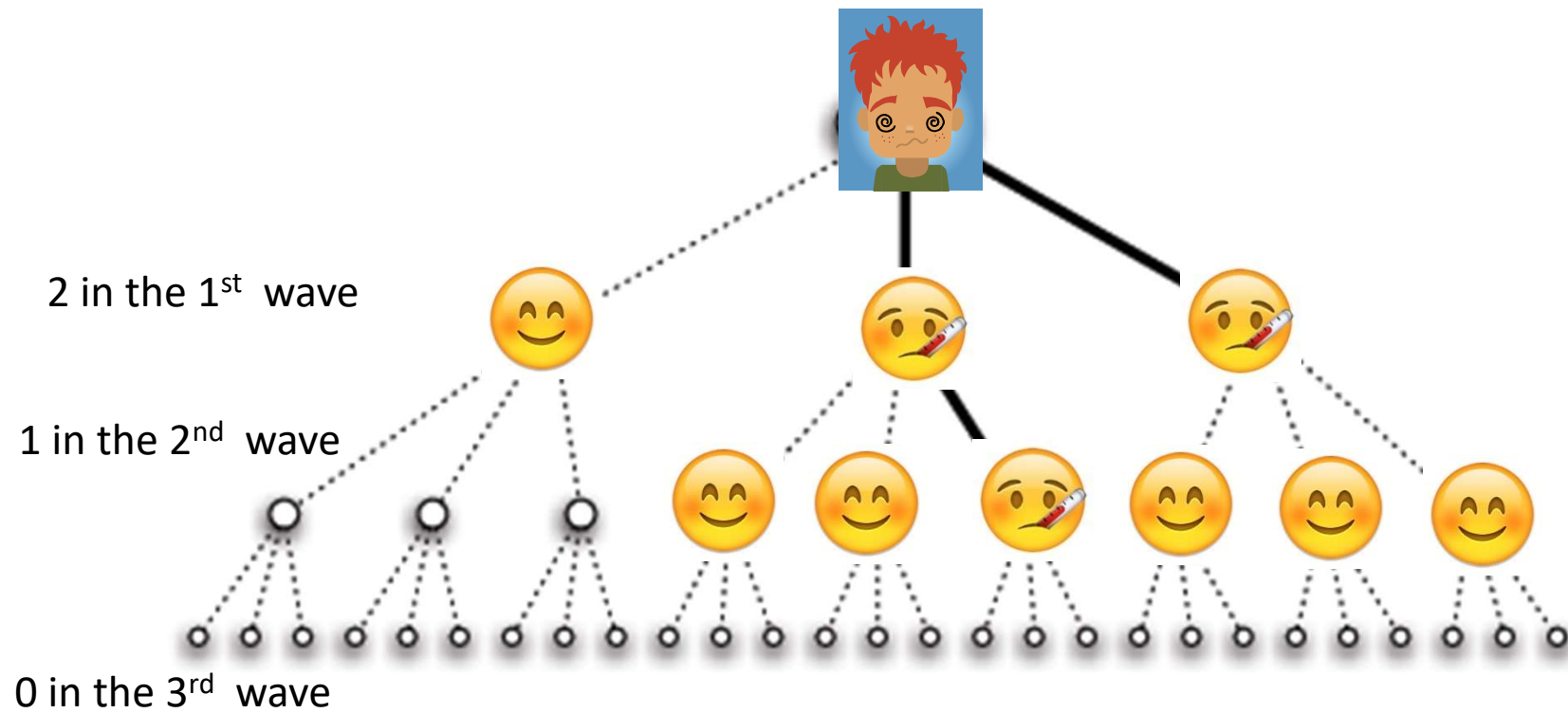


high contagion probability





low contagion probability





Dichotomy for Branching Processes

- Two possibilities for a disease in the branching process model:
 - it reaches a wave where it infects no one, thus **dying out** after a finite number of steps;
 - it continues to infect people in every wave, **proceeding infinitely** through the contact network.



The Basic Reproductive Number

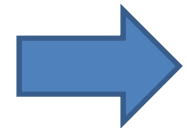
- Everyone meets k new people and infects each with probability p
- The **basic reproductive number** (R_0) = the expected number of new cases of the disease caused by a single individual = pk .

$$R_0 = pk$$



Dichotomy for Branching Processes

- R_0 = the expected number of new cases
- Claim:
 - If $R_0 < 1$, then with probability 1, the disease dies out after a finite number of waves.
 - If $R_0 > 1$, then with probability greater than 0, the disease persists by infecting at least one person in each wave.





Dichotomy for Branching Processes

- Critical value when $R_0 = 1$
 - when R_0 is slightly above 1
 - a positive probability of enormous **outbreak**
 - when R_0 is slightly below 1
 - can **eliminate** the risk of a large epidemic
- It can be worth investing large amounts of effort even to produce small shifts in the basic reproductive number.
- $R_0 = p k$
- Two basic kinds of public-health measures to reduce R_0
 - quarantining people, which reduces the quantity k ,
 - and encouraging behavioral measures such as better sanitary practices to reduce the spread of germs, which reduces the quantity p .





Customary values of R_0 of well-known infectious diseases^[1]

Disease	Transmission	R_0
Measles	Airborne	12–18
Diphtheria	Saliva	6–7
Smallpox	Airborne droplet	5–7
Polio	Fecal–oral route	5–7
Rubella	Airborne droplet	5–7
Mumps	Airborne droplet	4–7
Pertussis	Airborne droplet	5.5 ^[2]
HIV/AIDS	Sexual contact	2–5
SARS	Airborne droplet	2–5 ^[3]
COVID-19	Airborne droplet	1.4–6.6 ^{[4][5][6]}
Influenza (1918 pandemic strain)	Airborne droplet	2–3 ^[7]
Ebola (2014 Ebola outbreak)	Body fluids	1.5–2.5 ^[8]
MERS	Airborne droplet	0.3–0.8 ^[9]




