Modelling Epidemics

Introduction to Network Science

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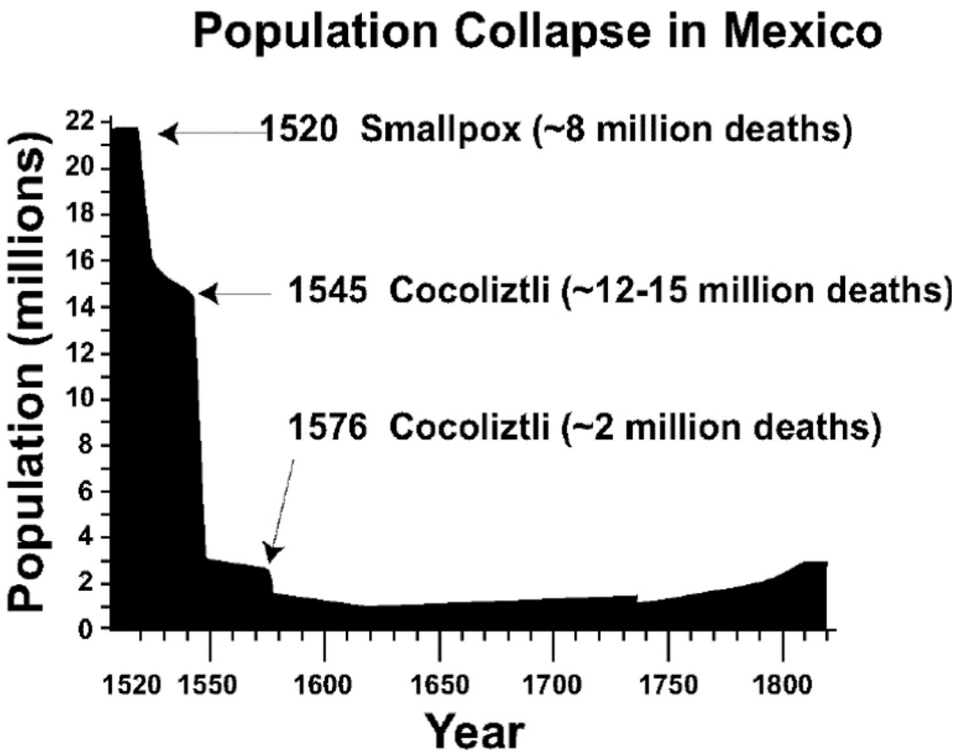
Content

- Compartmental epidemiological models
- Results on homogenepus mixing scenarios

Examples: human epidemics

- Influenza, measles, STIs, ...
- Smallpox and other diseases brought by Europeans to America since early 1500s
- The “Black Death” (next slide)



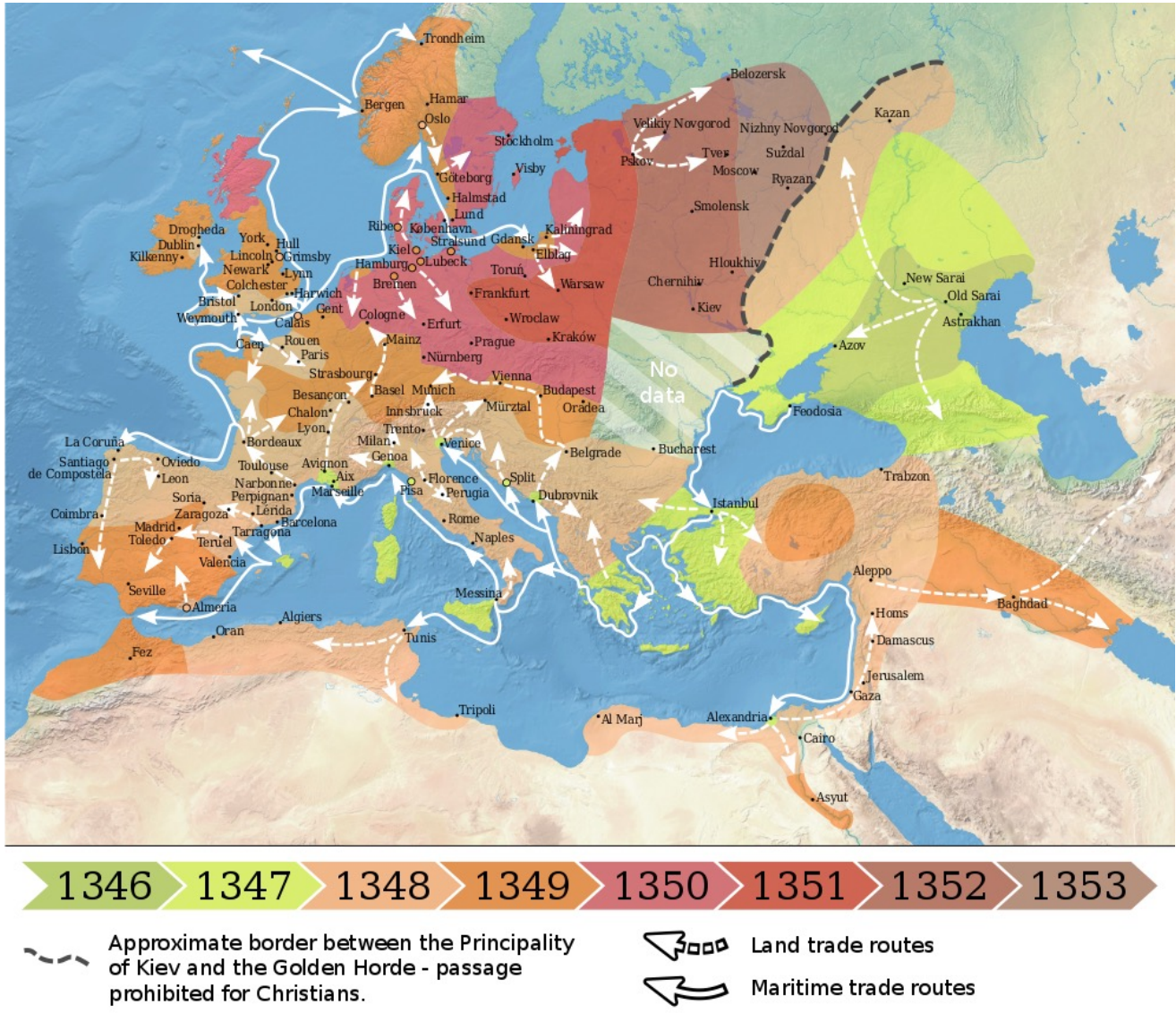
https://en.wikipedia.org/wiki/Cocoliztli_Epidemic_of_1545-1548

