Epidemics and Networks A Little Survey.

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Outline

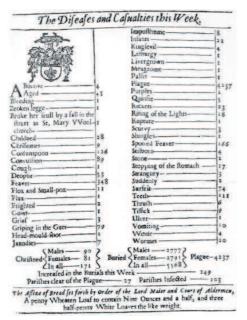
Introduction to epidemiology

Homogeneous population approaches

Spatial models

Epidemics on networks

Early history



Bills of Mortality for London, August 15-22, 1665 http://eee.uci.edu/clients/bjbecker/PlaguesandPeople/lecture7.html

John Graunt, 1620-1674

- Natural and Political Observations made upon the Bills of Mortality, 1662.
 - one of the earliest examples of statistical demography.

Early history

Daniel Bernoulli, 1700-1782

- Essai d'une nouvelle analyse de la mortalité causée par la petite vérole et des avantages de l'inoculation pour la prévenir, 1760
- presented a differential equations model of smallpox population dynamics

William Farr, 1807-1883

- ► Second report of the Registrar-General of England and Wales, 1840.
- ▶ fitted curves to outbreak data on smallpox and rinderpest in cattle



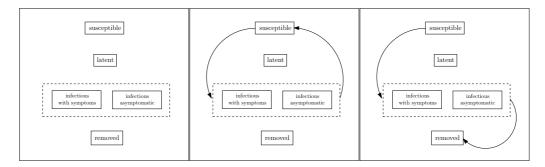
Bernoulli http://www.mathematik.ch/mathematiker/daniel_bernoulli.php



Farr
http://www.york.ac.uk/depts/maths/histstat/people/farr.gif

Infectious disease progression

The 19th century's key idea: a disease is transmitted from an ill individual to a healthy individual via an infectious microbe.



Example

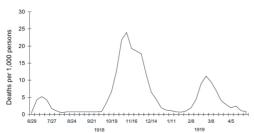
SIS model - appropriate for diseases that don't confer immunity or death, e.g. the common cold.

Measurements

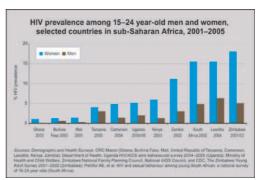
Population disease parameters

incidence rate frequency of occurrence of some event per individual during a period of time.

prevalence rate proportion of population affected by a disease at a given time. mortality rate number of deaths per individual per unit of time.



Combined influenza and pneumonia mortality curve, UK, 1918-1919. from Taubenberger, CID 2006



HIV prevalence curve in southern Africa, by nation, 2001-2005 from UNAIDS/WHO Aids Epidemic Update 2005

What is an epidemic?

An epidemic is "any marked upward fluctuation in disease incidence or prevalence" [Barker, 1973].

For SIS or SIRS models:

▶ is there a non-zero fraction of infected individuals in the long term?

For SIR models:

does the population of infectives increase from its initial size?

Model predictions and control

Questions you'd like your model to answer...

- ▶ Will the disease become an epidemic?
- ▶ What percentage of the population will be affected? What percentage will die?
- ▶ How long will the disease persist?

...and consequent public health decisions.

- ▶ What kinds of policies might inhibit disease transmission?
- ► Can a vaccination campaign prevent an epidemic? What kind of vaccination strategy should we use?
- ▶ Is quarantining necessary, or will more mild social regulations be just as effective?
- ▶ Are there preventative measures that will make an epidemic unlikely?

Law of mass action

"If the individuals in a population mix homogeneously, the rate of interaction between two different subsets of the population is proportional to the product of the numbers in each of the subsets concerned." [Daley & Gani, 1999]

- ▶ predicts that the rate at which the susceptible population becomes infected is proportional to the product of the sizes of the two populations.
- occurs in both deterministic and stochastic models of infection.

Example

- ► Kermack & McKendrick, 1927
 - ▶ a continuous-time deterministic SIR ODE model.
- ▶ Whittle, 1955
 - ▶ a SIR Markov process model.