Source : wikipedia

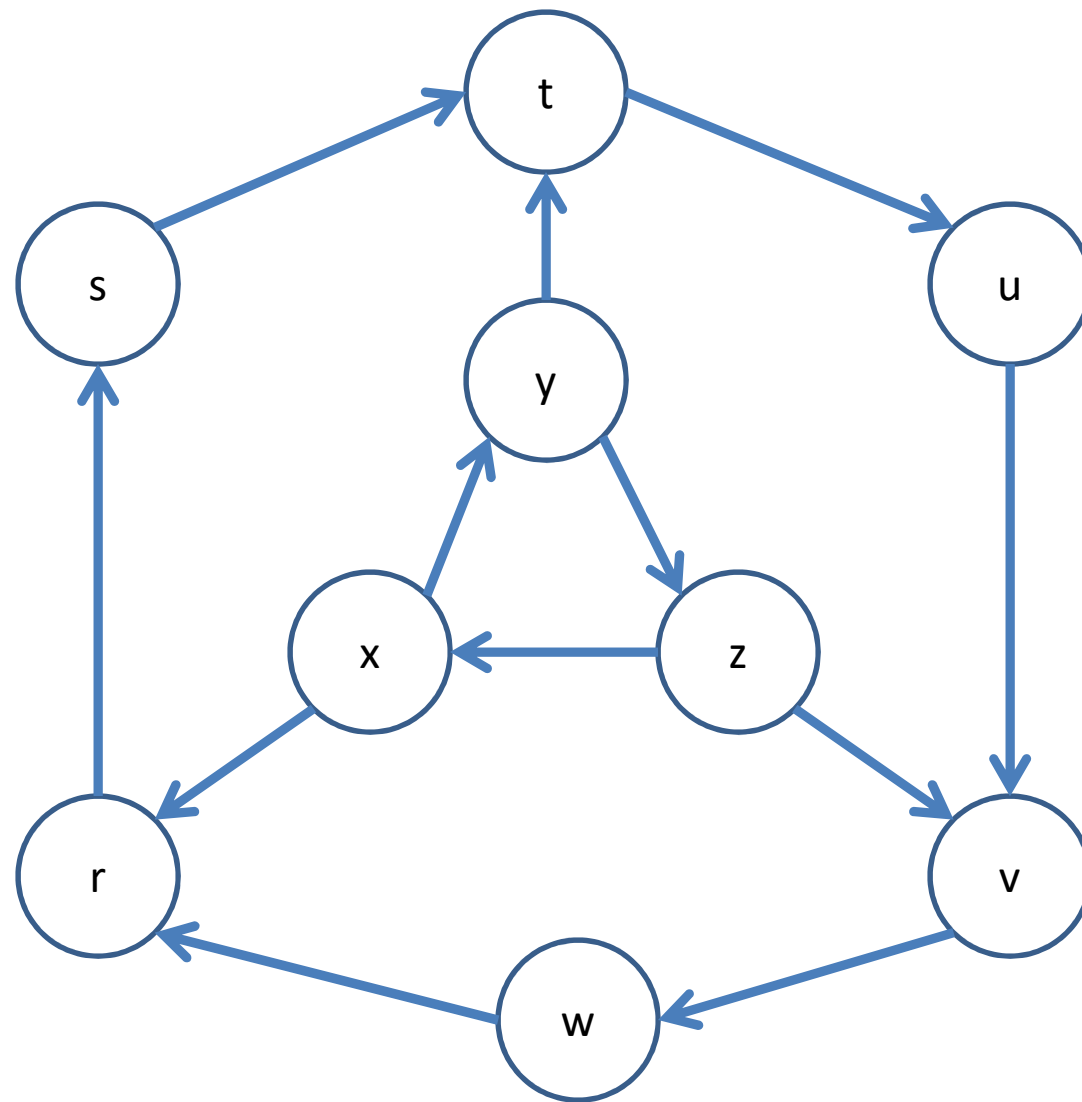


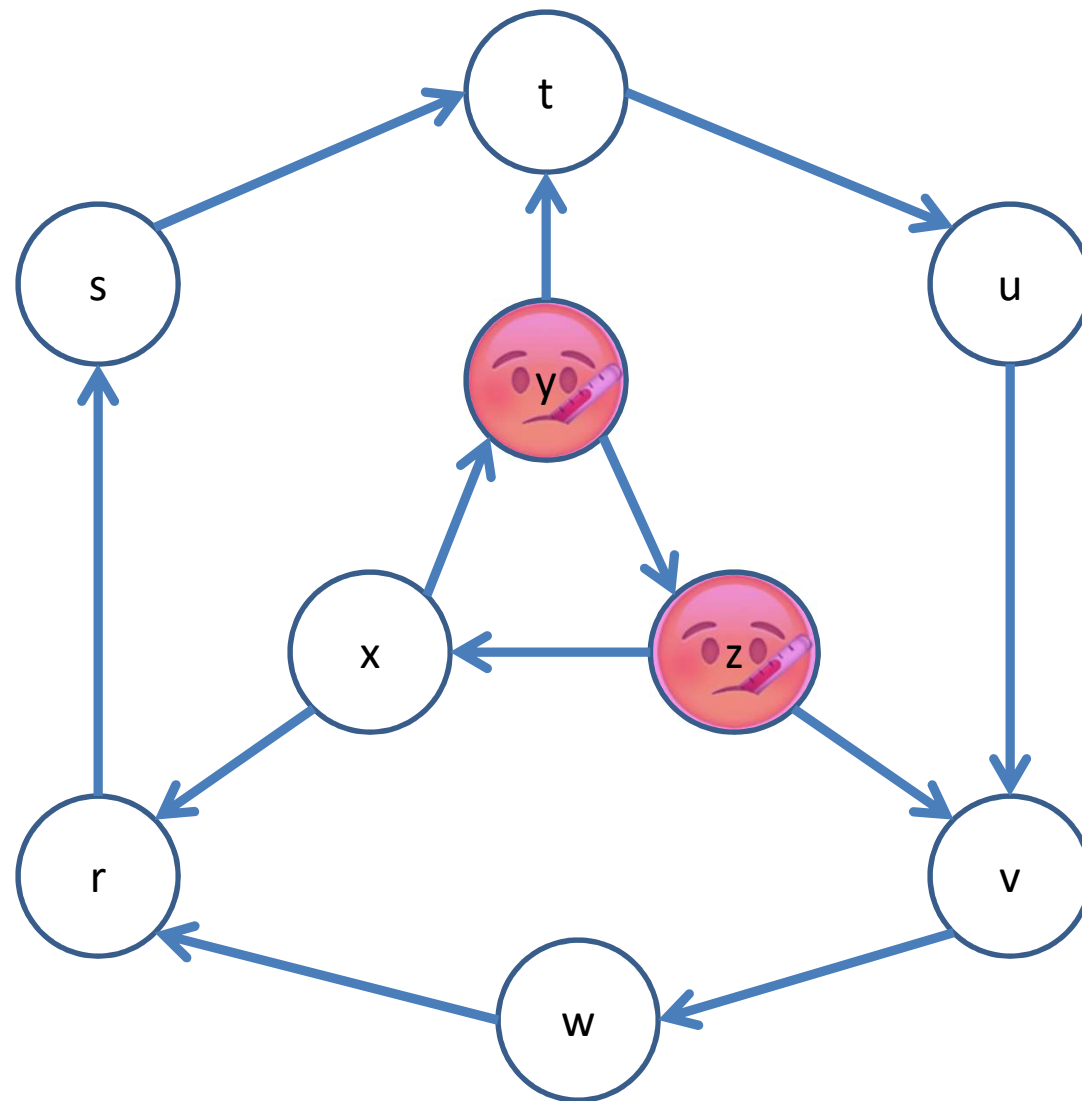
- Epidemic Models
 - SIR
 - SIS
 - SIRS



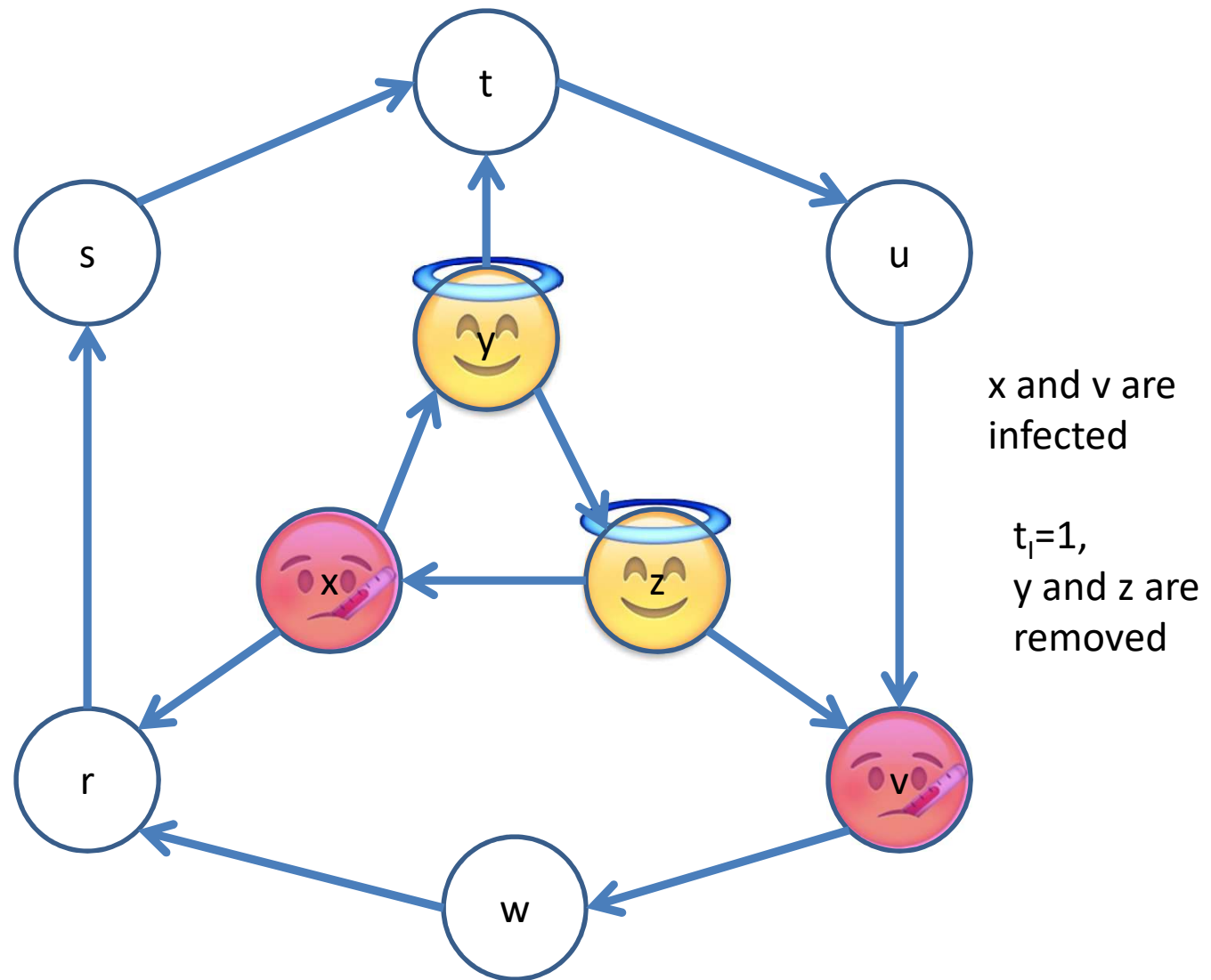
The SIR Epidemic Model

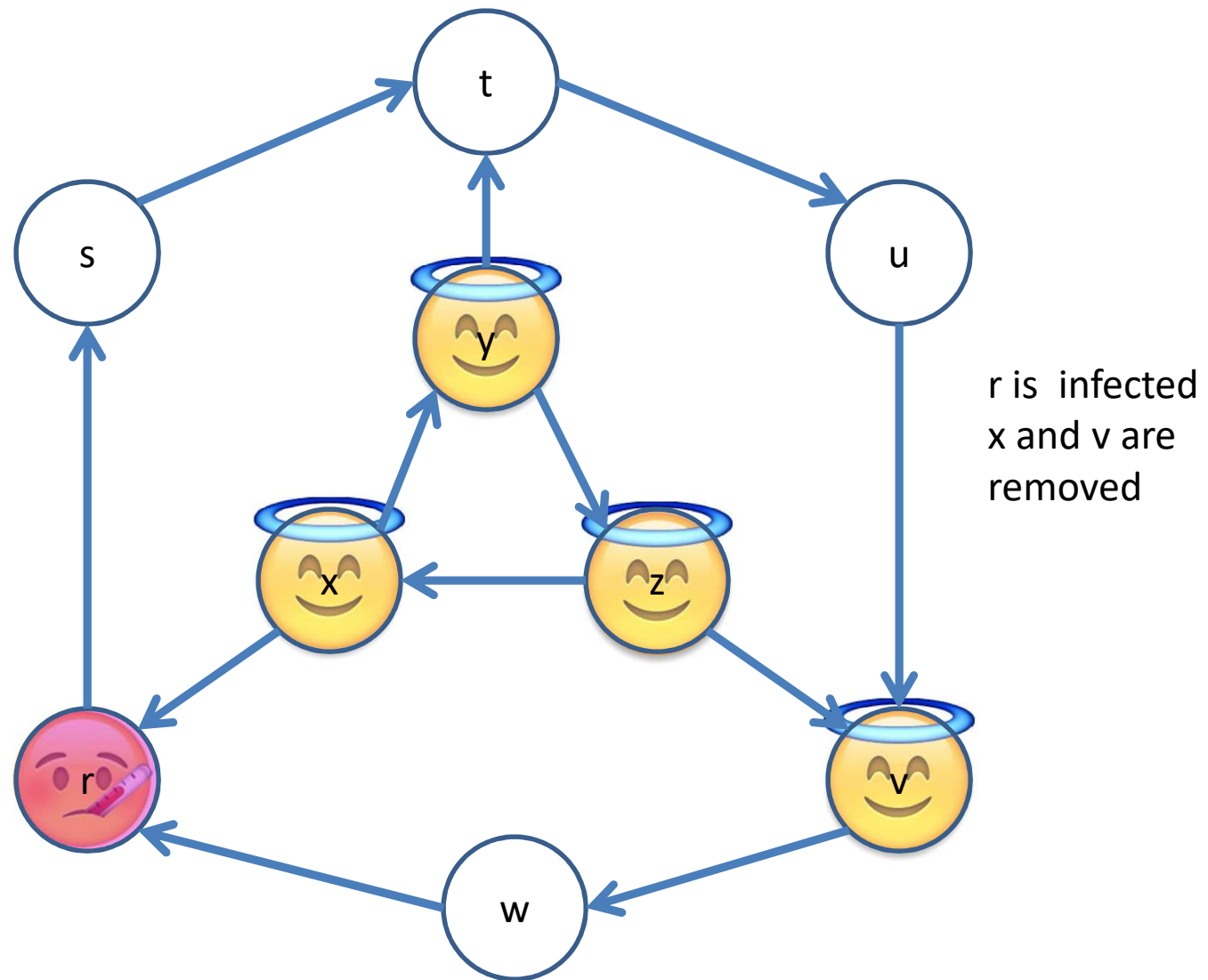
- **Susceptible**: Before the node has caught the disease, it is susceptible to infection from its neighbors. 
- **Infectious**: Once the node has caught the disease, it is infectious and has some probability, p , of infecting each of its susceptible neighbors. 
- **Removed**: After a particular node has experienced the full infectious period after t_i steps, this node is removed from consideration, since it no longer poses a threat of future infection. 

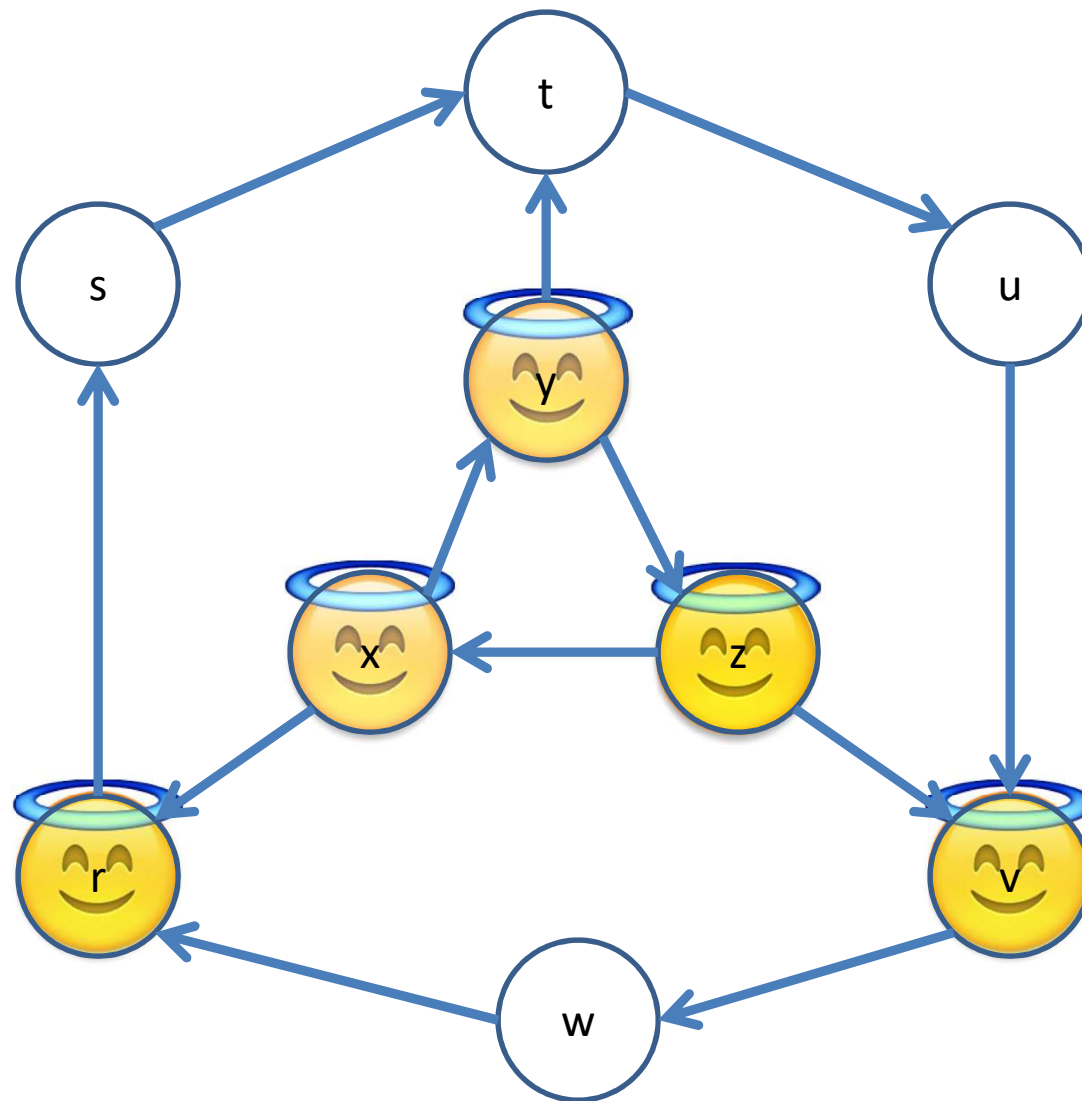




y and z are
initially infected







r is removed



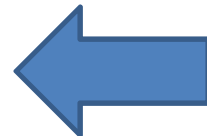
Extensions to the SIR model

- **Contagion probabilities** : non-uniform
 - uniform value $p \rightarrow$ separate probability $p_{v,w}$ to each pair of nodes v and w .
 - higher values of $p_{v,w}$ correspond to closer contact and more likely contagion, and lower values indicate less intensive contact.
- **Infectious period** : random in length
 - $t_i \rightarrow$ a probability q of recovering in each step while it is infected.
 - Separating the I state into a sequence of several states (e.g. early, middle and later periods of the infection) and allowing the contagion probabilities to vary across these states.



