Mathematical Models for Effectiveness of Contact Tracing on the Onset of an Epidemic

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Why do we need mathematical models in infectious diseases epidemiology?

- A population-based model integrates knowledge and data about an infectious disease
  - natural history of the disease,
  - transmission of the pathogen between individuals
  - better understand the disease and its population-level dynamics
  - evaluate the population-level impact of interventions: vaccination, antibiotic or antiviral treatment, quarantine, mask (ex: SARS, influenza), …

Why do we need mathematical models in infectious diseases epidemiology?

- "Mechanistic" models, i.e. models that try to capture the underlying mechanisms (natural history, transmission,) are used in order to better understand/predict the evolution of the disease in the population.

- provide useful tools for quantifying the spread of a potential epidemic and examine the effectiveness of control measures

- These models are dynamic → they can account for both direct **and** indirect "herd protection" effects induced by vaccination.

What questions need to be answered?

- Infectious diseases appear and disappear in a community in various ways:

- How severe would an epidemic be?

- How many individuals will be affected altogether and thus require treatment?

- What is the maximum number of people needing care and at any particular time ?

- How long will the epidemic last?

Stochastic and deterministic models

- **Stochastic epidemic models can reveal some important disease dynamics such as variability in the levels of an infection not predicted by deterministic models**

- **Stochastic models are Markovian process, that is, the a process in which the future is independent of the past, given the present.**

- **appropriate in small populations, where random events cannot be ignored**

- **Deterministic dynamics of diseases is a good approximation only when dealing with large populations**

Contact tracing is an important epidemic control measure

- Recommended policy for tackling outbreaks of emerging or re-emerging infectious diseases

- Appropriate and effective when dealing with low numbers of cases that are locally targeted

- Local contact structure to find other infected individuals focus are the potential next-generation cases

Transmission

Cases

- Index – the first case identified
- Primary – the case that brings the infection into a population
- Secondary – infected by a primary case
- Tertiary – infected by a secondary case

Contact tracing

- Screening and contact tracing using a stochastic branching process approximations
- Appropriate when number of infected individuals is small in relation to the total population size
- Initial phase/stage of the epidemic is described by a branching process that resembles a growing tree
- It is a stochastic event on the pattern of contacts between members of the population
- Infection looked at as a slow branching process while contact tracing at a much shorter scale
- Tracing can take forms forward, backwards or both (full tracing)
- Identify an index case
- Each contact is traced with a probability, say p_c

Contact tracing (ctd)

- Branching processes is suited for the epidemiological study since they require data on cases
- They assume individual-level processes are independent and identically distributed
- Provide a simple way (iterative method) to estimate outbreak characteristics such as the

  - basic reproduction number

  -Expected final size and duration of the epidemic

  -Probability of observing a major epidemic

Contact tracing

- Stochastic simulations and moment closures (pair approximation) methods are used to investigate the utility of contact tracing in SIR and SIS models

- Differential equation models that assume homogeneous mixing of the population to study contact tracing whereby traced contacts of individuals found through screening

- single-step contact tracing, a fixed fraction of the of the contacts of an index case (the patient identified as being infected) are identified and treated

- key parameter is the fraction of treated contacts
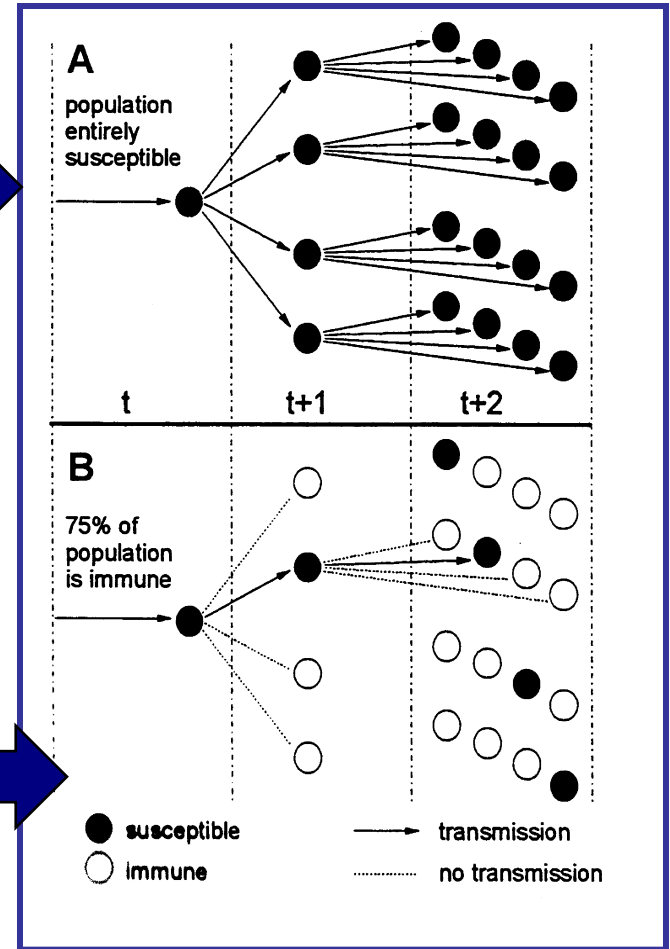
Potential for spread of an infection

- The ***basic reproduction number R_0*** =
  key quantity in infectious disease epidemiology:
  R_0 = *average number of new infectious cases generated by one primary case during its entire period of infectiousness in a totally susceptible population.*

- R_0 determines the required control effort

- $R_0 < 1 \rightarrow$ No invasion of the infection within the population; only small epidemics.