The “Black Death”

(Bubonic plague)

1300s

Probably originated in Central Asia, it spread throughout all of Europe between 1346 and 1353. The Black Death is estimated to have killed 30-60% of Europe’s population



SARS Outbreak (2003)

- February 21st: Chinese doctor who have bee several treating “atypical pneumonia” cases check-ins into hotel in Hong Kong

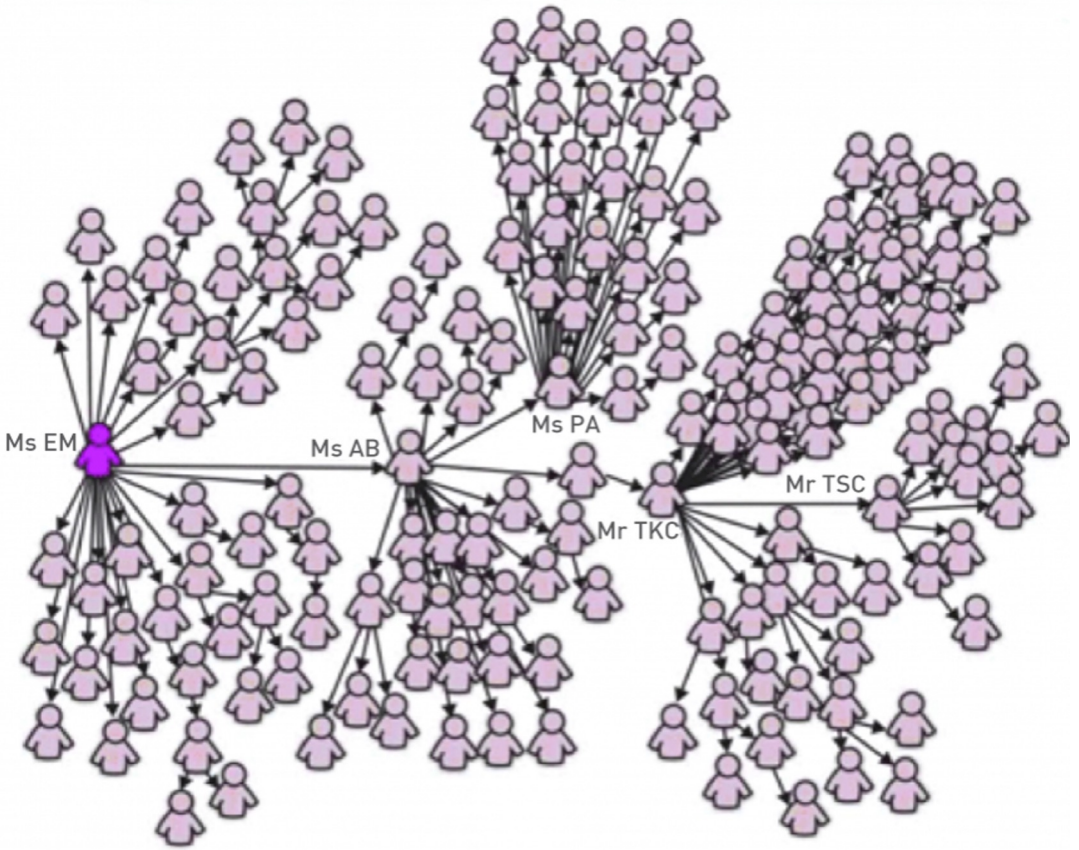
  - Hospitalized on Feb 22nd

  - Died on March 4th

- March 1st: “Ms. E. M.” returns to Singapore after visiting Hong Kong

  - Graph depicts 144 out of the first 206 SARS patients in Singapore

  - Ms. E. M. lived, various of her family members died



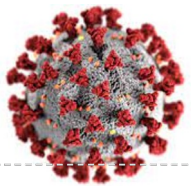
https://en.wikipedia.org/wiki/Timeline_of_the_SARS_outbreak

Daily confirmed COVID-19 cases

The number of confirmed cases is lower than the number of total cases. The main reason for this is limited testing.

Our World in Data

COVID-19



COVID vs Black Death

- The Black Death spread across Europe in **years**
- Covid spread across the world in **weeks**
- Covid reached even Antardide & remote islands
- What changed?

Modeling epidemics

- **Modeling an epidemic process (dynamics):**
  - Contagiousness
  - Length of infectious period,
  - Severity
  - ...
- **Modeling underlying network substrate** (static)
  - Structure of contacts in a population

Modeling epidemics

- **Modeling Epidemic process (dynamics):**
  - Branching process
  - SI model
  - SIR model
  - SIS model
- **Modeling underlying network substrate (static)**
  - Mean-field mixing (fully connected network)
  - Homogeneous networks (ER networks)
  - Heterogeneous networks (SF networks)

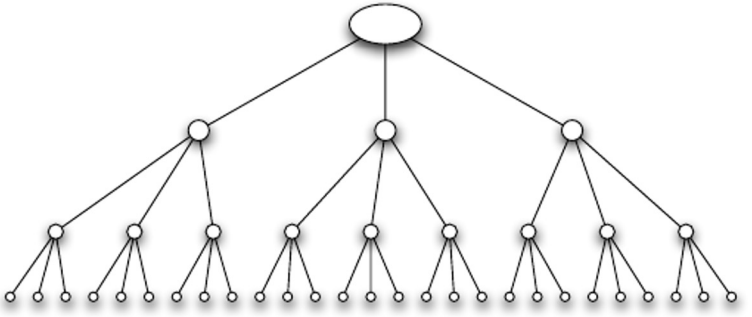
Diffusion of ideas vs diseases

- Adopting a new idea, behavior, fashion, product, taste, may also spread from person to person: **"social contagion"**
- There is a certain agency of the receiver
- In diffusion of diseases, we assume **there is no agency: each contagion is random**