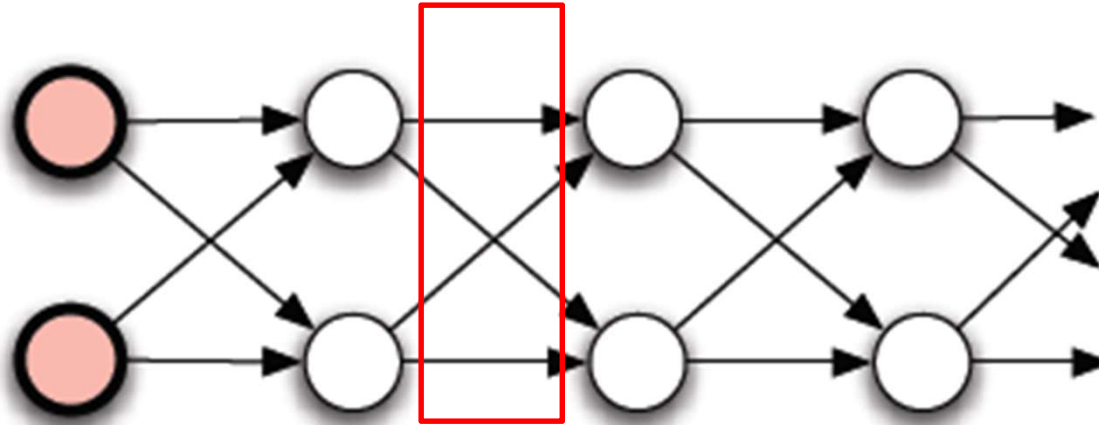
Dichotomy for Branching Processes

- R_0 = the expected number of new cases
- Claim:
 - If $R_0 < 1$, the disease dies out.
 - If $R_0 > 1$, the disease persists.
- Not necessary holds
 - Not a tree structure





Network structure : Channel



- Let $p = 2/3$, $t_1 = 1$.
- $R_0 = pk = 4/3 > 1$
- 4 edges at each time step
- a probability of $> (1/3)^4 = 1/81$, the disease will die out after a finite number of layers.

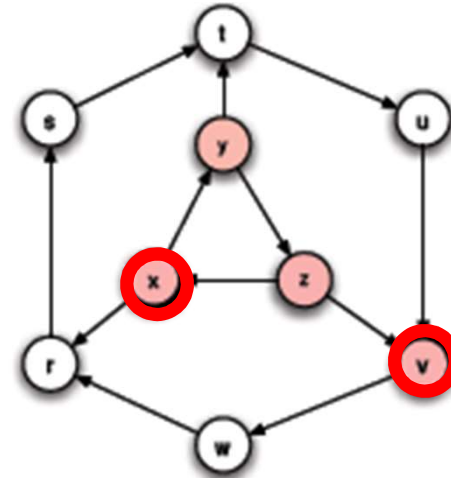
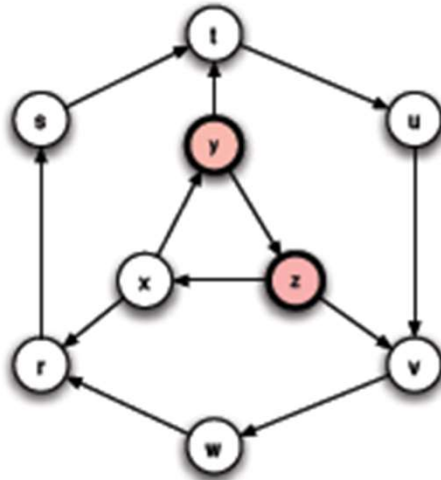


Percolation

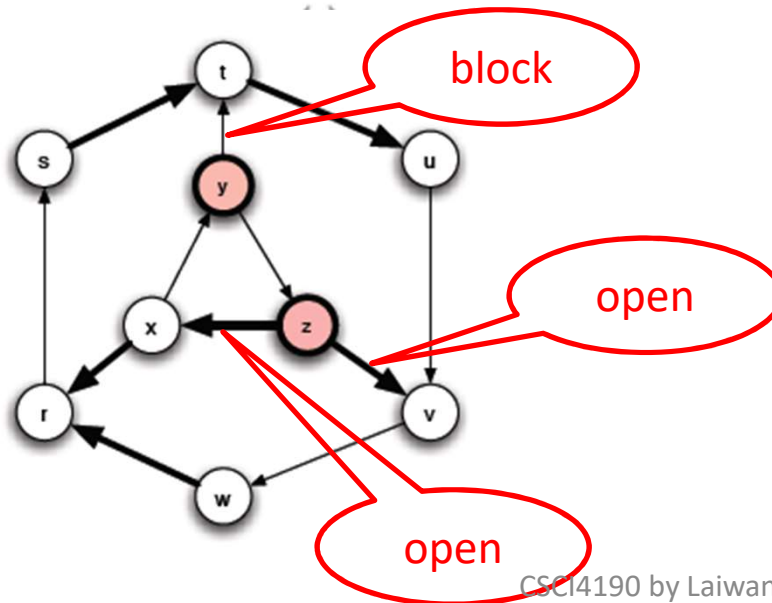
- Epidemic models
 - dynamic processes
- Percolation
 - static views of the epidemic models
 - in the event that v becomes infectious while w is susceptible, edge v - w is
 - open : if w is infected by v
 - block : otherwise
 - A node v will become infected during the epidemic if and only if there is a path to v from one of the initially infected nodes that consists entirely of open edges.



Percolation : static view of the model



Open pipes vs Blocked pipes



A node v will become infected during the epidemic if and only if there is a path to v from one of the initially infected nodes that consists entirely of open edges



- **SIR model**

- Susceptible
- Infectious
- Removed

- **SIS model**



- Susceptible
- Infectious



- No removed state, the node cycles back to the Susceptible state and is ready to catch the disease again

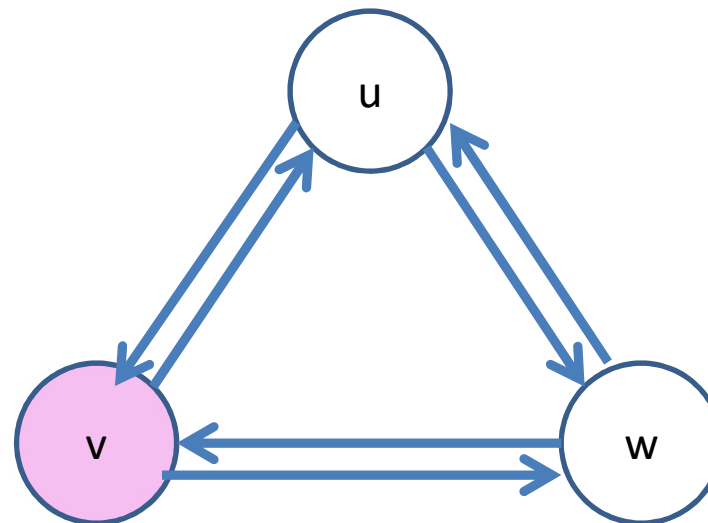


- The mechanics of the model follow the SIR process very closely.

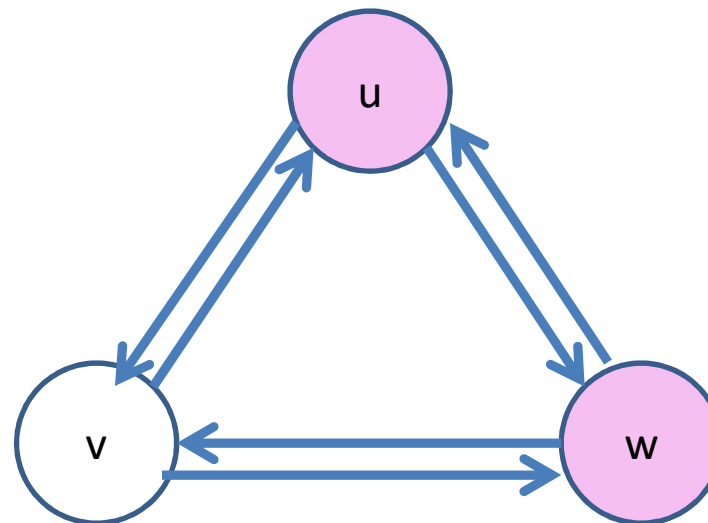


The SIS Epidemic Model

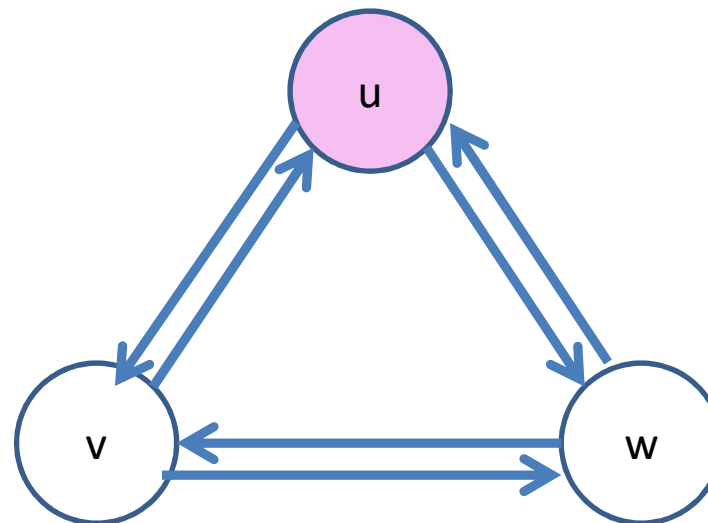
- Some nodes (v) are in the I state
 - remains infectious for t_i steps
 - After t_i steps, node v is no longer infectious, and it returns to the S state
- All others are in the S state
 - v has a probability p of passing the disease to each of its susceptible neighbors.



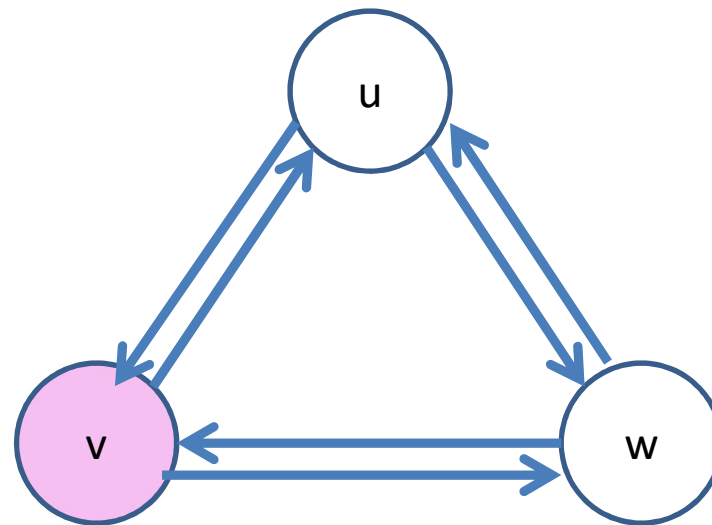
- v passes the disease to both u and w
- v recovers

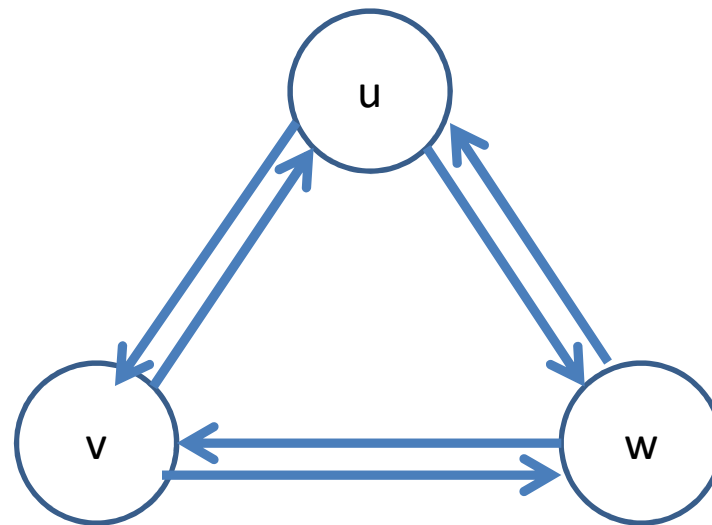


- w passes the disease to u
- w recovers



- u passes the disease to v
- u recovers

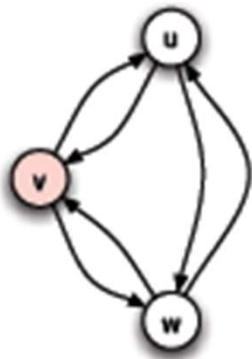




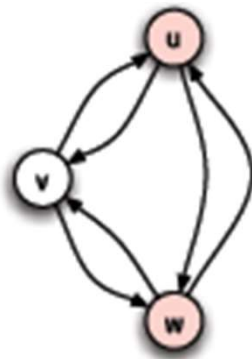
- v recovers



SIS Epidemic Model



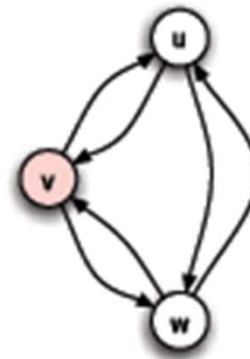
(a)



(b)



(c)



(d)



(e)

$v \rightarrow u, w \rightarrow u \rightarrow v$



Life Cycles of SIR and SIS Epidemics.