Kermack & McKendrick, 1927

- s the fraction of susceptible individuals in a population.
- *i* the fraction of infected individuals.
- r the fraction of removed individuals.
- β the contact rate of susceptible and infected individuals.
- γ the removal rate of infected individuals.

$$\rho = \frac{\gamma}{\beta}$$
 the relative removal rate.

$$\frac{ds}{dt} = -\beta si$$

$$\frac{di}{dt} = \beta si - \gamma$$

$$\frac{dr}{dt} = \gamma i$$

Theorem

► An epidemic occurs if and only if the initial fraction of susceptibles s₀ exceeds the relative removal rate:

$$s_0>
ho\longleftrightarrow R_0s_0\equivrac{eta}{\gamma}s_0>1$$

A digression on R_0

The basic reproductive ratio

- defined as "the average number of secondary cases caused by an infectious individual in a totally susceptible population" [Keeling, 2001].
- ▶ the initial rate of increase of a disease.

$$R_0 s_0 > 1$$

AIDS	2 – 5
smallpox	3 – 5
measles	16 - 18
malaria	> 100

Ranges of R_0 for some well-known diseases from Keeling, Plus Mag., 2001.

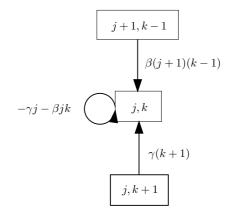
Example

If there existed a vaccine for malaria ($R_0 = 100$), then the fraction of the population that must be vaccinated to prevent an epidemic outbreak would be:

$$1 - \frac{1}{R_0} = 0.99$$

Whittle, 1955

- ▶ a continuous-time Markov SIR model.
- in state (s, i) = (j, k) and in the interval $(t, t + \delta t)$:
 - infections occur at rate $\beta jk\delta t$
 - removals occur at rate $\gamma k \delta t$.



Theorem

Given a large susceptible population, if

$$rac{\gamma}{eta}=
ho\geq extstyle s_0$$

there is zero probability of the disease infecting a finite percentage of the susceptible population.

Spatial approaches

Continuous space

- ▶ PDE models diffusion dynamics.
- traveling epidemic waves, chaotic dynamic behavior.

Discrete space

- ▶ lattice percolation models, contact processes and voter models.
- ▶ often analyzed via simulations.

Example

- ► Kendall, 1957
 - SIR model in continuous time and space.
- ▶ Rhodes & Anderson, 1997
 - simulations of a SIR model on a lattice with individual movement in discrete time.

Spatial (and network) model analysis often employs *mean-field approximations*, in which local correlations are neglected.

Kendall, 1957

- \blacktriangleright an infinite, uniform 2D population with σ individuals per unit area.
- ▶ define s(P, t) (resp. i(P, t), r(P, t)) to be the susceptible (resp. infected, removed) proportions of the population in an infinitesimal area dA around a point P.
- define $\tilde{i}(P)$ to be a spatially-weighted average of i with respect to P.

$$\frac{\partial s}{\partial t}(P,t) = -\beta \sigma s \tilde{i}$$

$$\frac{\partial i}{\partial t}(P,t) = \beta \sigma s \tilde{i} - \gamma i$$

$$\frac{\partial r}{\partial t}(P,t) = \gamma i$$

Theorem

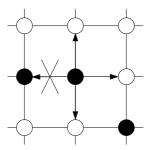
For an initial proportion of infectious individuals centered at the origin, and assuming some additional restrictions, the proportion of individuals contracting the disease will be larger than zero if and only if

$$\sigma > \rho = \frac{\gamma}{\beta}$$

Rhodes & Anderson, 1997

A SIRS model on a 2D toroidal lattice

- ightharpoonup L imes L lattice with population density
- at each time step, an individual chooses one of his four neighboring nodes and moves there if it is unoccupied.
- ▶ a susceptible becomes infected with probability *p* by each of his infected neighbors, independently.
- ▶ an infected recovers with probability p_r at each time step.
- a recovered individual becomes susceptible again with probability p_s at each time step.



Simulations indicate the existence of a threshold in σ , above which a non-zero fraction of the population is infected at steady state.