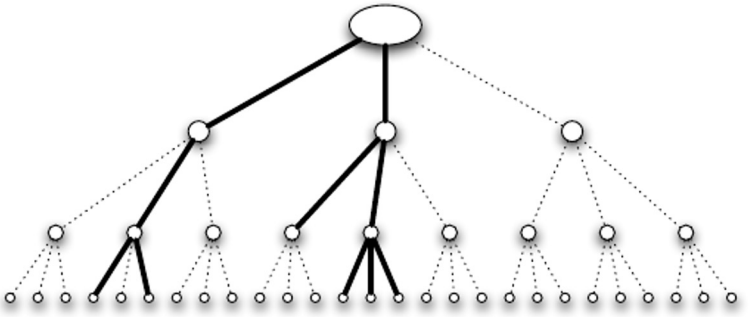
Epidemic model: branching process

Branching process

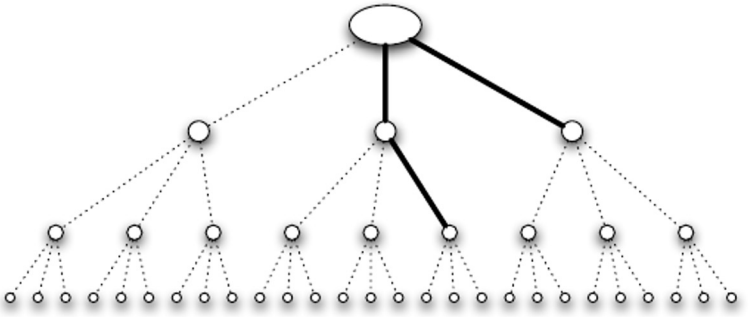
- Each person interacts with other *k* people
- Each interaction ends in infection with probability *beta*



(a) *The contact network for a branching process*



(b) *With high contagion probability, the infection spreads widely*



(c) *With low contagion probability, the infection is likely to die out quickly*

Example: k=3

Transmission rate or "Basic reproductive number" R_0

- Each person interacts with other k people
- Each interaction ends in infection with probability β

- What is the expected number of cases caused by a single individual, R_0?
- What do you think happens if $R_0 < 1$?
- What do you think happens if $R_0 > 1$?

Epidemic threshold

- The **basic reproductive number** is the average number of individuals that are infected by an infectious one during his infectious period, in a fully susceptible population.
- An epidemic outbreak **can occur only if** the basic reproductive number is **larger than 1**.

Disease	Transmission	R_0
Measles	Airborne	12-18
Pertussis	Airborne droplet	12-17
Diptheria	Saliva	6-7
Smallpox	Social contact	5-7
Polio	Fecal-oral route	5-7
Rubella	Airborne droplet	5-7
Mumps	Airborne droplet	4-7
HIV/AIDS	Sexual contact	2-5
SARS	Airborne droplet	2-5
Influenza (1918 strain)	Airborne droplet	2-3

Changing R_0 = *beta k*

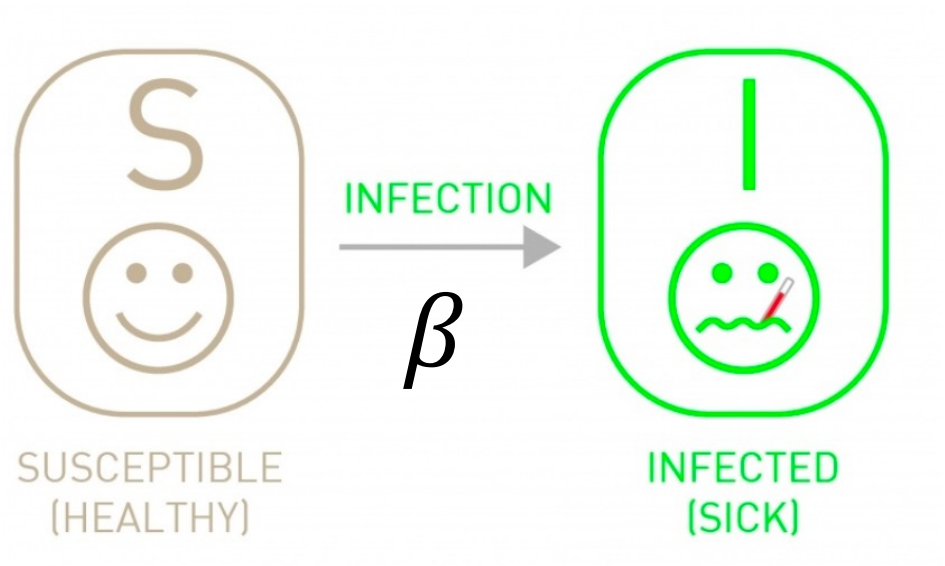
.Sanitary practices (to reduce what?)

.Quarantine (to reduce what?)

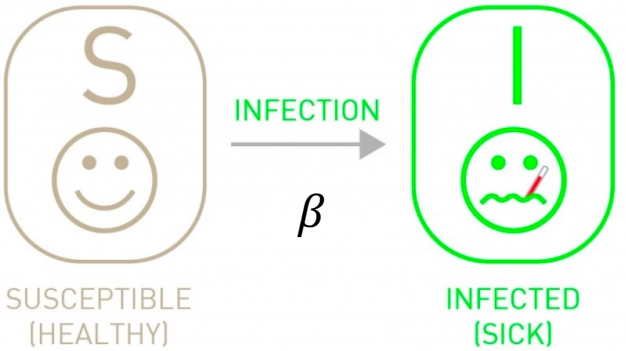
SARS-CoV-2


ORIGINAL VIRUS
IN WUHAN
2.4-2.6
THE VERSION THAT CAUSED
EUROPE'S FIRST WAVE
3
ALPHA
4-5
DELTA
5-8

The SI model



The SI model



.Susceptible node:

– each contact with an infected node
can result in infection with probability **beta**

.Infected node:

– has the disease and can spread it

– will stay sick forever

Notation

- Number of susceptible S(t)
  - Fraction of susceptible s(t) = S(t) / N
- Number of infected I(t)
  - Fraction of infected i(t) = I(t) / N
- s(t) + i(t) = 1

Network substrate

- Let’s assume a homogeneous mixing
  - All nodes have the same number of neighbors <k>
  - example: <k>=4, network is a degree regular d=4
  - example: fully connected graph <k> = N-1

How many susceptible neighbors a node has?

$$\langle k \rangle \frac{S(t)}{N} = \langle k \rangle s(t)$$

How many new infections are produced?