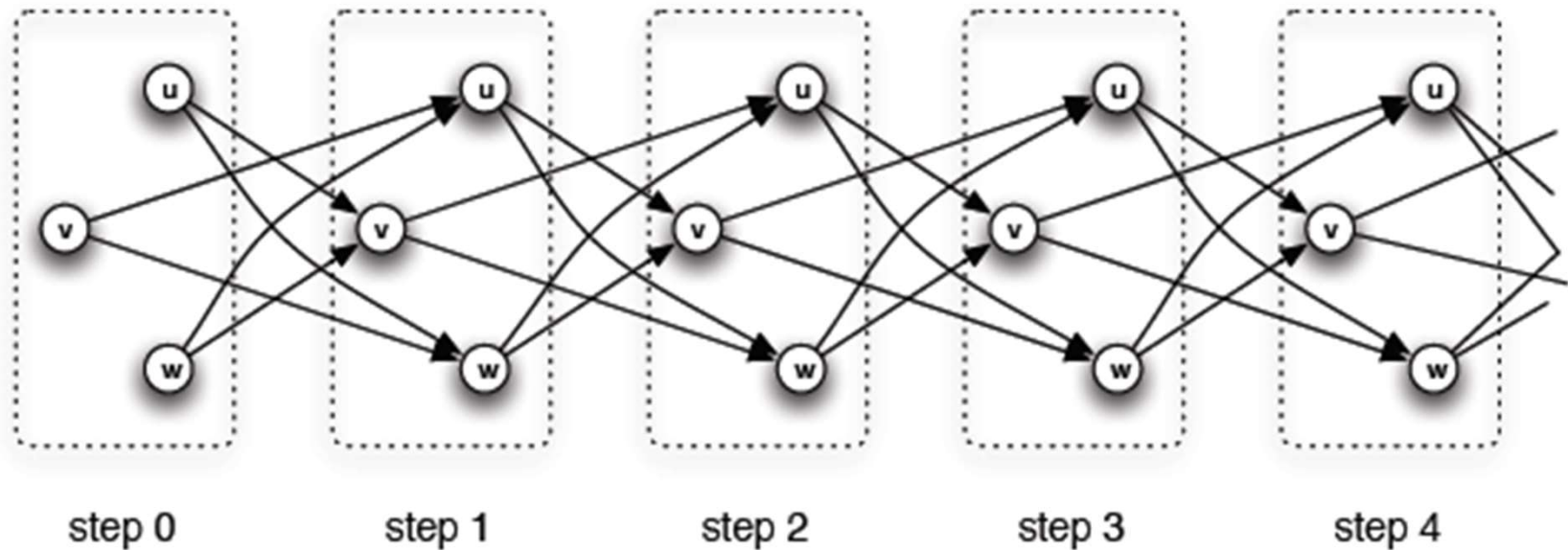
- SIR
 - on (finite-size) graphs -- it must come to an end after a small number of steps.
- SIS
 - can run for an extremely long time as it cycles through the nodes potentially multiple times.
 - a particular critical value of the contagion probability p (depending on the network structure), the network will shift from one that dies out quickly to one that persists for a very long time.



A Connection Between SIR and SIS Epidemics

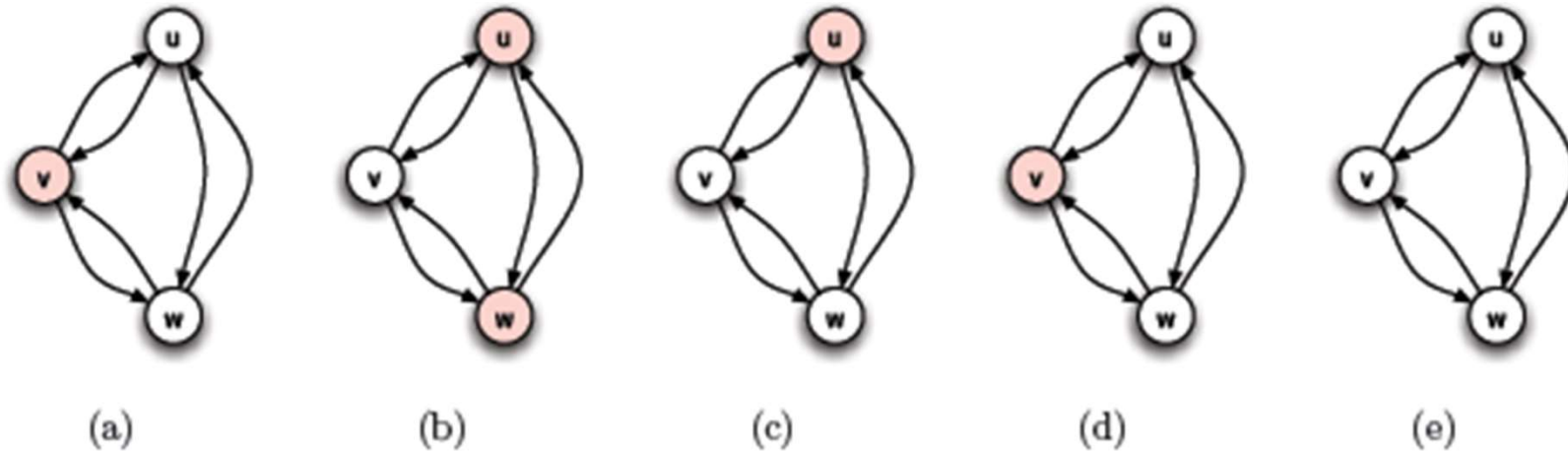


time-expanded contact network

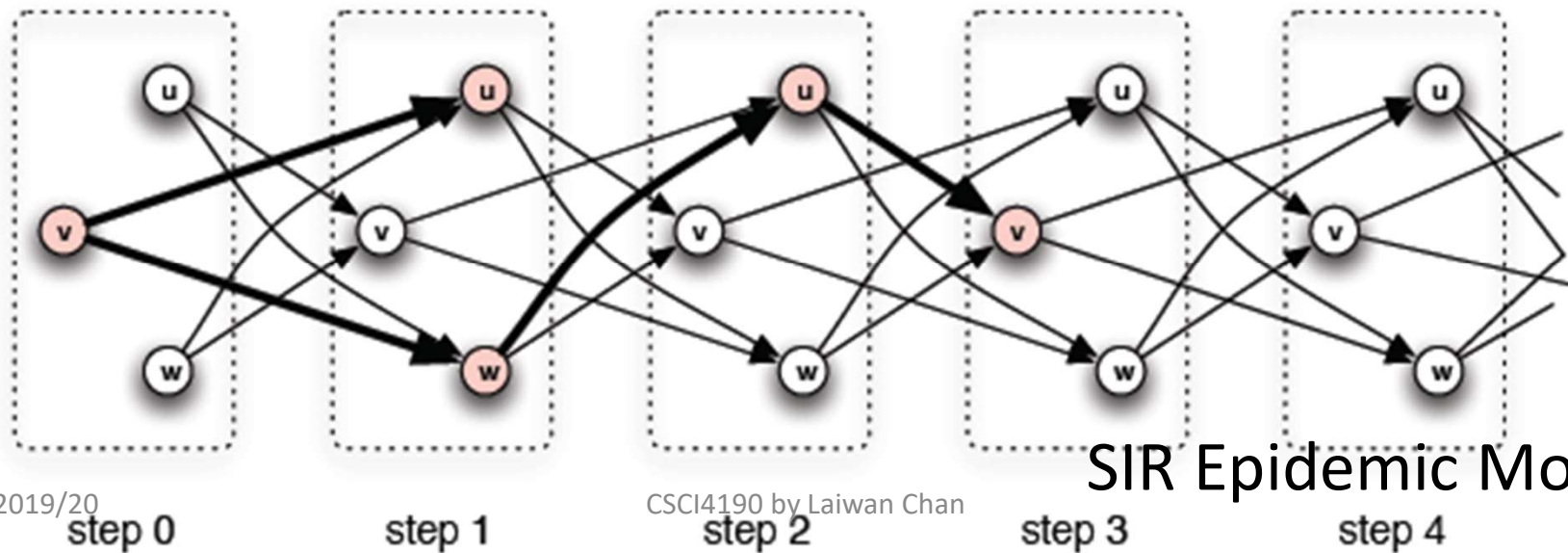




SIS Epidemic Model



$v \rightarrow u, w \rightarrow u \rightarrow v$



SIR Epidemic Model



The SIRS Epidemic Model

- Combine SIR and SIS
- Temporary immunity on infected individual
- Produce a model with oscillations



The SIRS Epidemic Model

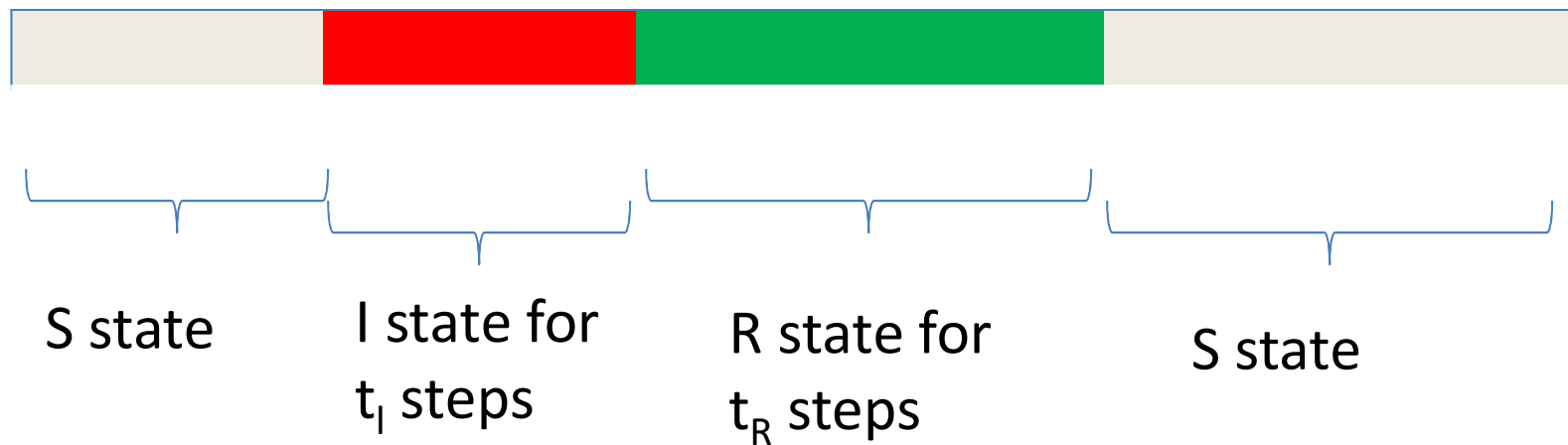
- Initially, some nodes are in the I state and all others are in the S state.
- Each node v that enters the I state remains infectious for a fixed number of steps t_i .
- During each of these t_i steps, v has a probability p of passing the disease to each of its susceptible neighbors.
- (The new feature of the model.) After t_i steps, node v is no longer infectious. It then enters the R state for a fixed number of steps t_R . During this time, it cannot be infected with the disease, nor does it transmit the disease to other nodes. After t_R steps in the R state, node v returns to the S state.





The SIRS Epidemic Model

- Some nodes (v) are in the I state
 - remains infectious for t_I steps
 - ~~– After t_I steps, node v is no longer infectious, and it returns to the S state~~
 - After t_I steps, node v is no longer infectious, and it returns to the R state for a t_R steps. During this time, it cannot be infected with the disease, nor does it transmit the disease to other nodes.
 - After t_R steps in the R state, node v returns to the S state.
- All others are in the S state
 - v has a probability p of passing the disease to each of its susceptible neighbors.



