A complex network diagram serves as the background for the slide. It consists of numerous nodes of varying sizes and colors (yellow, green, blue, orange, purple, grey) connected by thin grey lines. Some nodes are highlighted with larger, semi-transparent circles of the same color. The network is dense and interconnected, with some clusters and some isolated nodes.

# Lecture 17 · Spreading Phenomena

## Networks, Crowds and Markets

# Today's Lecture

1. Spreading phenomena
2. Modelling hypotheses
3. Epidemic modelling
  - 3.1 Susceptible-Infected (SI)
  - 3.2 Susceptible-Infected-Susceptible (SIS)
  - 3.3 Susceptible-Infected-Recovered (SIR)
4. Epidemics on networks (rumor spread)

# Spreading Phenomena

Despite their differences, many spreading processes follow similar patterns and can be described within a common framework.

PHENOMENA	AGENT	NETWORK
Venereal Disease	Pathogens	Sexual Network
Rumor Spreading	Information, Memes	Communication Network
Diffusion of Innovations	Ideas, Knowledge	Communication Network
Computer Viruses	Malware, digital viruses	Internet
Mobile Phone Virus	Mobile Viruses	Social / Proximity Network
Bedbugs	Parasitic Insects	Hotel–Traveler Network
Malaria	<i>Plasmodium</i>	Mosquito–Human Network

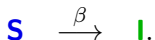
In the first part of this lecture the network will not appear explicitly.

# Modelling hypotheses

# Compartmentalization Hypothesis

Epidemic models classify each individual according to the stage of the disease. A simple classification is:

- **Susceptible (S)** – can become infected,
- **Infectious (I)** – currently contagious,
- **Recovered (R)** – has cleared the infection and is immune.



More detailed models add states such as **latent** individuals, who have been exposed but are not yet contagious.

# Homogeneous Mixing Hypothesis

**Homogeneous mixing** assumes that each individual has the same chance of coming into contact with any given infected individual.

This hypothesis removes the need to know the precise contact network on which the disease spreads. Instead, we assume that anyone can infect anyone else (as if the population formed a complete graph).

# Susceptible-Infected Model (SI)

$$S \xrightarrow{\beta} I.$$

## Susceptible-Infected Model (SI)

Consider a disease that spreads in a population of  $N$  individuals.

- $S(t)$  is the number of individuals who are susceptible at time  $t$ .
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If a single individual becomes infected at time  $t = 0$  (i.e.  $I(0) = 1$ ), how many individuals will be infected at some later time  $t$ ?

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Assume:

- Each individual makes on average  $c$  contacts per unit time,  $c > 0$ .
- The probability that the disease is transmitted from an infected to a susceptible individual in a unit time is  $\beta$ .
  - ▶ Over a small time interval  $\Delta t$  this probability is  $\beta\Delta t + o(\Delta t)$ .

## Susceptible-Infected Model (SI)

At each time  $t$  there are  $I(t)$  infected individuals.

Each of them gets in touch with  $c \frac{S(t)}{N}$  susceptible individuals.

Each new person gets infected in time  $\Delta t$  with probability  $\beta \Delta t + o(\Delta t)$ .

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We conclude:

$$I(t + \Delta t) - I(t) = I(t) c \frac{S(t)}{N} (\beta \Delta t + o(\Delta t)) = I(t) c \frac{S(t)}{N} \beta \Delta t + o(\Delta t).$$

Taking the limit  $\Delta t \rightarrow 0$ , we get the expression for the derivative.

$$\frac{dI(t)}{dt} = I(t) c \frac{S(t)}{N} \beta.$$

# Susceptible-Infected Model (SI)

Recall:  $\frac{dI(t)}{dt} = \beta c \frac{S(t)I(t)}{N}$ . Denote  $s(t) := S(t)/N$  and  $i(t) := I(t)/N$ .

The equation becomes

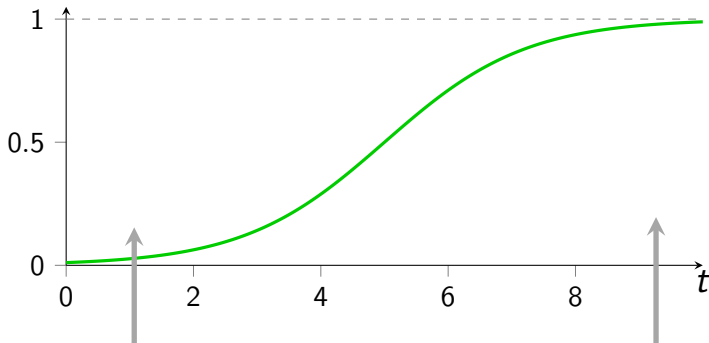
$$\frac{di}{dt} = \beta c s(t) i(t) = \beta c (1 - i(t)) i(t),$$

