Contagion and COVID-19

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$R_0$: Reproduction Number

- Number of other people that a diseased person will infect, in her lifetime

Reference: https://triplebyte.com/blog/modeling-infectious-diseases
How to Model COVID-19 Spread?

• **Estimate the $R_0$ from real data**

• **Case Study:** Diamond Princess cruise ship

*Estimation of the reproductive number of novel coronavirus (COVID-19) and the probable outbreak size on the Diamond Princess cruise ship: A data-driven analysis.*

Zhang S¹, Diao M², Yu W³, Pei L³, Lin Z⁴, Chen D⁵.

• Note that a lot is **ongoing research** and the findings may change as new evidence emerges.
Findings

• The median with 95% Confidence Interval of $R_0$ of COVID-19 was about **2.28 (2.06-2.52)** during the early stage experienced on the Diamond Princess cruise ship.
More Research, New Results

**Method:** Study of virus spread in China. Fit the SEIR model.

**Finding:** median $R_0$ value of 5.7 (95% CI 3.8–8.9).
COVID-19 vs Others

Reproduction\(^1\) and fatality\(^2\) for selected human viruses

Identification of cases early in the disease, intensification of viral-control methods, and deployment of treatments should drive down the reproduction number and reduce case fatality.

\(^1\)As determined at the beginning of an outbreak; can be reduced by effective intervention.

\(^2\)Case-fatality numbers are reflective of the outbreak setting and depend on a number of factors, including patient’s age, community immunity, health-system capabilities, etc. This graphic aims to offer a broad comparison.

Source: World Health Organization; McKinsey analysis

Reference: https://triplebyte.com/blog/modeling-infectious-diseases
Importance

• Estimating the number of cases and casualties
• Policy development, e.g., stay-at-home orders
• Measuring the effect of interventions
Modeling COVID-19 Spread

- Which model should we use?
  - SIR
  - SIS

- **Next few slides:** recap of SIR and SIS models
Simple model: Branching Process

- **First wave:** A person carrying a disease enters the population and transmits to all she meets with probability $q$. She meets $d$ people, a portion of which will be infected.

- **Second wave:** Each of the $d$ people goes and meets $d$ different people. So we have a second wave of $d \times d = d^2$ people, a portion of which will be infected.

- **Subsequent waves:** same process
Example with $k=3$

High contagion probability:
The disease spreads

Low contagion probability:
The disease dies out
Spreading Models of Viruses

Virus Propagation: 2 Parameters:

• *(Virus) Birth rate* $\beta$:
  – probability that an infected neighbor attacks

• *(Virus) Death rate* $\delta$:
  – Probability that an infected node heals
SIR Model

- **SIR model**: Node goes through phases
  - Models chickenpox or plague:
    - Once you heal, you can never get infected again

- **Assuming perfect mixing**: The network is a complete graph

- **The model dynamics are**:
  \[
  \begin{align*}
  \frac{dS}{dt} &= -\beta SI \\
  \frac{dI}{dt} &= \beta SI - \delta I \\
  \frac{dR}{dt} &= \delta I
  \end{align*}
  \]
SIS Model

- **Susceptible-Infected-Susceptible (SIS) model**
- Cured nodes immediately become susceptible
- **Virus “strength”:** $s = \beta / \delta$
- **Node state transition diagram:**

  - Infected by neighbor with prob. $\beta$
  - Cured with prob. $\delta$
SIS Model

- Models flu:
  - Susceptible node becomes infected
  - The node then heals and become susceptible again

- Assuming perfect mixing (a complete graph):
  \[
  \frac{dS}{dt} = -\beta SI + \delta I \\
  \frac{dI}{dt} = \beta SI - \delta I
  \]
Modeling COVID-19 Spread

• Which model should we use?
  – SIR
  – SIS

• Answer: SIS