(for every infected, iterate through its susceptible neighbors, infect with probability β)

$$i(t) \langle k \rangle s(t) \beta$$

infected susceptible neighbors infection probability

Prove that $i(t) = \dfrac{i_0 e^{\beta\langle k\rangle t}}{1 - i_0 + i_0 e^{\beta\langle k\rangle t}}$

Begin from: $\dfrac{di(t)}{dt} = i(t)\,\langle k\rangle\,(1 - i(t))\beta$

First, place all terms with $i(t)$ on the left side

Second, use $\dfrac{1}{x \cdot (1-x)} = \dfrac{1}{x} + \dfrac{1}{1-x}$

Third, integrate from $t = 0$ to t and denote by $i_0 = i(t = 0)$

$$\int \frac{1}{x} dx = \log x + C \qquad \int \frac{1}{1-x} dx = -\log(1-x) + C$$

Behavior in the limit $t \to \infty$

- What is the limit of $i(t) = \dfrac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$ when $t \to \infty$?

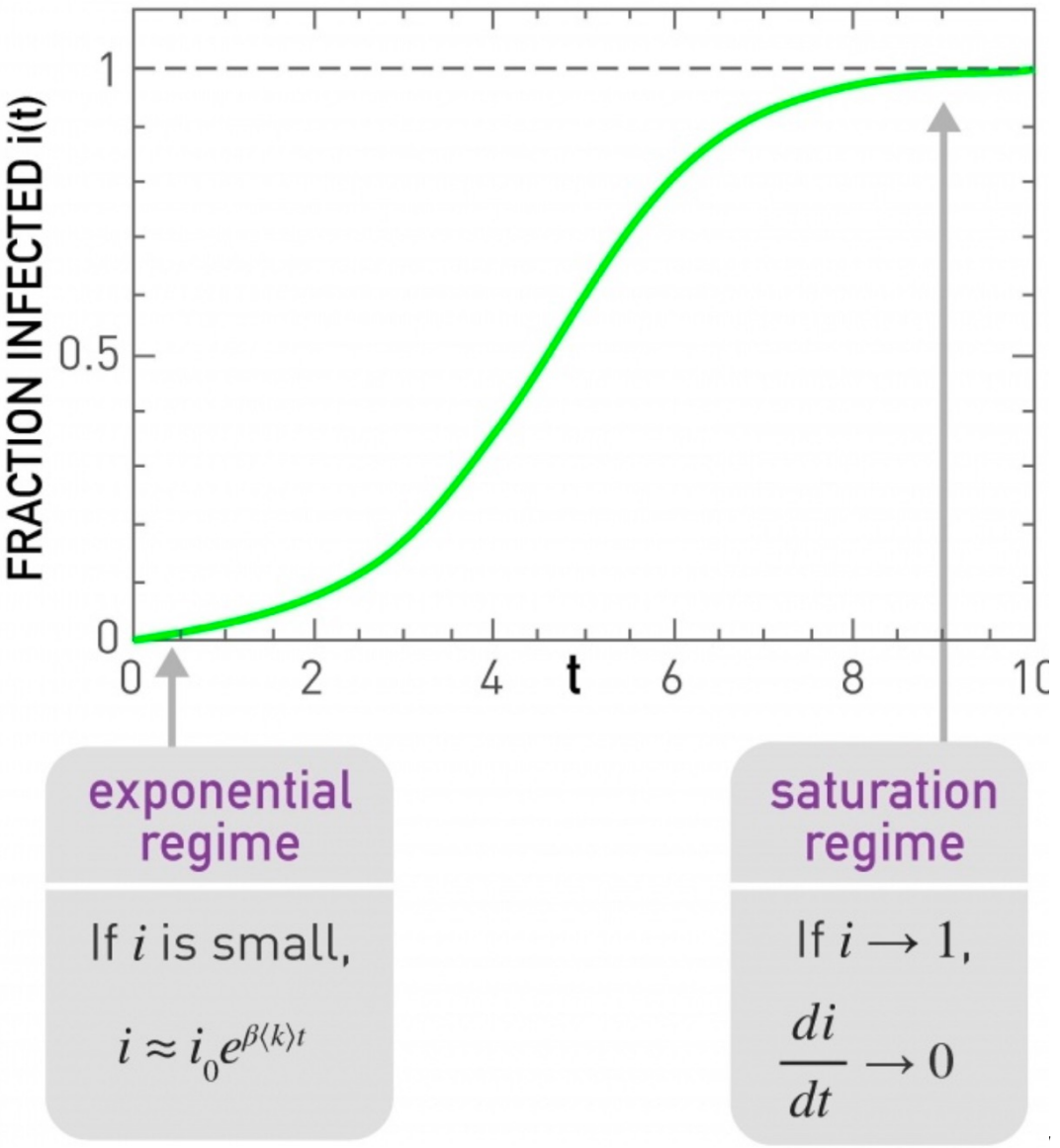
- Hint: similar to $f(t) = \dfrac{e^t}{1 + e^t}$

Infected as a function of time (SI)