with solution

$$i(t) = \frac{i_0 e^{\beta c t}}{1 - i_0 + i_0 e^{\beta c t}},$$

where  $i_0 = i(0)$ . **Verify this!**

FRACTION INFECTED  $i(t)$



**exponential  
regime**

If  $i$  is small,  
$$i \approx i_0 e^{\beta c t}$$

**saturation  
regime**

As  $i \rightarrow 1$ ,  
$$\frac{di}{dt} \rightarrow 0$$

In the SI model the epidemic ends only when everyone is infected.

# Susceptible-Infected-Susceptible Model (SIS)



# Motivation for a different model

Most pathogens are eventually defeated by the immune system or by treatment. We therefore allow individuals to recover at rate  $\mu$ .

- The probability of recovering in time  $\Delta t$  is  $\mu\Delta t + o(\Delta t)$ .

Once an individual recovers:

- they become susceptible again;
- they cease to spread the disease.



# Susceptible-Infected-Susceptible Model (SIS)

The equation to be solved is now

$$\frac{di}{dt} = \beta c(1 - i(t))i(t) - \mu i(t) = (\beta c - \mu)i(t) - \beta c i^2(t).$$

Set

$$r := \beta c - \mu, \quad i^* := 1 - \frac{\mu}{\beta c}.$$

**Case  $\beta c > \mu$  (endemic regime).** Then  $r > 0$  and  $i^* \in (0, 1)$ . For  $i(0) = i_0 \in (0, 1)$  the solution is

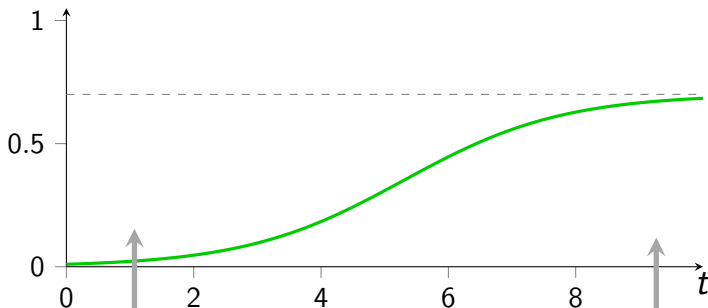
$$i(t) = \frac{i^*}{1 + \left(\frac{i^* - i_0}{i_0}\right) e^{-rt}},$$

which increases monotonically to the equilibrium  $i^*$ .

**Case  $\beta c \leq \mu$  (disease-free regime).** The only equilibrium in  $[0, 1]$  is  $i = 0$ , and every solution with  $0 < i_0 < 1$  decreases monotonically to 0.

## Endemic state: $\mu < \beta c$

FRACTION INFECTED  $i(t)$



**exponential  
outbreak**

If  $i$  is small,  
 $i \approx i_0 e^{(\beta c - \mu)t}$

**endemic  
state**

$$i(\infty) = 1 - \frac{\mu}{\beta c}$$

# The Basic Reproductive Number

## Basic reproductive number

$$R_0 := \frac{\beta c}{\mu}$$

is the average number of new infections caused by one infected individual in an otherwise susceptible population.

- We can show that  $1/\mu$  is the average infectious period.

# The Basic Reproductive Number

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- We can show that  $1/\mu$  is the average infectious period.

If  $R_0 > 1$ , the epidemic reaches an endemic state.

- If each infected individual infects on average more than one healthy person, the pathogen is poised to spread and persist.

If  $R_0 < 1$  the epidemic dies out.

- If each infected individual infects on average fewer than one additional person, the pathogen cannot persist in the population.

## Examples of $R_0$ for some diseases

DISEASE	TRANSMISSION	$R_0$
Measles	Airborne	12–18
Pertussis	Airborne droplet	12–17
Diphtheria	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

Likely, we will never about any pathogen with  $R_0 < 1$ .

## Exercise

Given the following function in the SIS model of an epidemic that affects 50 million people:

$$i(t) = \frac{0.125e^{0.35t}}{1 + 0.25e^{0.35t}},$$

where  $t$  is time in years.

- a) What is the state of the epidemic (endemic or disease-free)?
- b) How many people were infected at the beginning of the disease?
- c) At what time will more than 20 million people be infected?
- d) What is the stationary state? How long will it take to get close to the stationary state?