ELU 501
Data science, graph theory and social network studies

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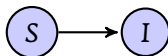
Part

Lecture 6
Epidemic models

Compartmental epidemiological models

- *S susceptible* ⟨🇫🇷 *susceptible*⟩
- *I infectious* ⟨🇫🇷 *infectieux*⟩
- *R recovered* ⟨🇫🇷 *immunisé*⟩ or *dead* ⟨🇫🇷 *mort*⟩
- *M maternally-derived immunity* ⟨🇫🇷 *immunité à la naissance*⟩
- *C carrier* ⟨🇫🇷 *porteur*⟩
- *E exposed* ⟨🇫🇷 *exposé*⟩ = infected but not infectious.

The SI model

$$S \longrightarrow I$$

- The *SI model* is the one of *susceptible* and *infected*.
- Let $S(t)$ and $X(t)$ be the number of susceptible and of infected individuals at time t in a population of n.
- Each person meets β persons per unit of time.
- If there are X infected to start with then the average rate of new infections per unit of time is $\beta SX/n$.

- Justification of the $\beta SX/n$ formula: each person meets β others $\Rightarrow \beta S/n$ susceptible ones. This happens for every infected, so that *globally* the disease will increase by $X\beta S/n$ by unit of time.
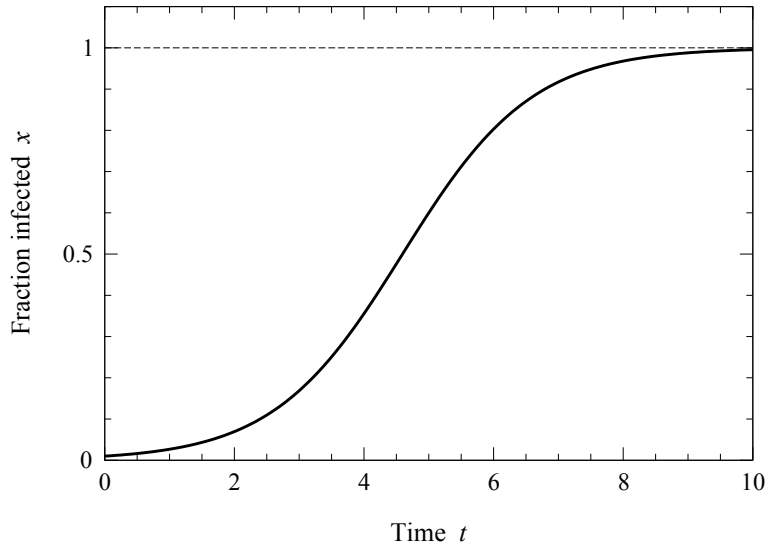
The SI model

$$S \longrightarrow I$$
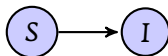
Hence we have

$$\frac{dX}{dt} = \beta \frac{SX}{n}$$

$$\frac{dS}{dt} = -\beta \frac{SX}{n}$$
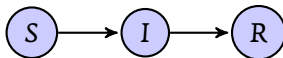
By using $s = S/n$ and $x = X/n$, we get the solution

$x(t) = \frac{x_0 e^{\beta t}}{1 - x_0 + x_0 e^{\beta t}}$ which is a logistic function.

The SI model

Time t

From [Newman, 2010, Fig. 17.1].

The SIR model

$$S \longrightarrow I \longrightarrow R$$

- The *SIR model* is the one of *susceptible*, *infected* and *recovered* (or dead).
- Each person meets with β persons per unit of time and infected recover (or die) at a constant average rate of γ.
- If there are X infected to start with then the average rate of new infections per unit of time is $\beta SX/n$.

The SIR model

- How long does an infected take to start recovering (and hence stop infecting others)? The probability of not recovering at δt is $1 - \gamma\delta t$ and hence the probability of not recovering in a total time t is $\lim_{\delta t \to 0}(1 - \gamma\delta t)^{t/\delta t} = e^{-\gamma t}$. If we add the condition "recovering at time t" we get $\gamma e^{-\gamma t}$.

