COMPUTATIONAL SOCIAL SCIENCE

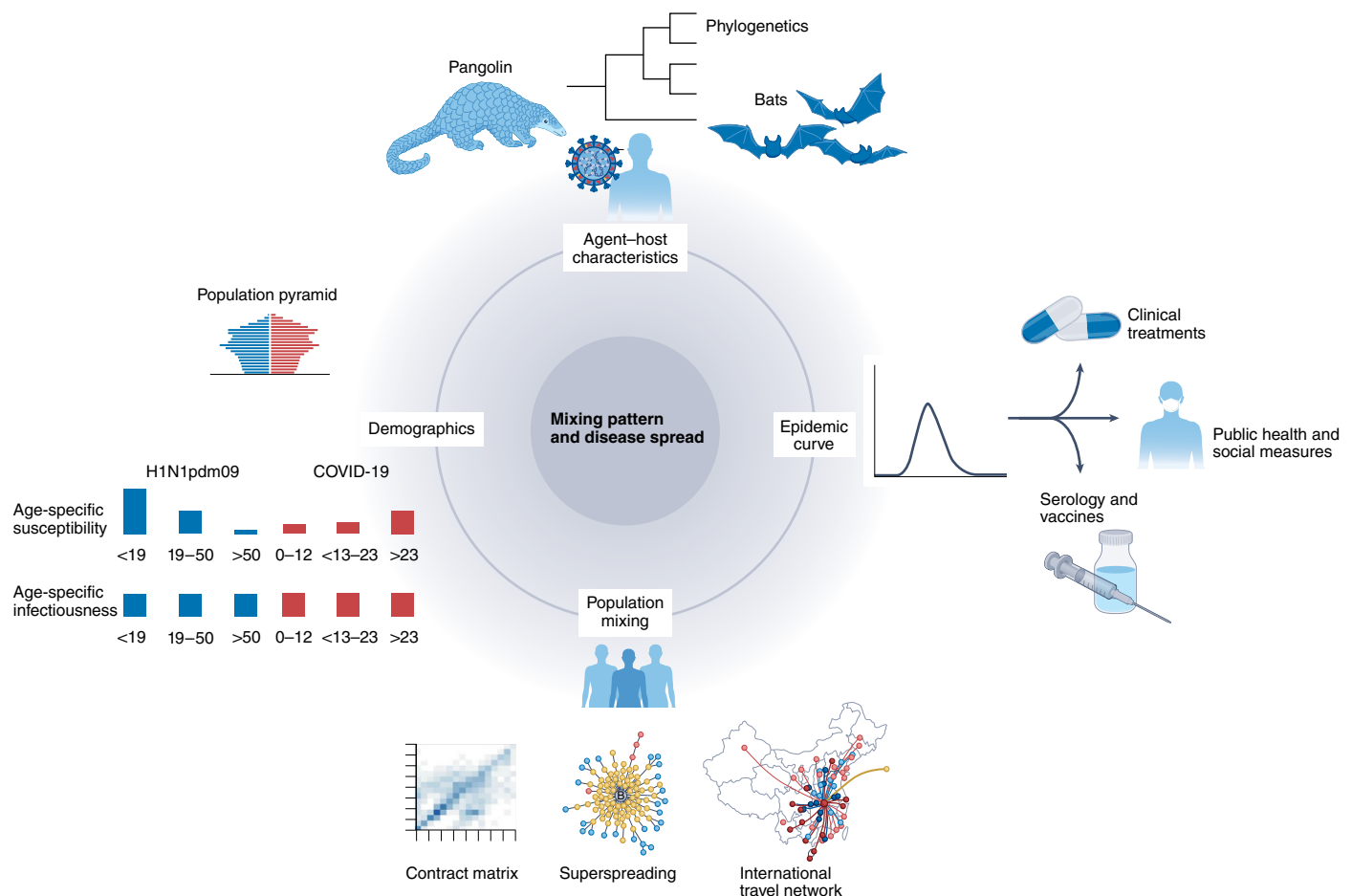# Mixing patterns and the spread of pandemics

Integrating social mixing data into epidemic models can help policy makers better understand epidemic spread. However, empirical mixing data might not be immediately available in most populations. In a recent work, a network model methodology is proposed to construct micro-level social mixing structure when empirical data are not available.

