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Approaching disease transmission with network science

Shivkumar Vishnempet Shridhar & Nicholas A. Christakis

Social connections are an important means for people to cope with adversity and illness. Thus, technologies, such as social network analysis, that can leverage close, face-to-face social networks could help optimize healthcare interventions and reduce healthcare-related costs, particularly in low-resource settings.

Network science of pathogen transmission

Airborne pathogens, such as SARS-CoV-2, or sexually-transmittedinfections, such as human immunodeficiency virus, spread across social ties and cause millions of deaths. However, the relevance of interpersonal ties is not limited to infectious diseases. Connected individuals also influence each other's behaviour; for example, tobacco and alcohol consumption behaviours can spread through social contagion in siblings, spouses, friends or co-workers¹. Social contagion influences behaviours as diverse as contraceptive use in Cameroon² or vaccine adoption in the USA³.

The biological contagion of commensal microbes might also play a role in the contagion of what are otherwise seen as chronic diseases, ranging from obesity and depression to dementia and atherosclerosis – all of which are becoming increasingly prevalent in many parts of the world. The sharing or transmission of gut microbiome strains occur in parallel with familial and social interaction connections, with one capable of predicting the other⁴. Social networks might thus act as a common highway for both biological and social contagions. Therefore, identifying how microbes spread might reveal transmissible aspects of conditions previously thought to be non-communicable, such as depression or obesity. Leveraging social network analysis and microbiome biology could therefore provide new opportunities for intervening against chronic illness.

In communicable diseases, a small number of people (or 'hubs') in a network are responsible for most of the spread. Because contact networks often have substantial overlap with social networks, social networks can also influence the basic reproduction number (R_0) of pathogens (that is, the number of cases expected to be generated by one case)⁵. Agent-based models (stochastic models that simulate interactions between objects) can predict the spread of epidemics or chronic conditions and identify which individuals might be targeted for interventions. These models can be used to develop epidemiological mappings of disease spreading owing to their ability to capture the nature of human social interactions. That is, agent-based models, along with information on social interactions and pathogen characteristics, can be used in ensemble simulations to map out all possible scenarios of disease end states, making this approach a valuable epidemiological technique.

By incorporating network information at the individual level (such as the number of social connections a person has), targeted intervention (either treatments or testing) can be delivered. For example, childhood vaccination rates in an Indian trial went up after trustworthy 'gossipers', who were responsible for diffusing vaccine-related information, were seeded within the community⁶. Other network-based strategies, such as picking individuals and their nominated friends as targets, can also increase adoption of interventions, such as the use of iron supplementation⁷. These approaches are more efficient than targeting the entire population or targeting random individuals, thus saving valuable resources and time in dealing with epidemics. Software tools, such as Trellis, have been developed for the purpose of mapping networks and selecting targets⁸. Other targeting strategies that leverage network dynamics to select the group that should receive an intervention are also available. For instance, physically separating target groups in crowded areas, such as grocery stores or hospitals, into subgroups that are serviced by different staff or at different venues can limit direct contact and help restrict the potential spread of infection. These strategies might not only help reduce R₀, but also provide an alternative to mass lockdowns, which often lead to reduced healthcare access, loss of jobs, economic burdens or adverse mental health, thereby helping in the redirection of resources towards vaccination and treatment strategies9.

Network science in diagnostics

The COVID-19 pandemic highlighted the need for speedy and accurate testing at the population level, especially in low-resource settings where access to healthcare may be limited. Point-of-care diagnostics, such as SalivaDirect, a saliva-based SARS-CoV-2 detection method that does not require expensive saliva collection tubes or specialized reagents and equipment for nucleic acid extraction, provide a cheap, easy-to-use, scalable and accurate solution compared with real-time quantitative reverse transcription polymerase chain reaction (qRT-PCR)¹⁰. Pooled testing strategies that leverage network information (for example, choosing people with many connections to focus on, or making the composition and size of the pooled groups depend on the number of connections people in the groups have) could further reduce testing costs.

Social connections can be further leveraged to enhance testing uptake; for instance, a randomized trial (NCT03741725) among men who have sex with men at an urban sexually-transmitted-infections clinic in China evaluated a 'pay-it-forward strategy', offering individuals a gift in the form of a test for sexually transmitted diseases. The participants were then asked whether they would like to give the same gift (that is, a future test) to another person. This strategy increased gonorrhoea and chlamydia testing uptake compared with the standard-of-care, in which testing was offered at a fee, and it could be a useful tool for scaling up preventive services that carry a fee¹¹.

Conclusions

Bioengineering challenges in confronting infectious and non-infectious diseases may be overcome by understanding and leveraging social connections, which are involved in the spreading of diseases and behavioural traits, to identify points and timings of intervention.

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Competing interests

The authors declare no competing interests.