- The differential equations become

$$\frac{ds}{dt} = -\beta sx \qquad \text{Les personnes susceptibles}$$

$$\text{d'être infectés diminuent}$$

Les personnes infectées augmentent

de la même proportion, et diminuent

$$\frac{dx}{dt} = \beta sx - \gamma x$$

$$\frac{dr}{dt} = \gamma x. \quad \text{Les personnes guéris augmentent}$$

The SIR model
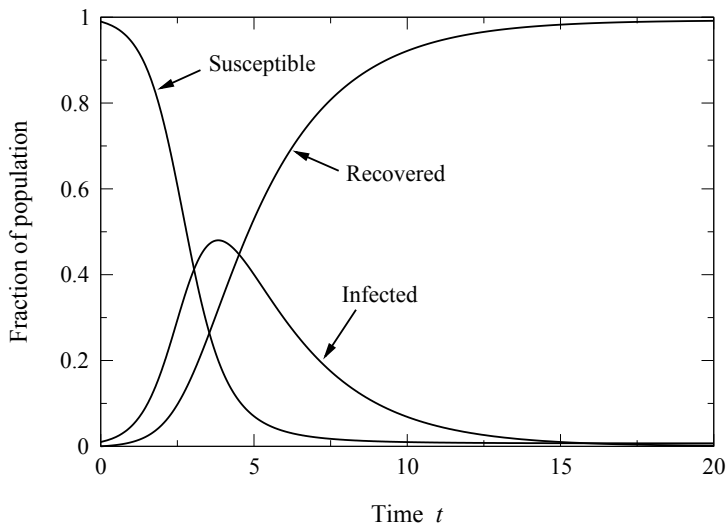
From [Newman, 2010, Fig. 17.2], here
$\beta = 1$, $\gamma = 0.4$, $s_0 = 0.99$, $x_0 = 0.01$, $r_0 = 0$.

The basic reproduction number

- The *basic reproduction number* R is the average number of people to which an infected passes the disease before recovering (or dying).
- It depends not only on the "virus strength" but also on *sanitary conditions*.
- If R < 1 the disease will die out. The value $R_0 = 1$ is called *epidemic threshold*.
- In the SIR model,

$$R = \beta\gamma \int_0^\infty te^{-\gamma t}dt = \frac{\beta}{\gamma}.$$

Disambiguation

Read on `http://aeema.vet-alfort.fr/index.php/component/glossary/Glossaire-1/S/SEUIL-EPIDEMIQUE-300/`:

SEUIL EPIDEMIQUE (angl. epidemic threshold)

Incidence d'une maladie à partir de laquelle on peut considérer qu'un processus épidémique est en cours.

Exemple : utilisé pour la grippe hivernale. Pour l'Homme, Serfling a proposé une méthode de calcul permettant, à partir de données enregistrées pendant plusieurs années pour une endémie, de déterminer l'incidence attendue. Le seuil épidémique est obtenu en ajoutant 1,65 fois l'écart-type à l'incidence attendue. On considère qu'il y a épidémie lorsque l'incidence enregistrée est supérieure au seuil épidémique pendant trois semaines consécutives.

Remarque 1 : la définition d'un seuil épidémique implique que la maladie soit l'objet d'une surveillance régulière et qu'elle survienne périodiquement.

Remarque 2 : pour certains auteurs, cette expression est utilisée pour désigner le nombre ou la densité de sujets réceptifs nécessaire pour qu'une épidémie puisse survenir.
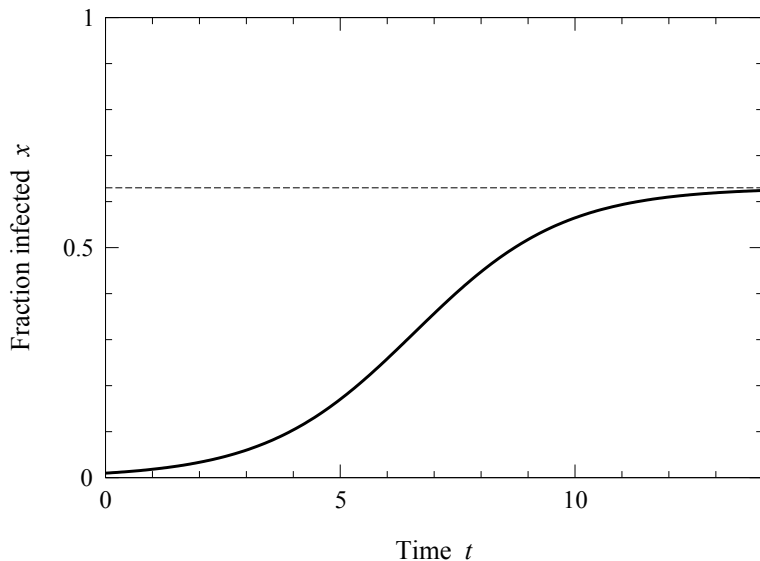
The SIS model
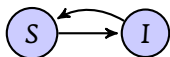
- The *SIS model* is the one of *susceptible*, *infected* which can return to susceptible state, and then get reinfected, etc.
- Each person meets with β persons per unit of time and infected recover at a constant average rate of γ.
- The differential equations are