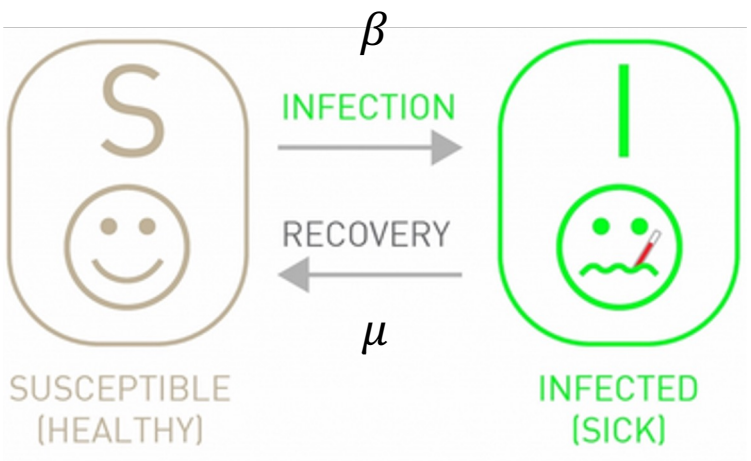
$$i(t) = \frac{i_0 e^{\beta \langle k \rangle t}}{1 - i_0 + i_0 e^{\beta \langle k \rangle t}}$$

Characteristic time
(to infect 1/e ≃ 36% of people):

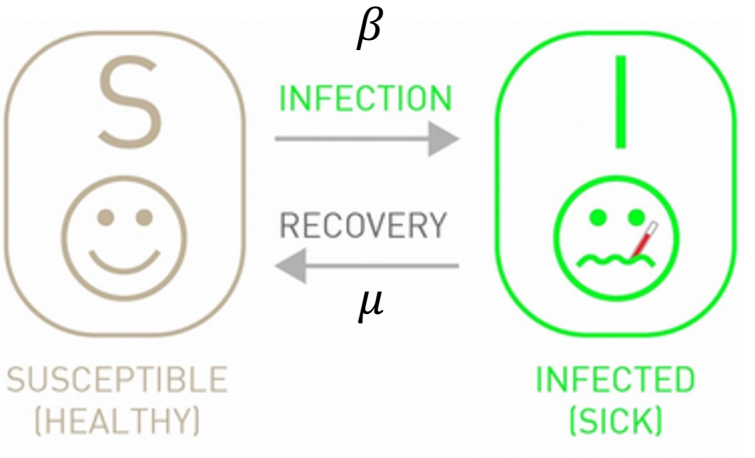
$$\tau = \frac{1}{\beta \langle k \rangle}$$



The SIS model



The SIS model



- **Susceptible node:**

– each contact with an infected node
can result in infection with probability **beta**

- **Infected node:**

– have the disease and can spread it

– each time step, it recovers with probability **mu**
(it becomes susceptible again)

Infection dynamics

$$\frac{di(t)}{dt} = \beta \langle k \rangle i(t)(1 - i(t)) - \mu i(t)$$

- μ is the recovery rate, i.e., the probability of becoming susceptible again in an unit of time

$$i(t) = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta\langle k\rangle - \mu)t}}{1 + Ce^{(\beta\langle k\rangle - \mu)t}}$$

- C is a constant that depends on i_0

Behavior in the limit $t \to \infty$

- What is the limit of when $t \to \infty$?

$$i(t) = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta\langle k\rangle - \mu)t}}{1 + Ce^{(\beta\langle k\rangle - \mu)t}}$$