- $R_0 > 1 \rightarrow$ Endemic infection; the bigger the value of R_0 the bigger the potential for spread of the infection within the population.

R_0 is a threshold value at which there is a « bifurcation » with exchange of stability between the « infection-free » state and the « endemic » state.

Evaluation of the potential for spread of an infection

$R_0 = 4$
with whole population susceptible

$R_0 = 4$
with 75% population immune
(25% susceptible)

A
population entirely susceptible

t   t+1   t+2

B
75% of population is immune

● susceptible   → transmission
○ immune   ·····> no transmission

Evaluation of the potential for spread of an infection

- Vaccination reduces the proportion of susceptibles in the population.

- The minimal immunization coverage needed to eliminate an infection in the population, p_c, is related to R_0 by the relation
$$p_c = 1 - (1 / R_0)$$

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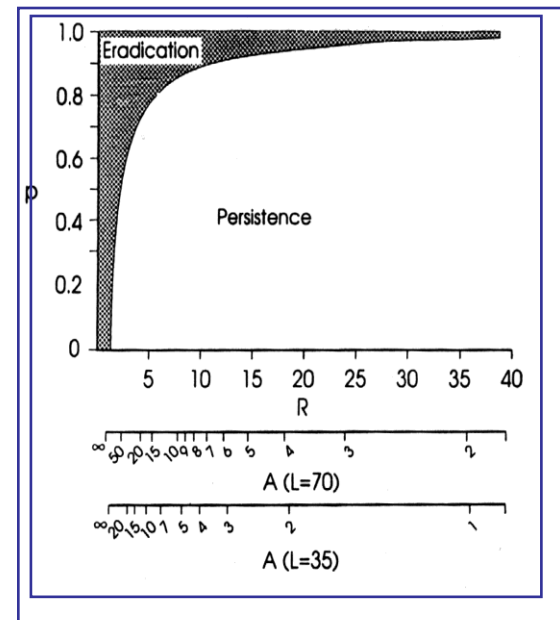
Networks structures

- **Network structures identify the potential transmission routes on how the disease is likely to be spread from one individual to another**
- **They easily depict the complexity of the real world**

Importance

- capture some aspects of population heterogeneity
- identify connections between individuals (or groups of individuals) allow an infectious disease to propagate
- gives opportunities for a disease to spread
- Networks are either static or dynamic through time
- Static contact network models are appropriate for human interactions for a well represented disease generation time

Network Structure

- Contact tracing relate disease generation time in which all contacts within one disease generation are identified and tested for potential transmission

- A node in a contact network represents an individual host

- An edge (connection or link) between two nodes represents an interaction which may allow disease transmission

- Number of edges (contacts) attached to the node is its degree

- A network referred to as a tree, with a single node at the top called a root.

Mathematical models in infectious diseases epidemiology and semi-algebraic methods

- Nature of the network between individuals is important in determining R0 and the final size of an epidemic
- **Number of connections per node k is a significant potential efficacy of contact tracing and disease control strategies**
- **Contacts of the infected patients are identified, located,and either treated, vaccinated or isolated to preventt their additional infecting patients**
- **Parameter of the branching process depend on the time since infection**
- **Tau- is the generation interval- the duration between onset of symptoms of a secondary case and its primary case.**
- **Local contact network structure affects the duration of generation interval**

The SIR Epidemic Model

- First studied, Kermack & McKendrick, 1927
- Consider a disease spread by contact with infected individuals
- Individuals recover from the disease and gain further immunity from it.
- S = fraction of *susceptibles* in a population
- I = fraction of *infecteds* in a population
- R = fraction of *recovereds* in a population

$$S + I + R = 1$$

SIR Epidemic model (ctd)

- *Differential equations* (involving the variables *S*, *I*, and *R* and their rates of change with respect to time *t*) are

$$\frac{dS}{dt} = -\rho SI, \quad \frac{dI}{dt} = \rho SI - \alpha I, \quad \frac{dR}{dt} = \alpha I$$

- We define the parameters:

☐ $\rho =$ the *infection rate*

☐ $\alpha =$ the *removal rate*

- *Basic reproduction number* is obtained from these parameters:

- $N_R = \rho / \alpha$

SIR Epidemic model

- This number represents the average number of infections caused by one infective in a totally susceptible population. As such, an epidemic can occur only if $N_R > 1$.

- If only a fraction S_0 of the population is susceptible, the *reproduction number* is $N_R S_0$, and an epidemic can occur only if this number exceeds 1.

- Suppose a fraction V of the population is vaccinated against the disease. In this case, $S_0 = 1 - V$ and no epidemic can occur if
$$V > 1 - 1/N_R$$

End

Thank you for your

Attention

Acknowledgements

(1) DAAD

(2) Mbarara University of Science & Technology

(3) Conference Organizers