It cannot be infected
nor does it transmit
the disease to other
nodes



SIRS



S state

I state for
 t_I steps

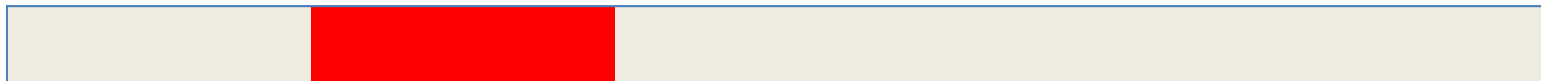
R state for
 t_R steps

S state

SIR



SIS



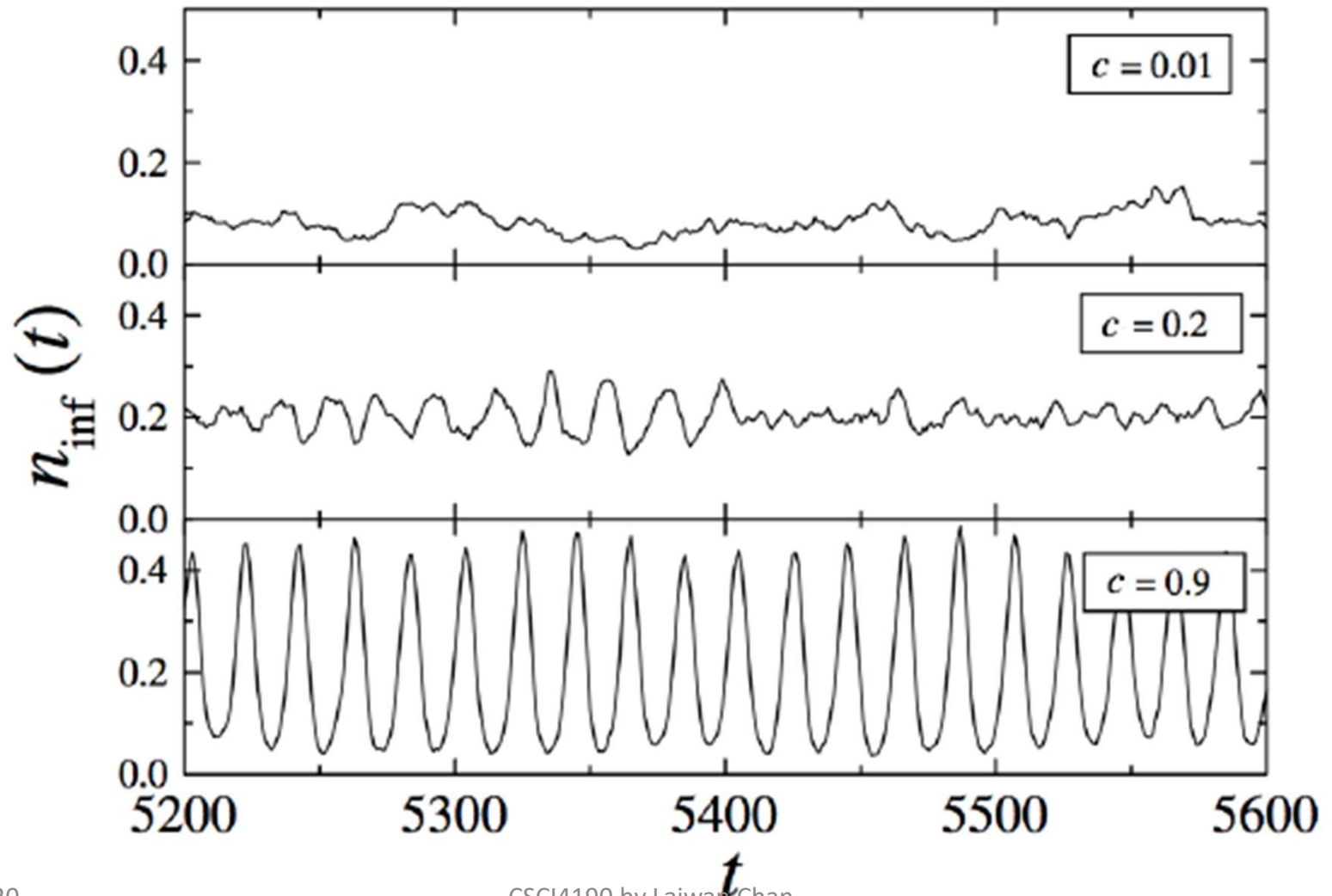


Small-World Contact Networks

- Network structure
 - Homophily
 - local and clustered
 - similar social and geographic characteristic
 - long-range links
 - weak ties linking different parts of the network
 - probability c : fraction of long-range weak ties
 - small c : disease transmit via the short-range local edges
 - Very large c : oscillations



Synchronization





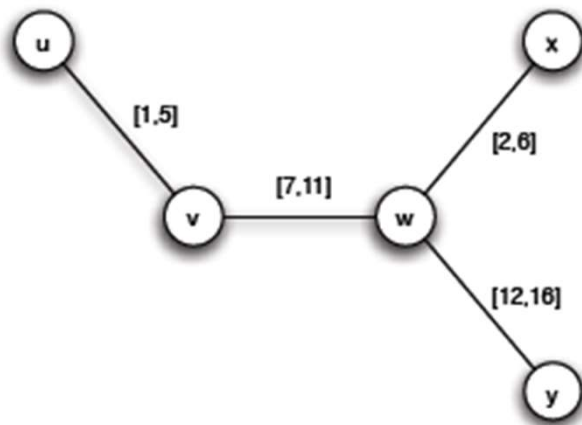
Transient Contacts and the Dangers of Concurrency

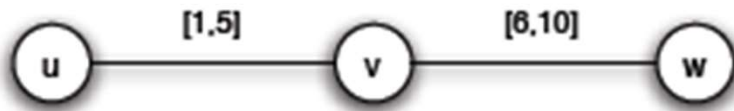
- contact network
 - if diseases are relatively contagious and spread quickly : **static network**
 - epidemic progresses over many years : contacts can **shift** significantly
 - E.g. HIV/AIDS, diffusion of information, ideas and behaviour



Transient Contacts and the Dangers of Concurrency

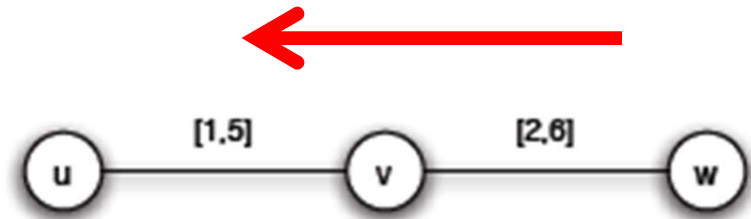
- **transient contacts** — contact networks in which each edge is annotated with the **period of time** during which it existed
- the **time range** for one endpoint of the edge to have passed the disease to the other.





Partnerships happen
Serially

Only allow spreading
from u to w

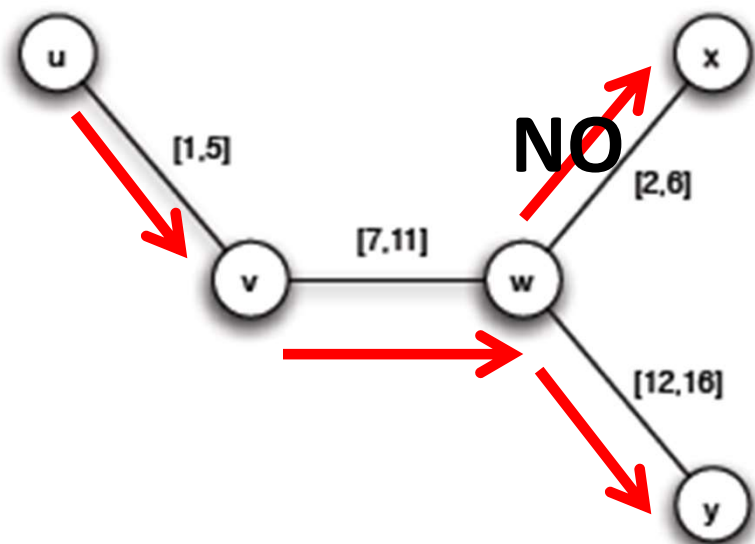


Partnerships happen
concurrently

Either u or w spread the
disease to the other



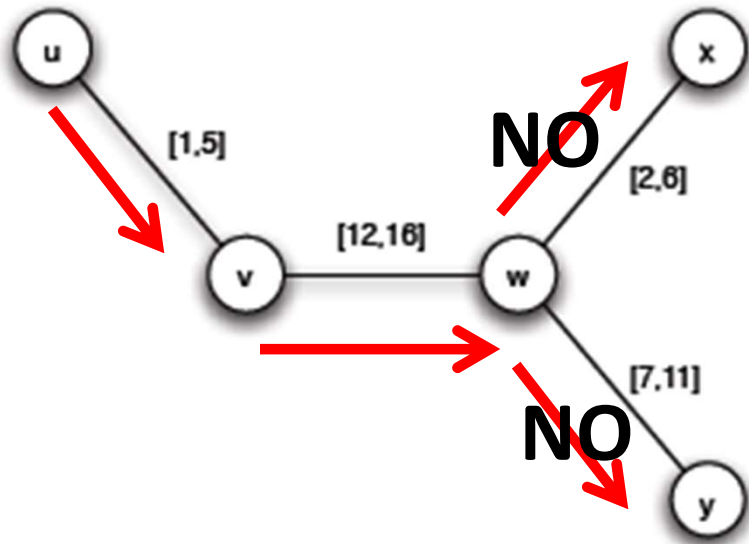
Transient Contacts and the Dangers of Concurrency



time	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
u-v																	
v-w																	
w-x																	
w-y																	



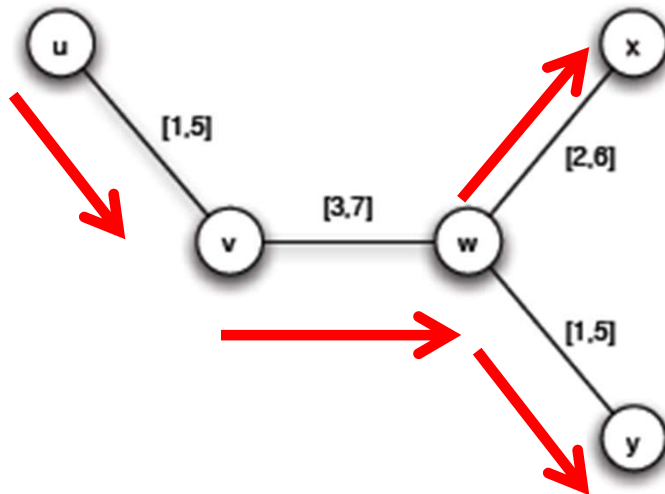
Transient Contacts and the Dangers of Concurrency



time	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
u-v																	
v-w																	
w-x																	
w-y																	



Transient Contacts and the Dangers of Concurrency



time	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
u-v																	
v-w																	
w-x																	
w-y																	

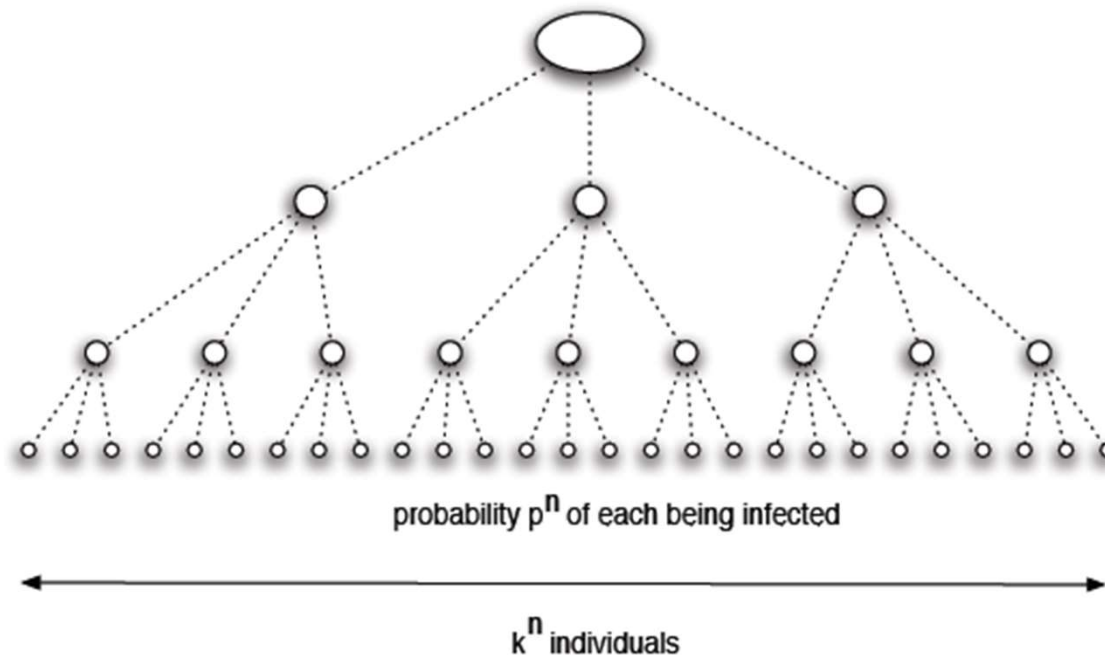


Analysis of Branching Processes

- q_n = the probability that the epidemic survives for at least n waves
- $q^* = q_n$ as n goes to infinity
- q^* = the probability that the epidemic persists indefinitely.
- To prove
 - (a) If $R_0 < 1$ then $q^* = 0$.
 - (b) If $R_0 > 1$ then $q^* > 0$.