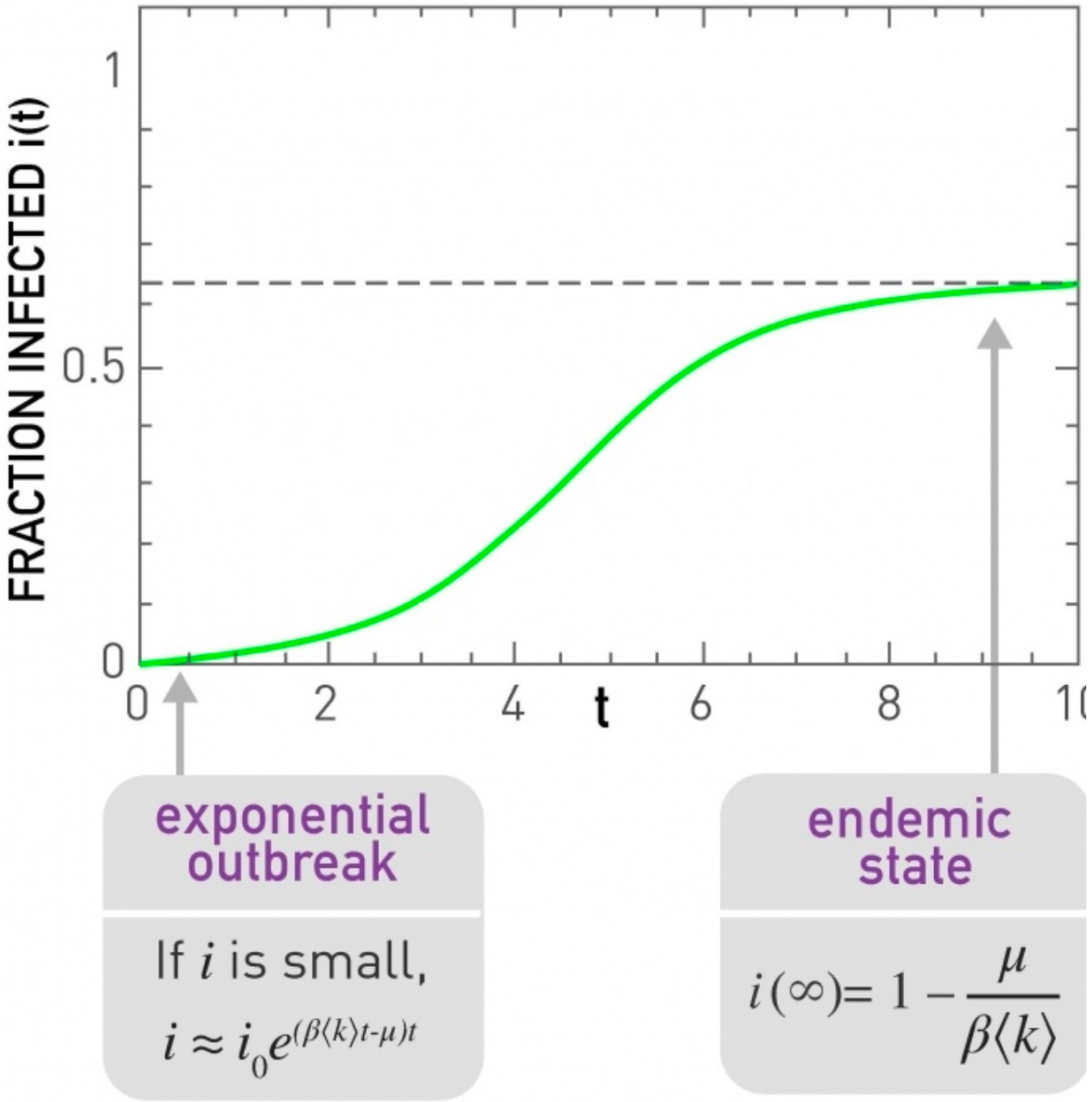
- Hint: similar to

$$f(t) = \alpha \frac{e^t}{1 + e^t}$$

Infected as a function of time (SIS)

$$i(t) = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta\langle k\rangle - \mu)t}}{1 + Ce^{(\beta\langle k\rangle - \mu)t}}$$

This is in the case $\mu < \beta \langle k \rangle$



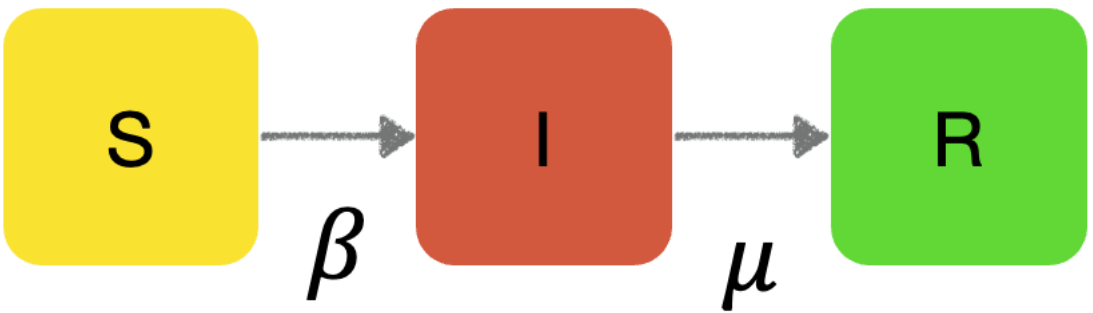
What happens if $\mu > \beta \langle k \rangle$

- Remember: $$\frac{di(t)}{dt} = \beta \langle k \rangle i(t)(1 - i(t)) - \mu i(t)$$

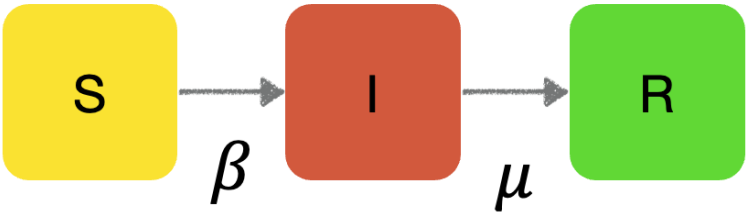
Epidemic threshold

- Assumption: early phase of the epidemic, almost all are susceptible $I \simeq 0, S \simeq N$
- Each infected individual can transmit the disease to <*k*> people at each iteration: expected number of people infected by a single person after one iteration is $\beta\langle k\rangle$
- If there are *I* infected individuals, we expect to have $I_{sec} = \beta\langle k\rangle I$ new infected people after one iteration and $I_{rec} = \mu I$ recovered people
- **Threshold condition for epidemic spreading:** $\beta\langle k\rangle I > \mu I \implies R_0 = \frac{\beta}{\mu}\langle k\rangle > 1$
  $I_{sec} > I_{rec}$
- $R_0 = \beta\langle k\rangle/\mu$ is the **basic reproduction number**
- If $R_0 < 1$, the **initial outbreak dies out in a short time**
  if $R_0 > 1$, the **epidemic keeps spreading**

The SIR model



The SIR model



•Susceptible node:

– each contact with an infected node
can result in infection with probability **beta**

•Infected node:

–The node has the disease and can spread it

–each time step, it recovers with probability **mu**

•Removed node:

– has no longer the disease, and cannot catch it or propagate it again
(permanent immunity -or- death)

Infection dynamics in SIR

$$\frac{di(t)}{dt} = \beta \langle k \rangle i(t)(1 - r(t) - i(t)) - \mu i(t)$$

$$\frac{dr(t)}{dt} = \mu i(t)$$

$$\frac{ds(t)}{dt} = -\frac{di(t)}{dt} - \frac{dr(t)}{dt} = -\beta \langle k \rangle i(t)(1 - r(t) - i(t))$$