$$\frac{ds}{dt} = \gamma x - \beta s x$$
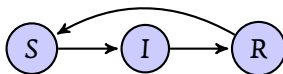
$$\frac{dx}{dt} = \beta s x - \gamma x.$$

- We get the solution $x(t) = x_0 \frac{(\beta-\gamma)e^{(\beta-\gamma)t}}{\beta-\gamma+\beta x_0 e^{(\beta-\gamma)t}}$.

The SIS model

From [Newman, 2010, Fig. 17.3].

The SIRS model

- The *SIRS model* is the one of *susceptible*, *infected*, *recovered* which can return to susceptible state, and then get reinfected, etc.
- Each person meets with β persons per unit of time and infected recover at a constant average rate of γ (= inverse of average recovery time). Let δ the average rate at which people lose immunity.
- The differential equations are

$$\frac{ds}{dt} = \delta r - \beta s x$$

$$\frac{dx}{dt} = \beta s x - \gamma x$$

$$\frac{dr}{dt} = \gamma x - \delta r.$$

- There is no analytic solution for this model.

Epidemic models on networks

- Let us take the SIS model on a graph of adjacency matrix A:
- Vertices are people and edges are relationships between them.
- Let λ be the probability of being infected on each edge of the graph, and μ the probability of a vertex recovering (= returning to state S), on one unit of time.
- Let $p_i^{(t)}$ be the probability of vertex i of being in state I (infected) at time t.
- It depends on $p_i^{(t-1)}$ and on $p_j^{(t-1)}$ for all vertices j neighbors of i.
- $(1-\mu)p_i^{(t-1)}$ is the probability of being I at time t if no other influence.
- $1-(1-\mu)p_i^{(t-1)}$ is the probability of being S at time t if no other influence. We keep this as (1).

Epidemic models on networks

- For each neighbor j probability of infecting i at time t is $\lambda p_j^{(t-1)}$.
- For each node j (not necessarily neighbor) probability of infecting i at time t is $\lambda A_{ij} p_j^{(t-1)}$.
- For each node j probability of not infecting i at time t is $1 - \lambda A_{ij} p_j^{(t-1)}$.
- Probability for i of not being infected by other nodes at time t is $\prod_j (1 - \lambda A_{ij} p_j^{(t-1)})$.
- Using (1), probability of i of being in state S is $(1 - (1-\mu)p_i^{(t-1)}) \prod_j (1 - \lambda A_{ij} p_j^{(t-1)})$.
- Probability of i of being in state I at time t is
$$p_i^{(t)} = 1 - \left(1 - (1-\mu)p_i^{(t-1)}\right) \prod_j (1 - \lambda A_{ij} p_j^{(t-1)}).$$

Python EoN

```python
import networkx as nx
import EoN
import matplotlib.pyplot as plt
N= 100
rho = 0.05
gamma = 1
beta = 10
G = nx.barabasi_albert_graph(N,1)

sim = EoN.fast_SIR(G, beta, gamma, rho = rho, tmax = 10, \
    return_full_data=True)
ani=sim.animate(ts_plots=['SIR'], IonTop=False, \
    node_size=10)
ani.save('SIR_ba-g1-b10-N1.mp4', fps=5,\
    extra_args=['-vcodec', 'libx264'])
```

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