Network preliminaries

Graph terminology

Recall:

ightharpoonup the adjacency matrix of a network of n nodes is the $n \times n$ matrix A defined by

$$[A]_{ij} = \left\{ egin{array}{ll} 1 & (i,j) ext{ is an edge} \ 0 & ext{otherwise} \end{array}
ight.$$

▶ the degree of a node in an *undirected graph* is the number of edges adjacent to that node.

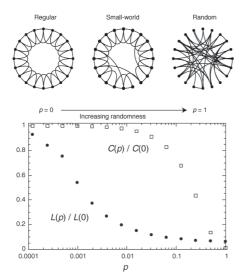
Network parameters

degree distribution P(k) is the probability that a node in the network has degree k.

path length *L* is the number of edges in the shortest path between two vertices, averaged over all vertex pairs.

clustering coefficient C is the average node clustering coefficient, C_v , where C_v is the fraction of possible edges between *neighbors* of node v that actually exist in the graph.

Small-world networks - Watts & Strogatz, 1998



- ▶ the rewiring model: for each vertex and each adjacent edge, rewire the other end of the edge to any other vertex with probability p.
- demonstrates both high clustering and short path lengths.

In general, the *small-world* designation refers to a network's clustering and path length properties, but does not imply a degree distribution! (e.g., the degree distribution of the Watts-Strogatz model has an exponential tail.)

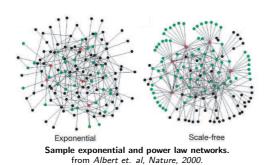
Degree distributions

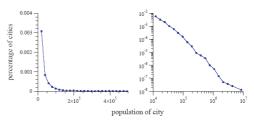
Exponential network

- ▶ the degree distribution is tightly clustered about its mean, and then falls away exponentially.
- ▶ a feature of classical Erdös-Rènyi random graphs (a Poisson distribution).

Power-law (scale-free) distributions

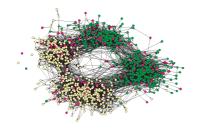
- ightharpoonup occurs when the degree distribution, $P(k)\sim k^{u}$, plotted on a log-log scale, is a straight line.
- described as having a fat tail distribution is skewed with few nodes of very high degree.
- right can be obtained through many different mechanisms.





Frequency of populations of cities in the U.S., 2000 (plotted on linear and log scales). from Newman, Contemp. Phys., 2005.

A highlight of some network epidemic models



Student social network, with clustering along racial and age group divisions. from Moody, American Journal of Sociology, 2001.



 $\begin{array}{c} \textbf{Map of the Moscow subway system.} \\ \textbf{from } \textit{http://www.mosmetro.ru.} \end{array}$

Example

- ► Pastor-Satorras & Vespignani, 2001/2002
 - continuous-time SIS model on infinite, undirected exponential and scale-free networks.
- Wang et al. & Ganesh et al., 2005
 - Markovian SIS models applied to arbitrary networks.
- Watts, et al., 2005
 - a stochastic SIR model operating on a metapopulation.

Pastor-Satorras & Vespignani, 2001/2002

The network SIS model

For a network with an infinite number of nodes and degree distribution P(k):

- ▶ a susceptible node is infected by each of its neighboring infectious nodes with probability β_0 .
- \triangleright an infected node becomes susceptible again with probability γ .

Using a mean-field differential equations approach, when will the infection persist in the network and when will it die away?

Pastor-Satorras & Vespignani, 2001/2002

Exponential networks

- since the degree distribution is clustered around its mean, \bar{k} , assume that all nodes have degree \bar{k} .
- let i(t), s(t) denote the expected density of infected, susceptible nodes at time t:

$$\frac{di(t)}{dt} = \beta_0 \bar{k}i(t)s(t) - \gamma i(t)$$

• observe that this model is identical to the homogeneous deterministic model that we started with, with the infectivity parameter β now equal to $\beta_0 \bar{k}$.

Results

When $\frac{\beta_0 \bar{k}}{\gamma} s_0 > 1$, the network will reach a steady state in which i(t) > 0.