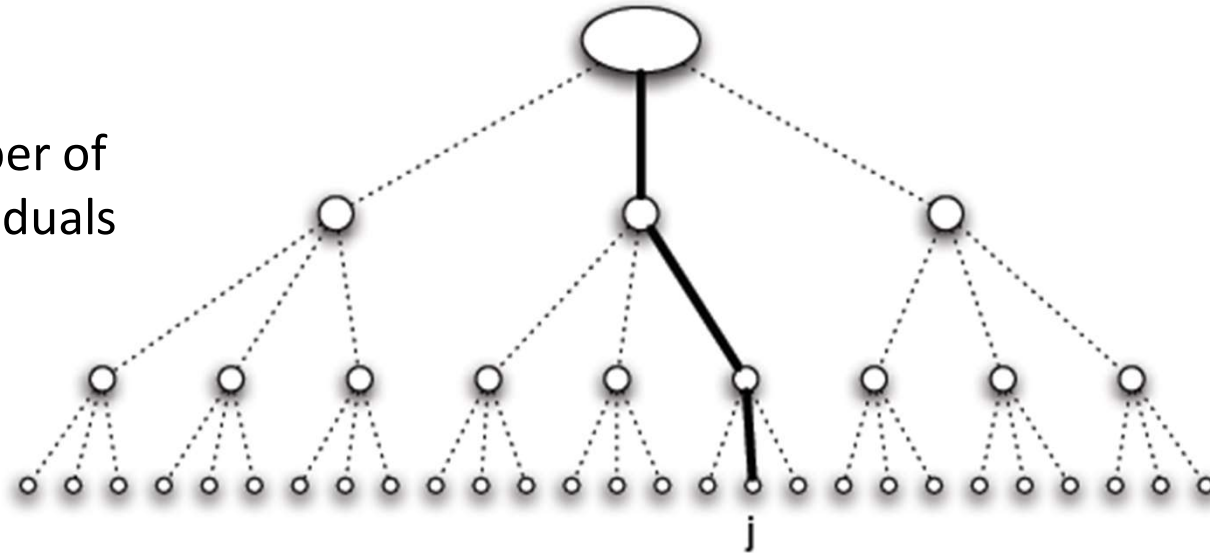
Analysis of Branching Processes



At level n , the number of individuals is $m = k^n$



X_n = the number of infected individuals at level n .



Individual j is infected if each contact from the root to j successfully transmits the disease

$$X_n = Y_{n1} + Y_{n2} + \dots + Y_{nm}$$

$$E[X_n] = E[Y_{n1}] + E[Y_{n2}] + \dots + E[Y_{mn}]$$

$Y_{nj} = 1$ if j is infected,
 $Y_{nj} = 0$ otherwise



- $$E[Y_{nj}] = 1 \cdot \Pr[Y_{nj} = 1] + 0 \cdot \Pr[Y_{nj} = 0]$$
$$= \Pr[Y_{nj} = 1] = p^n$$

$\Pr[Y_{nj}=1]$ = Probability that individual j at level n get infected = p^n

- $$E[X_n] = E[Y_{n1}] + E[Y_{n2}] + \dots + E[Y_{mn}]$$
$$= p^n k^n = R_0^n$$



- $E[X_n] = 1 \cdot Pr[X_n = 1] + 2 \cdot Pr[X_n = 2] + 3 \cdot Pr[X_n = 3] + \dots$
- $E[X_n] = Pr[X_n \geq 1] + Pr[X_n \geq 2] + Pr[X_n \geq 3] + \dots$
- $E[X_n] \geq Pr[X_n \geq 1] = q_n$
- $E[X_n] = R_0^n \geq q_n$
- If $R_0 < 1$, $E[X_n] = R_0^n$ converges to 0 as n grows
It leads to $q^* = 0$
- If $R_0 > 1$, $E[X_n] = R_0^n$ goes to infinity as n grows
 $E[X_n] \rightarrow \infty$ may not necessarily implies $q^* > 0$



Example

- It is possible that $E[X_n] \rightarrow \infty$,
but $\text{prob}[X_n > 0]$ goes to zero
- X_n are random variables taking the values 4^n
with probability 2^{-n} and 0 otherwise
 - $E[X_n] = 4^n \cdot 2^{-n} = 2^n$
 - $\text{prob}[X_n > 0] = 2^{-n}$



A Formula for q_n

- (Event *) : The disease spreads through the root node's first contact j and then continues to persist down to n levels in the part of the tree reachable through j .



A Formula for q_n

- (Event $*$) : The disease spreads through the root node's first contact j and then continues to persist down to n levels in the part of the tree reachable through j .
- For the event $(*)$ to hold, it would require that j catches the disease directly from the root, which happens with probability p .

probability of event $*$ = pq_{n-1}

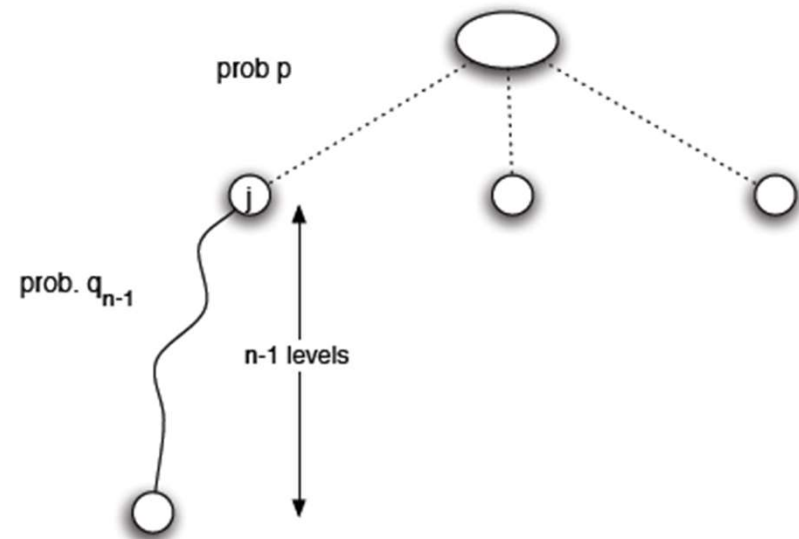
probability of failing event $*$ = $1 - pq_{n-1}$