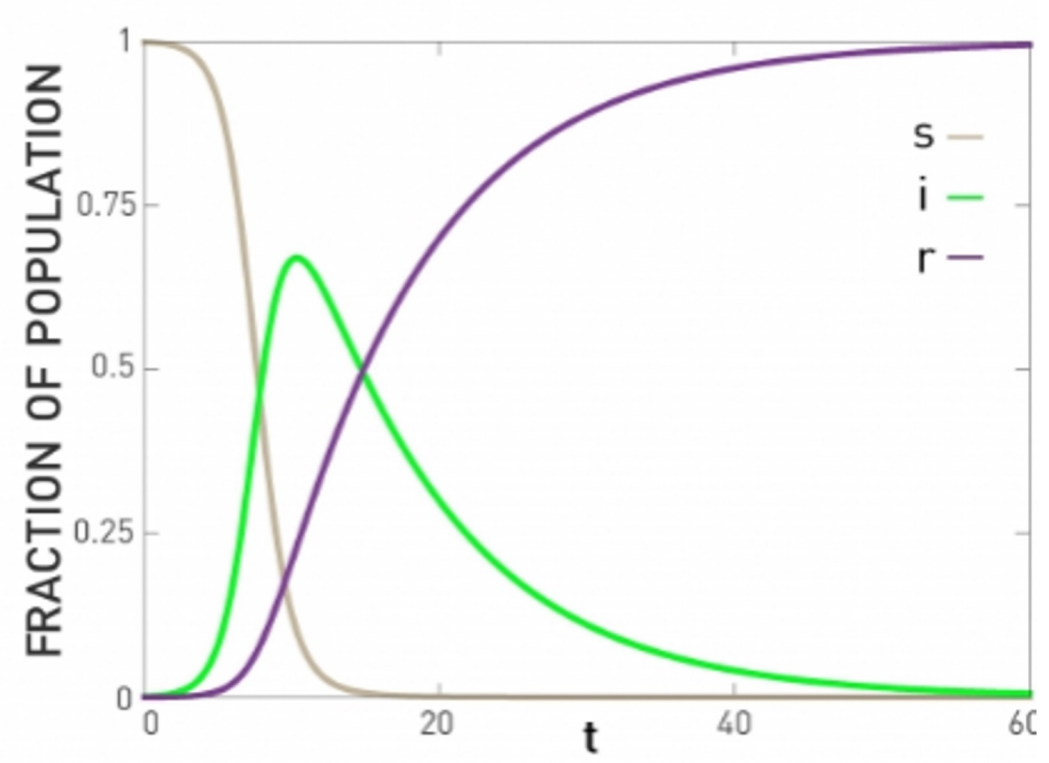
- No closed form solution

Infection dynamics (SIR)

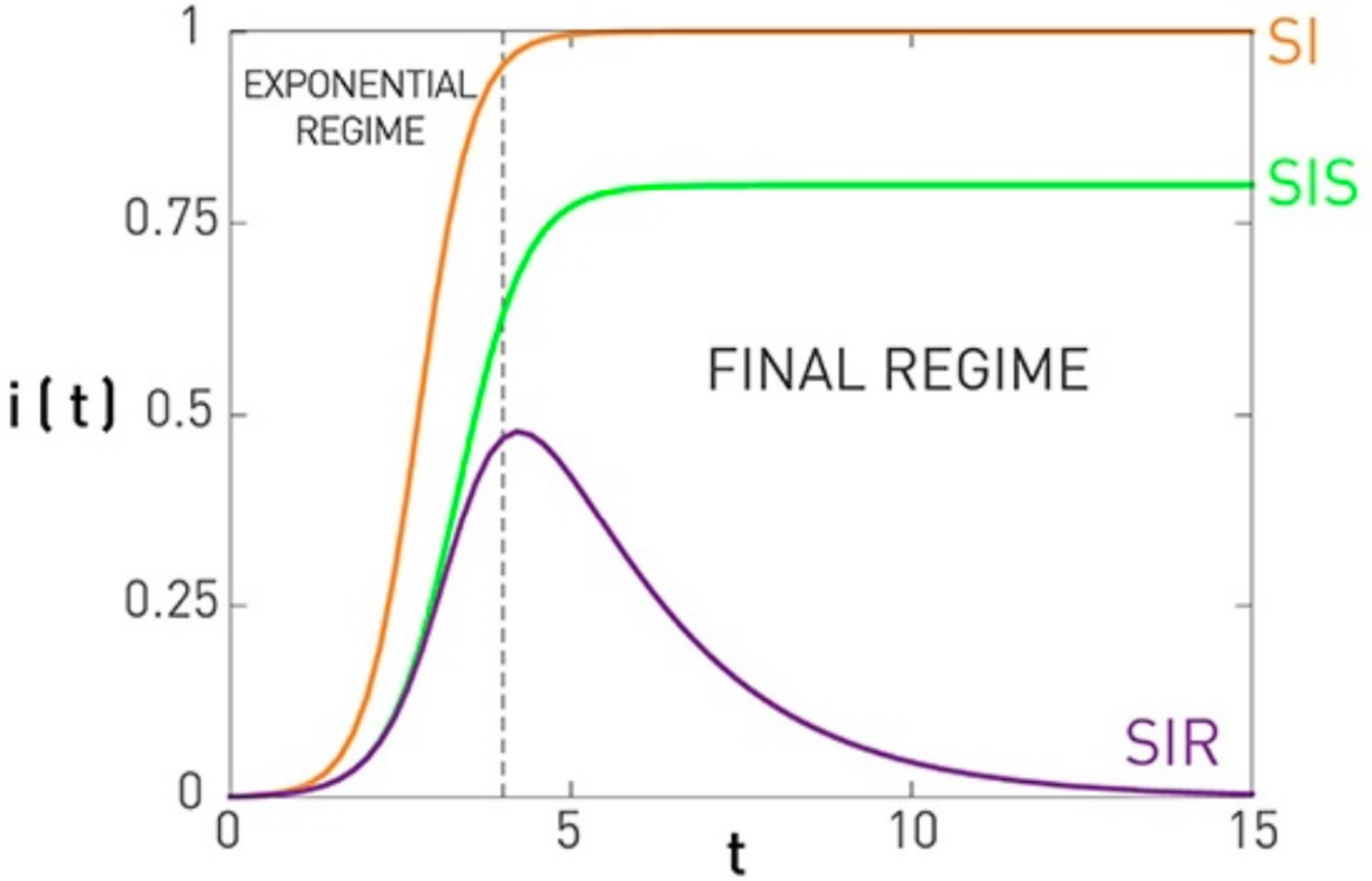
$$\frac{di(t)}{dt} = \beta \langle k \rangle i(t)(1 - r(t) - i(t)) - \mu i(t)$$