(recall that the deterministic model exhibited a threshold at $rac{eta}{\gamma}s_0>$ 1, where eta a per-proportion rate)

Pastor-Satorras & Vespignani, 2001/2002

Power-law degree distribution

- ▶ since $P(k) \sim k^{-\nu}$ is highly skewed, can no longer assume that each node has roughly the same degree.
- define:
 - m the minimum degree of the nodes in the network.
 - $i_k(t)$ the fraction of degree-k nodes which are infected
 - $\Theta(i(t))$ the probability that any given link points to an infected node.

$$\frac{di_k(t)}{dt} = \beta_0 k s_k(t) \Theta(i(t)) - \gamma i_k(t)$$

Results

- for $2 < \nu \le 3$, the network will reach a steady state in which i(t) > 0 for every set of parameter values!
- for $3 < \nu$, the infection will be endemic in the network if and only if

$$\frac{eta_0}{\gamma} > rac{
u-1}{m
u}$$

May & Lloyd, 2002 present an SIR model with infection parameter β_0 and recovery parameter γ and find that the *fraction of the network ever infected* has the same threshold behavior as Pastor-Satorras & Vespignani's model!

Wang et al. & Ganesh et al., 2005

Wang et al., 2005 - a discrete time model

Consider an arbitrary network with adjacency matrix A and largest eigenvalue λ_A .

- \blacktriangleright at each time step, an infected node infects each of its susceptible neighbors with probability β independently.
- ightharpoonup at each time step, infected nodes may be cured with probability γ .
- \triangleright $p_i(t)$ the probability that node j is infected at time t.

Assuming that all p_j are small, the Kolmogorov equations for this system can be written as:

$$ho_j(t) pprox
ho_j(t-1) + eta \sum_{k: (k,j) \in E}
ho_k(t-1) - \gamma
ho_j(t-1)$$

in matrix form:
$$P_t \approx [(1-\gamma)I + \beta A]P_{t-1}$$

Theorem

If $\frac{\beta}{\gamma} < \frac{1}{\lambda_A}$, an epidemic cannot occur on the network.

note: agrees with Pastor-Satorras & Vespignani for the special case of an Erdös-Rènyi random graph, which has an exponential distribution with mean \bar{k} and for which $\lambda_A = \bar{k}$.

Wang et al. & Ganesh et al., 2005

Ganesh et al., 2005 - a continuous time model

Given an arbitrary network with adjacency matrix A with largest eigenvalue λ_A .

let $X_i(t)$ denote the state of node j at time t:

$$X_j(t) = \left\{ egin{array}{ll} 1 & j ext{ infected at time } t \ 0 & ext{otherwise} \end{array}
ight.$$

 \blacktriangleright an infected node infects its neighbors at rate β and recovers at rate γ .

$$X_j$$
 : $0 o 1$ at rate $eta \sum_{k:(k,j) \in E} X_j$

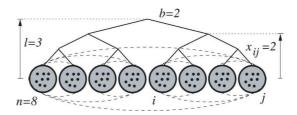
$$X_i$$
 : $1 \rightarrow 0$ at rate γ

Theorem

If $\frac{\beta}{\gamma} > \frac{1}{\lambda_A}$, the probability that the disease has not died out by time t decays exponentially with t.

Watts et al., 2005

- ▶ at each time step, individuals interact within their group i in a standard stochastic SIR fashion, then travel to another group j chosen with probability proportional to $e^{-x_{ij}/\xi}$, where
 - x_{ij} is the ultra-metric distance between groups i and j ξ is a parameter representing propensity for travel



▶ simulations demonstrate resurgent epidemics, underscore importance of stochasticity in disease transmission

Conclusion

The aim of this talk...

▶ to give a flavor of the types of models and results that are central to epidemic theory



Co-link map of NGO's interested in climate change. http://govcom.org

...and critical topics we've given short shrift to.

- large-scale simulation projects
- incorporating active control into these simple models to change the response
- choosing an appropriate model for a given disease
- the demographic challenges of measuring the spread of a disease
- related models for e.g. the spread of gossip in social networks, viruses in computer networks, political ideas between organizations
- including seasonal variations, non-human transmission vectors...