probability of failing for all k nodes
= $(1 - pq_{n-1})^k$

$$1 - q_n = (1 - pq_{n-1})^k$$

or

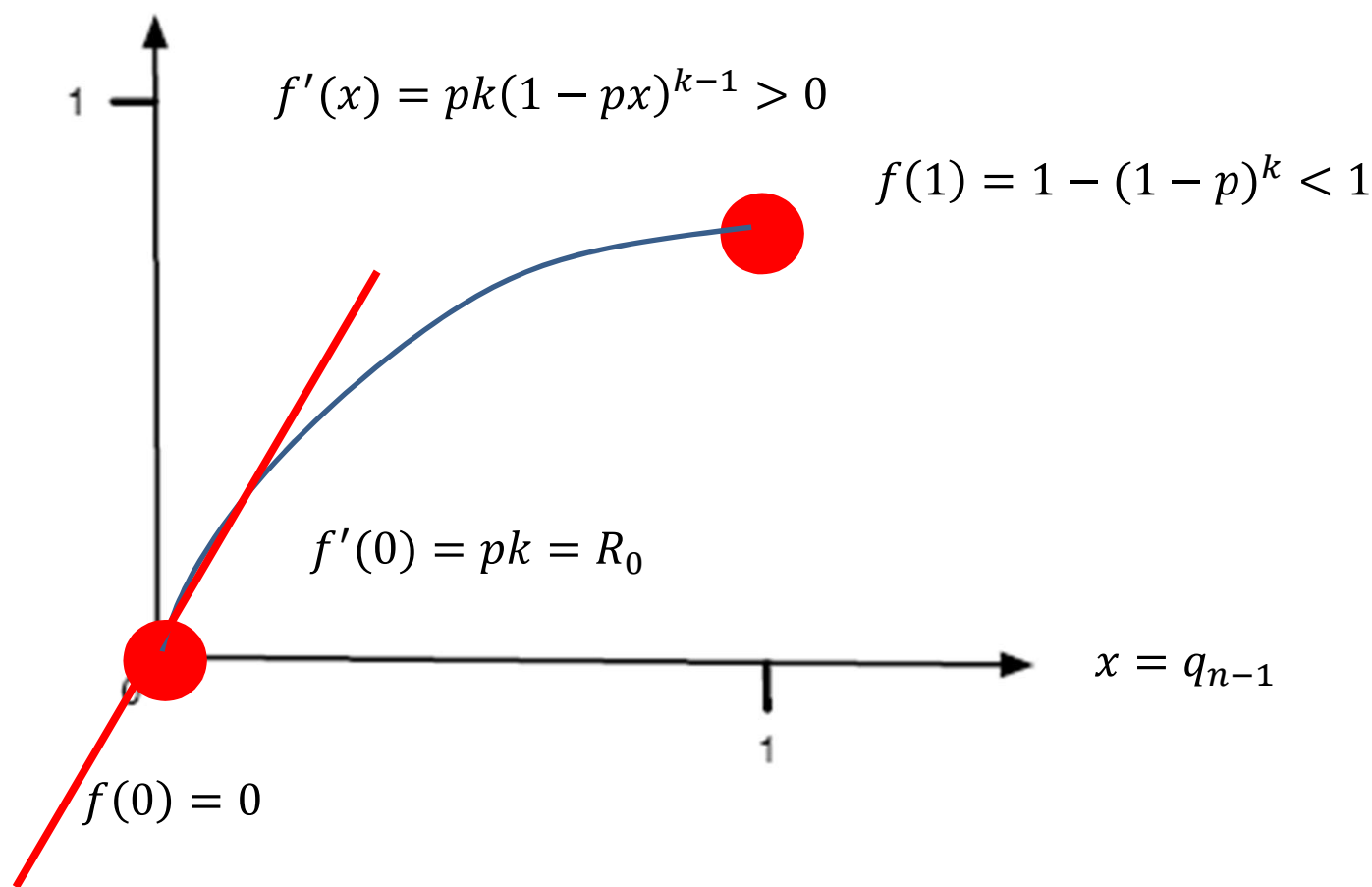
$$q_n = 1 - (1 - pq_{n-1})^k$$

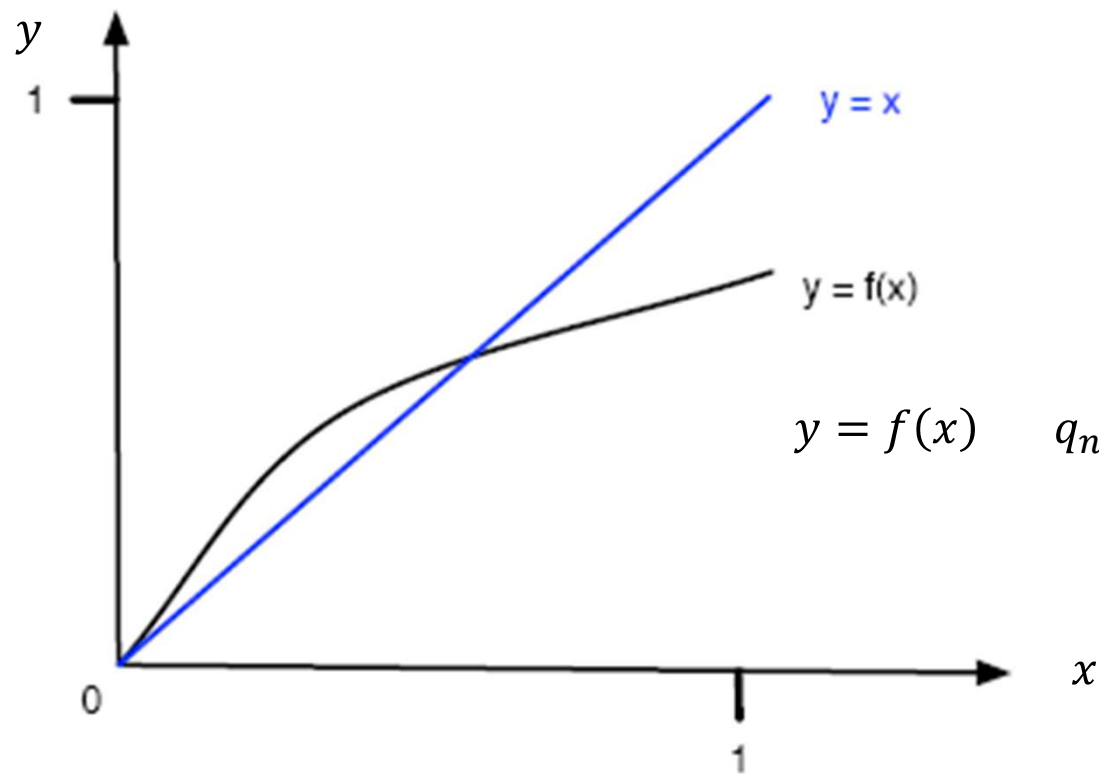




$$q_n = f(q_{n-1}) = 1 - (1 - pq_{n-1})^k$$

$$y = q_n = f(x) = 1 - (1 - px)^k$$

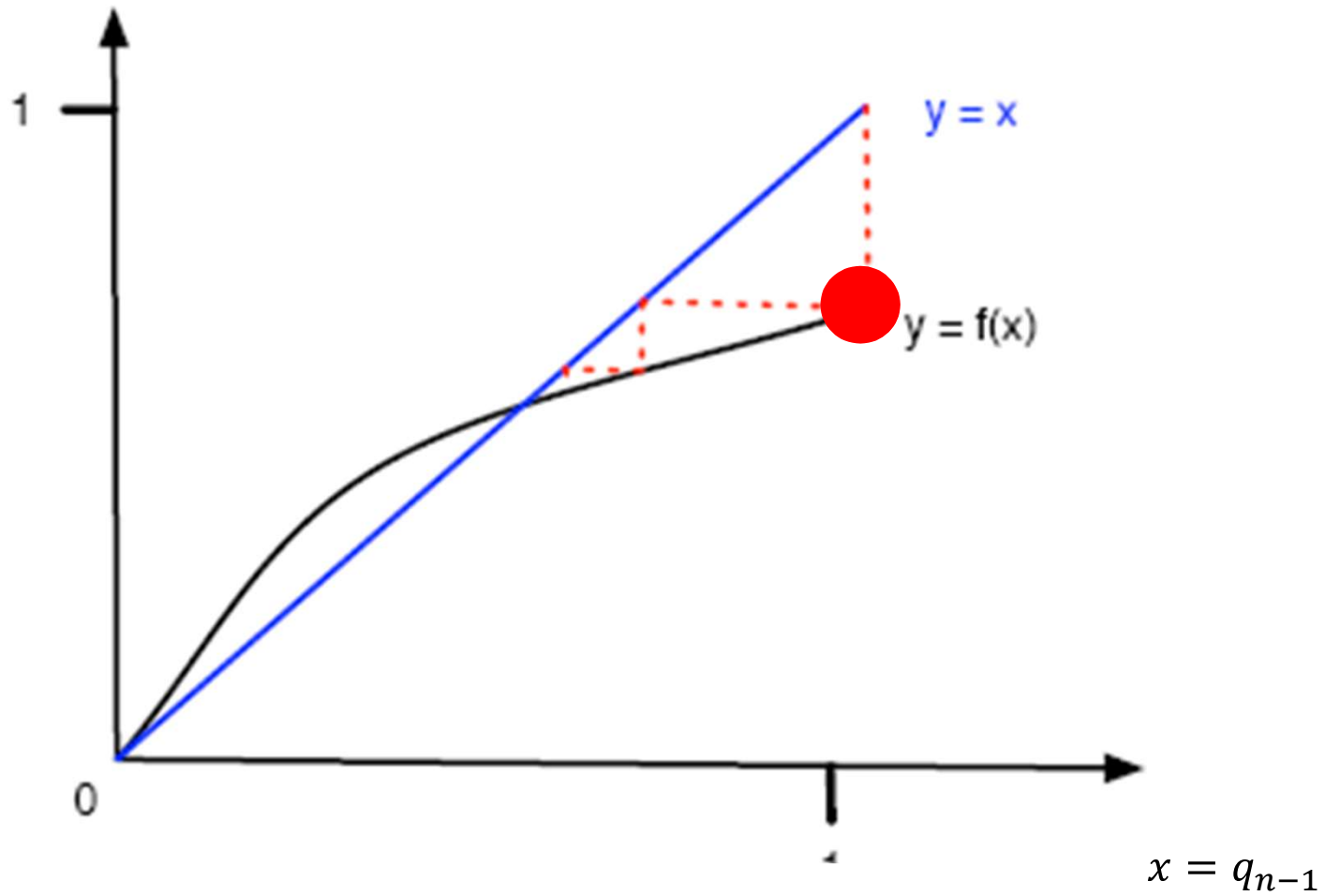




$$y = f(x) \quad q_n = 1 - (1 - pq_{n-1})^k$$

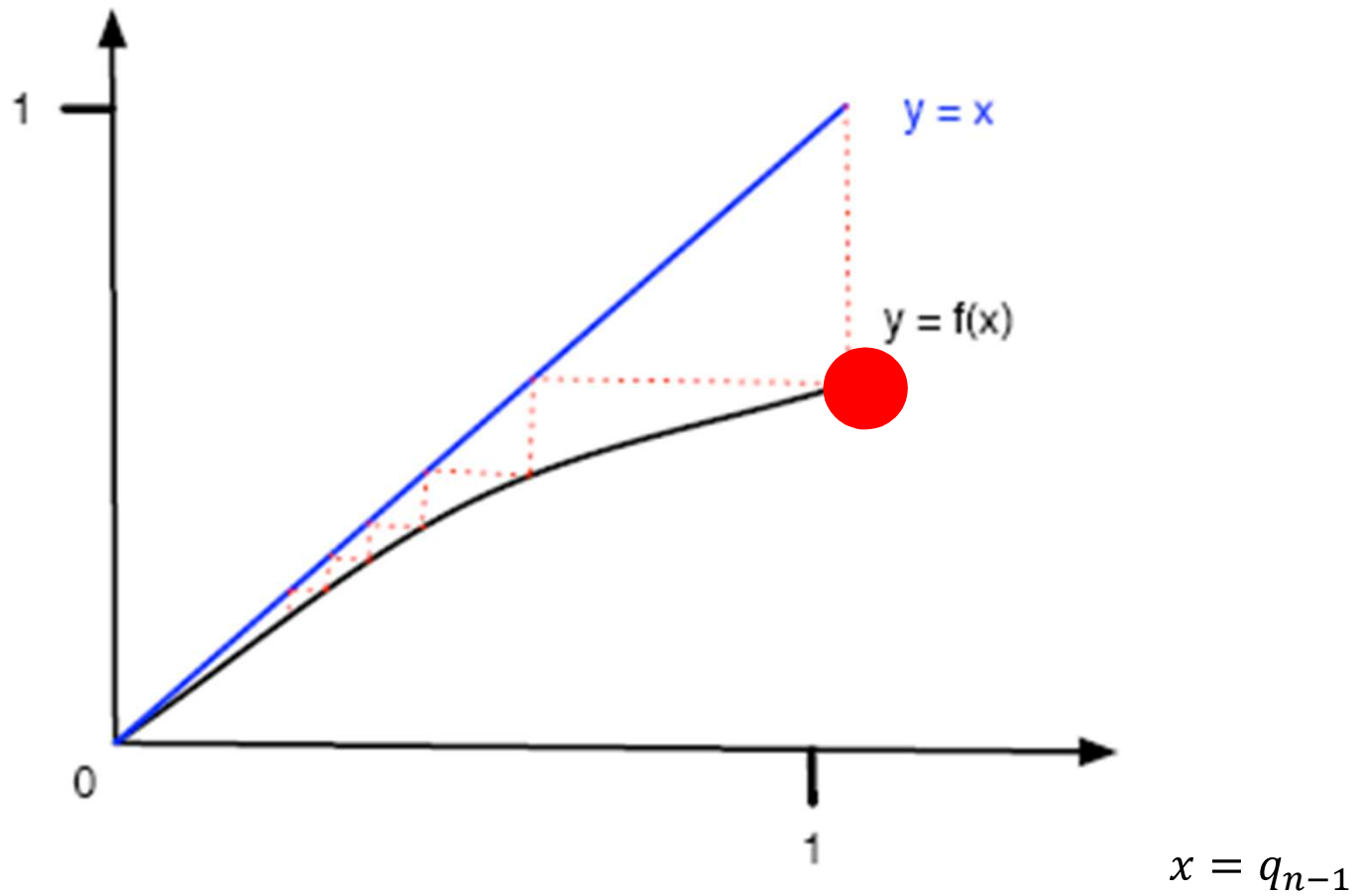


$$R_0 > 1$$





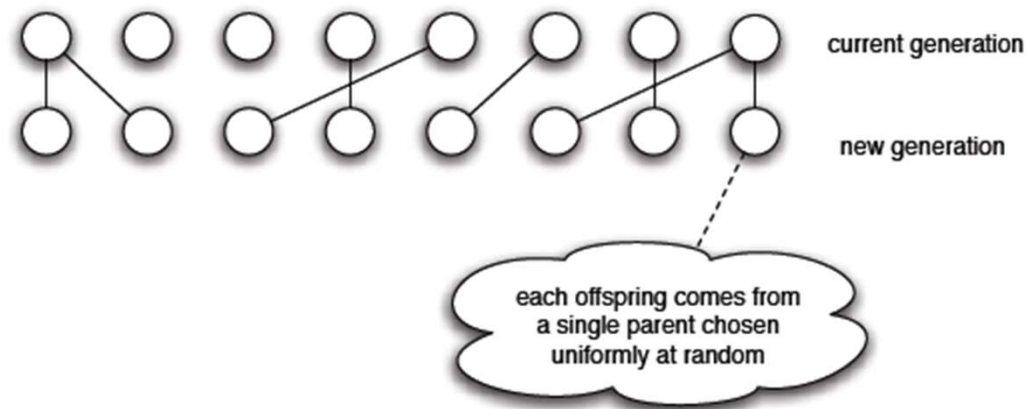
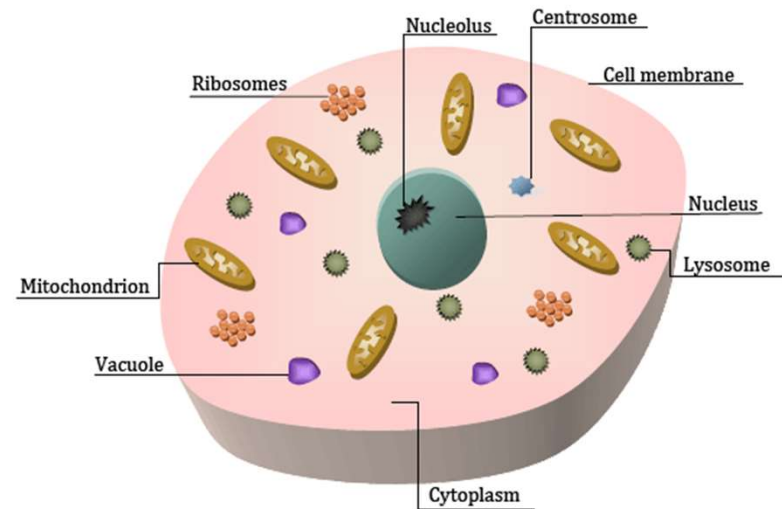
$$R_0 < 1$$





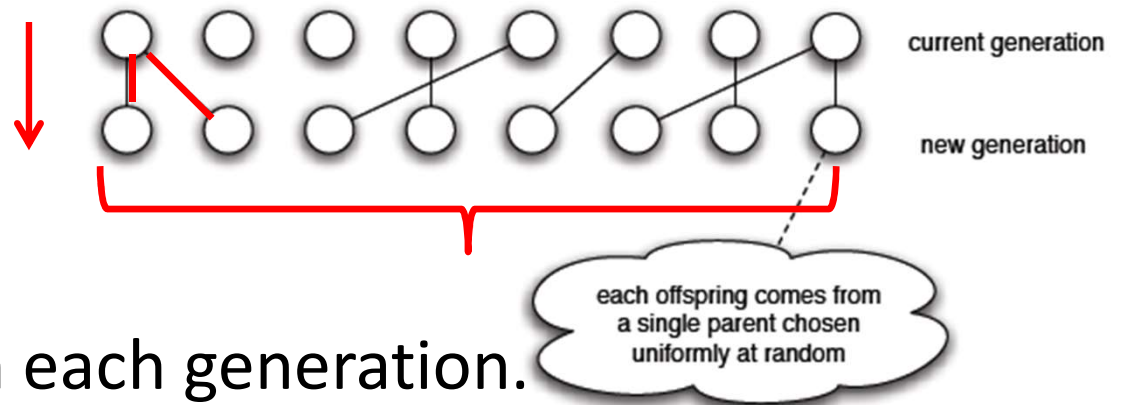
Genealogy, Genetic Inheritance, and Mitochondrial Eve