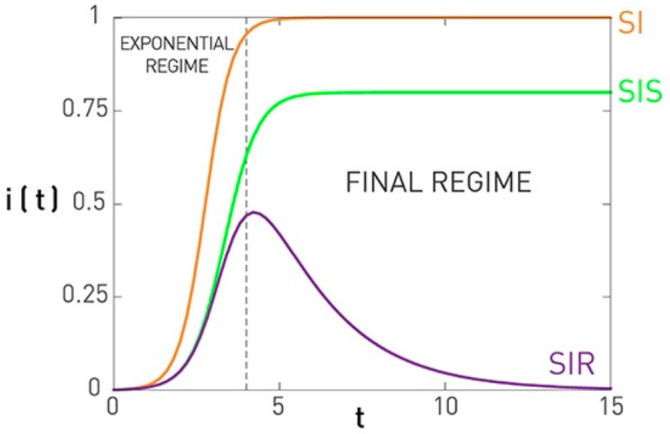
$$\frac{dr(t)}{dt} = \mu i(t)$$

$$\frac{ds(t)}{dt} = -\beta \langle k \rangle i(t)(1 - r(t) - i(t))$$



Comparison of *i(t)*

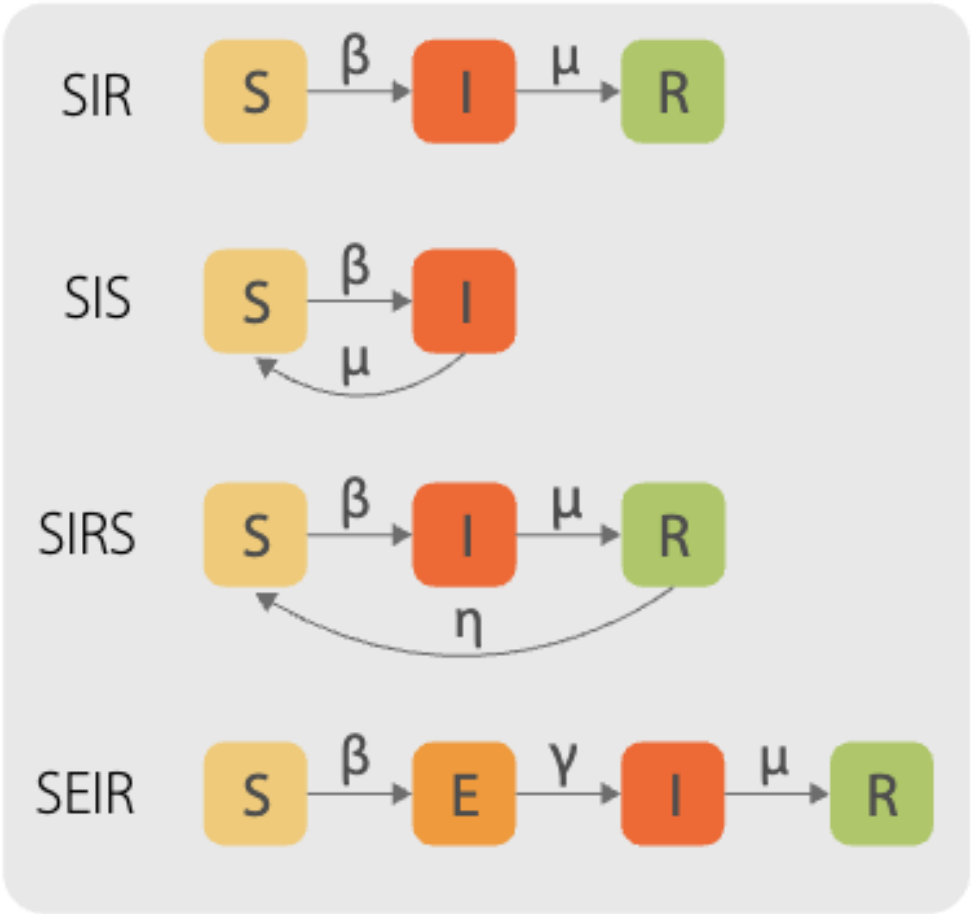




Comparison of *i(t)*

	SI	SIS	SIR
Exponential Regime: Number of infected individuals grows exponentially	$i = \frac{i_0 e^{\beta\langle k\rangle t}}{1 - i_0 + i_0 e^{\beta\langle k\rangle t}}$	$i = \left(1 - \frac{\mu}{\beta\langle k\rangle}\right)\frac{Ce^{(\beta\langle k\rangle - \mu)t}}{1 + Ce^{(\beta\langle k\rangle - \mu)t}}$	No closed solution
Final Regime: Saturation at $t \to \infty$	$i(\infty) = 1$	$i(\infty) = 1 - \frac{\mu}{\beta\langle k\rangle}$	$i(\infty) = 0$
Epidemic Threshold: Disease does not always spread	No threshold	$R_0 = 1$	$R_0 = 1$

More models…



- Can include incubation period
- non-permanent immunity (susceptible again)
- Can include a state for hospitalization

Things to remember

- SI, SIS, SIR models
- Which are the states in each process and which are the possible transitions
- Regimes under different parameters
- Practice executing by hand and write code if it helps you remember better each process

Sources

- A. L. Barabási (2016). Network Science – Chapter 10
- D. Easley and J. Kleinberg (2010). Networks, Crowds, and Markets — Chapter 21
- URLs cited in the footer of slides

Practice on your own

Under the **SIS** model, $i(t) = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta\langle k\rangle - \mu)t}}{1 + Ce^{(\beta\langle k\rangle - \mu)t}}$

1. When $\mu < \beta \langle k \rangle$ what is the limit of $i(t)$?
2. How is this state called?
3. What happens when $\mu > \beta \langle k \rangle$?
4. What conditions lead to large values of $i(t)$?

Practice on your own (cont.)

- In the **SIRS** epidemic model, there are three possible states for a node: susceptible, infected, and recovered. Susceptible nodes can become infected, infected nodes can become recovered, and ***recovered nodes can become susceptible again*.**

- During one unit of time, with probability β an infected node can infect one of its contacts, with probability μ, an infected node can recover, and with probability σ, a recovered node can become susceptible again.

- Let s(t) be the fraction of susceptible nodes, i(t) be the fraction of infected nodes, r(t) the fraction of recovered nodes, and <k> the average degree of the graph. Write the equations, simplifying them appropriately, for:

$$1.\frac{di(t)}{dt} \quad 2.\frac{dr(t)}{dt} \quad 3.\frac{ds(t)}{dt}$$

- 4. Is σ > μ sufficient to say that the recovered will tend to zero in the long run?