Research Paper Presentation

Overview – The research paper *“Networks and epidemic models”* by Matt J. Keeling and Ken T. D. Eames describes how an epidemiology of directly transmitted infectious diseases and a network can be compared. The paper dives deep into various aspects of the network and epidemic, lets explore various sections of the research paper ahead.

Introduction – The epidemiology of directly transmitted infectious diseases and network can be compared with a network as they both contain a lot of similarities. The foundations of epidemiology and early epidemiological models were based on random mixing. Each individual has a finite set of contacts to whom they can pass infection. Knowledge of the structure of the network allows models to compute the epidemic dynamics at the population scale.

Standard Graph Model – Most disease models are based on compartmentalization of individuals or host according to their disease status. Many of the details of the progression of infection are neglected, but the simplification has had a long and successful history. The susceptible-infectious-recovered (SIR) model is appropriate for infectious diseases that confer lifelong immunity. In a random-mixing model, each individual has a fixed number of contacts to whom they can transmit infection. Networks, on the other hand, have a finite set of permanent contacts from whom infection can be transmitted.

Standard Network Model – The study of networks has its origins in epidemiology and graph theory. In epidemiology, individuals are referred to as 'hosts' and 'contacts', whereas graph theory uses the term 'nodes' or 'edges'. The size of an individual's contacts is their 'neighborhood'. Research in graph theory has provided a wealth of tools and mechanisms for describing networks, many of which have epidemiological applications. We can use an 'adjacency matrix' or 'sociometric', A, to describe the connections within a population. The matrix A summarizes all connections within the network. A graph is said to be connected if any individual (or node) can be reached from any other by following network links. This is equivalent to infection being able to reach the entire population from any starting point. Percolation theory is about the formation of connected structures within networks. Edges within this lattice may be treated as transmission events, with p representing a transmission probability. The size of connected clusters that emerge in percolation models relate to the size of an epidemic within the network.

Three main techniques have been employed to gather network information are as follows

Infection tracing – After an epidemic, field-based epidemiologists place emphasis on determining the source of infection for each case. Because all connections represent actual transmission events, this method does not suffer from problems with the definition of links. However, interactions that did not happen to lead to the transmission of infection in this particular case will be omitted from the network.

Contact tracing – Contact tracing has been commonly applied not as a network evaluation device but as a control tool, most often in the case of STDs. This means that the contacts of uninfected individuals are not sought, and thus only a subset of the full mixing network will be uncovered. Long-term and large-scale data collection has enabled portions of sexual networks from Manitoba, Canada and Colorado Springs, USA, to be traced. These networks highlight the heterogeneities present in sexual networks and show the importance of core groups (interconnected groups) and 'long-distance' connections in disease transmission.

Diary -based tracking – Data collection is at the discretion of the subjects and definition of close contact may not be the same for all individuals. The benefits of this are that the responsibility for collecting the data lies with the subjects rather than the researcher and allows a larger number of individuals to be sampled in detail.

The use of simulated network – The role of core groups (interconnected individuals with a large number of contacts) in the dynamics and persistence of STDs is explored. The simulation model is used to examine the spread of smallpox, and places particular emphasis on transmission within households and family groups. Populations of 2000 individuals are generated with a given age distribution and household size that match the values for the United States. All network-based simulations are limited by fact that there is no simple way to ascertain the sensitivity of the epidemiological results to the details of the network structure. Such simulations are therefore always vulnerable to questions of 'what if?'. A range of idealized networks and analytical tools have been developed that can reveal elements of network structure that are important determinants of epidemic dynamics.

Idealized Network – Several types of computer-generated networks have been studied in the context of disease transmission. In the most tractable version of the random network, each individual has a fixed number of contacts through which infection can spread. The dynamics of diseases on random networks can be studied as a simple branching process. Both the early growth rate of the disease and the final epidemic size are reduced when compared with the random-mixing model. Lattices are homogeneous at the individual level and because of the localized nature of connections are highly clustered.

The contact process is an abstraction of the SIS model, with sites that can be characterized as 'on' or 'off'. The forest-fire model has strong parallels with the SIR disease model: trees burn, leaving empty sites that can be recolonized, which can be interpreted as SIR infection with births.

Pairwise approximations – Pairwise approximations are attempts to model the spread of infection on generic networks where higher-order structure has been ignored. Rather than modelling a network of interactions in its entirety, pairwise models examine the various types of connected pairs found within a population. In an SIS model, the number of SI pairs can change by infection from outside the pair, infection within the pair or recovery. Pairwise models have been shown to be accurate approximations of many network-based epidemics (Eames & Keeling 2002). The advantage of this method is that the complete network is not required so long as the pairs within the network are well sampled. By including connected individuals as its basic variables, the pairwise model can capture the correlations between neighboring individuals that emerge in a system.

The future – The authors argue that if we are attempting to predict population-level dynamics from individual-level observations, then it is vitally important that network structure is taken into account. However, this is not necessarily a problem when they are used for long-term epidemiological research. Advances in mobile phone technology mean that it may soon be possible to accurately track the movement of people in real time, allowing us to build comprehensive networks for many airborne disease

Learning and Interesting Facts – Its interesting to see how a network can mapped with real world problem and helps to solve and analyze them. Social Network Model is a powerful tool and has wide range of applications associated with it. Graph theory plays a major role in keeping track of as fast as ever evolving global changes, trends and behaviors.