- spread of diseases
- spread of information
- genetic inheritance
 - Mitochondrial Eve





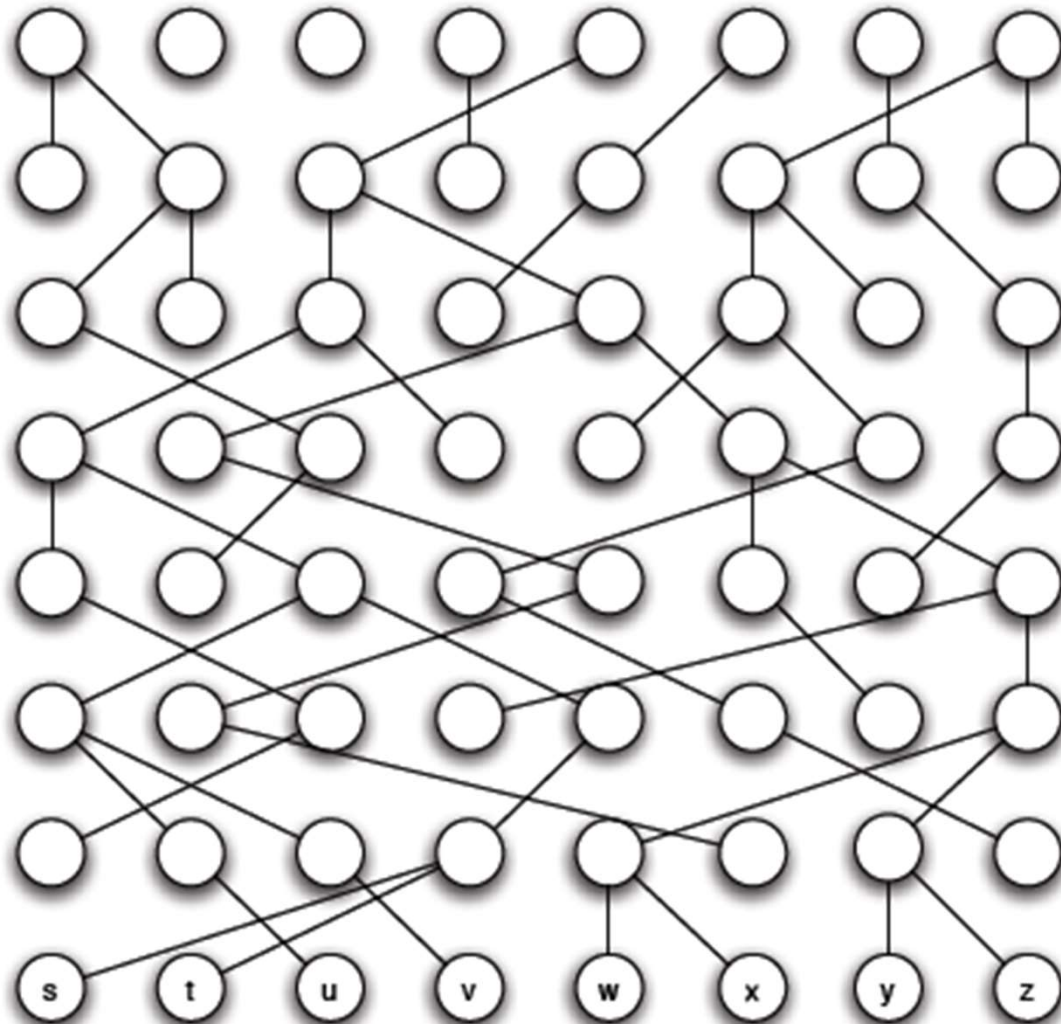
Wright-Fisher model



- Assumptions :
 - a fixed size N in each generation.
 - time moves from one generation to the next.
 - each new generation is formed by having the current set of N individuals produce N offspring in total.
 - each offspring is produced from a single parent.
 - certain individuals in the upper generation can have multiple children, while others may have none.



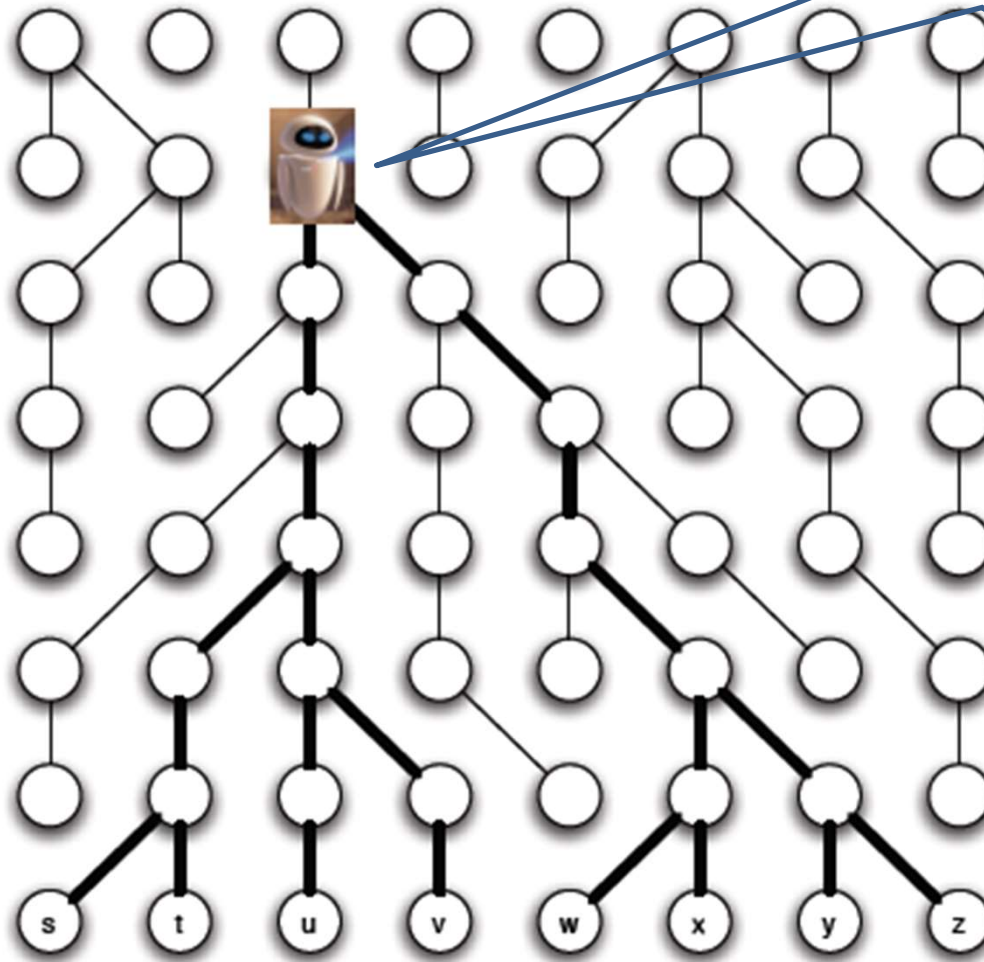
- a neutral model
 - no individual has a selective advantage in reproduction
- model species that engage in asexual reproduction
 - from a single parent
- in sexually reproducing populations
 - the inheritance of mitochondrial DNA among women
- purely “social” forms of inheritance
 - master-apprentice relationships, e.g. a single primary advisor for Ph.D. students in an academic field

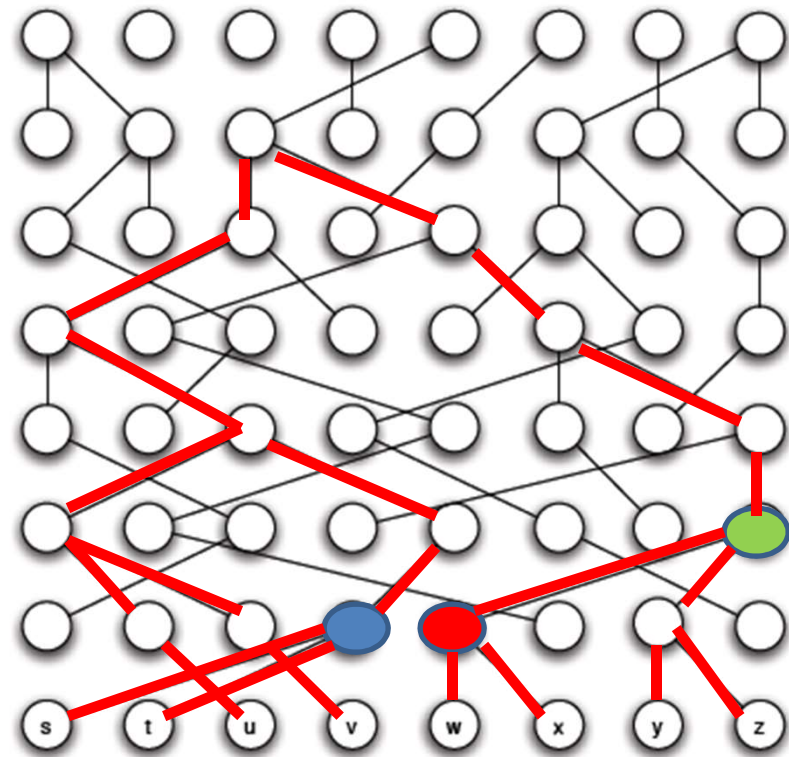




ancestries

Most recent
common
ancestor





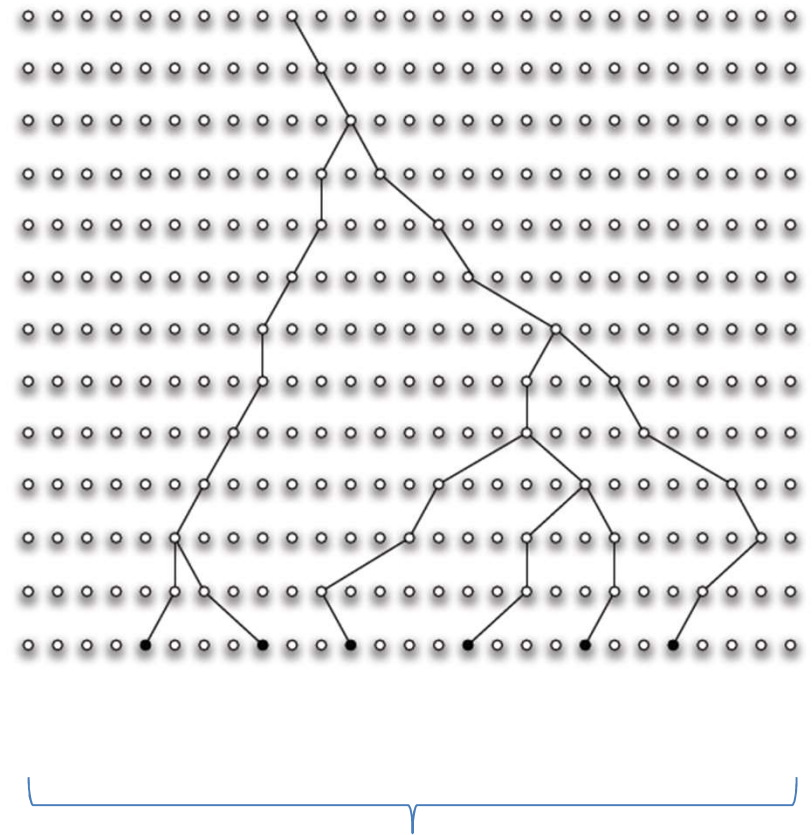


- A small sample of k individuals in a large population of size N ;
- We will consider the time until the lineages of these k merge into a common ancestor
- There are N individuals in each generation. For each of the k individuals in the initial sample, we choose a parent for each uniformly at random from the previous generation.
- We continue working backward in time this way, extending each of the k lineages through earlier generations
- We stop when we first reach a point where the number of lineages has been reduced to one



Analysis of Coalescent Processes

- an estimate of the expected number of generations one has to go back in order to find the most recent common ancestor for a set of individuals in the model



N=27 individuals