Kathy Leung, Jayson S. Jia and Joseph T. Wu

The ongoing COVID-19 pandemic has highlighted the importance of understanding the transmission dynamics of infectious diseases, which is fundamentally driven by the social and physical mixing patterns of individuals in the population. Human mobility and social network data offer the prospect of directly observing mixing patterns as well as understanding the underlying structure of social contact. Indeed, mixing pattern data, such as contact rates between individuals and flows of populations between regions of interest, have been integrated into mathematic models to provide nowcasts and forecasts of the pandemic[1]. These data provide unique opportunities to understand how mixing patterns vary across socio-economic and demographic micro-segments, which may directly affect social mixing tendencies and epidemic

Fig. 1 | Understanding human mixing patterns and the spread of diseases. Cao and Heydari provide an explainable model for investigating the heterogeneities in regional and global dynamics of the COVID-19 pandemic. The interactions among social demographics, population mixing, vaccine coverage, past waves of outbreaks and characteristics of circulating variants could be potentially integrated to their proposed model, which will provide even bigger insights into disease spread.

spread[1–3]. As reported in this issue of *Nature Computational Science*, Cao and Heydari have developed a network model to show that the micro-level structure of person-to-person interactions, measured by the average household size and in-person social contact rate, is a potential explanatory factor for variations in human mixing patterns[4]. As the pandemic transits to endemicity, their findings provide important insights to explain the heterogeneities in regional and global dynamics of the COVID-19 pandemic.

Fundamentally, the social network perspective posits that the structure of social networks has significant effects on epidemic spread patterns. For instance, school children are the 'bridge' linking household and community transmission[5]. Furthermore, social networks have behavioural, social and information spill-over effects that also have epidemiological implications: as an example, US counties with more social connections with Italy and China tend to adhere more to mobility restrictions[1,6]. As another layer of complexity, pandemic and health policies (such as distancing) have affected social mixing: the pandemic has weakened weak ties that typically link communities, while reinforcing close-knit, clustered networks[7]. Recent empirical research modeling the spread of SARS-CoV-2 has considered how such nuances in social network structural dynamics directly affect infection dynamics[8], suggesting that intervention strategies based around network structural considerations can both directly and indirectly curb the social behaviours that lead to transmissions.

One of the best-known approaches for integrating social mixing data into epidemic models is to estimate social contact matrices from POLYMOD-type diary-based contact surveys[1,2,9]. However, representative empirical contact data are not always available[2]. To fill such data gaps, synthetic contact matrices have been constructed by inferring contact patterns from more widely available survey or census data on key socio-demographics characteristics[10]. To further capture contact changes over time, mobile-derived geolocation data (from sources such as Facebook, Google, Apple, WeChat, Alipay and Safegraph) have been widely used by researchers to study the COVID-19 pandemic, and have shown great potential in generating accurate nowcasts and short-term forecasts of the epidemics, even when population mixing varies widely as a result of disruptive pandemic controls[1,3].

Nevertheless, empirical data do not always accurately reflect the underlying social mixing and behaviours. For example, mobility measured by the use of public transportation was reduced to low levels during Chinese New Year holidays, while COVID-19 transmission was actually enhanced by increased mixing from family gatherings in Hong Kong[1]. Complementary to the data-driven approaches above, Cao and Heydari proposed an explainable model by predicating that social structure is a major determinant of contact mixing[4]. Briefly: a representative network model is built as the basic social structure of disease transmission based on survey and census data; the transmission of the virus is approximated by strong and weak links between individuals in the constructed network; and the non-pharmaceutical interventions (NPIs) are modeled by sequential disconnection from the weakest to strongest links in the order of connectivity. Moreover, since empirical mixing data are not always available, this network model can also serve as a viable alternative for simulating epidemics to inform decision making and control measures. Ultimately, this approach has the potential to generate new insights into our understanding of human mixing patterns. During the early stages of a pandemic, especially when NPIs are the only available measures, the network model can also help identify the most cost-effective NPIs tailored to the social structure of different populations.

The study itself, however, has some notable limitations. First, the framework has not been formally validated by calibrating against empirical epidemiological data. Second, although a Government Stringency Index (GSI) could potentially be used as proxies for effects of interventions to estimate the changes in effective reproductive number, such a relationship might depend strongly on the specific interventions adopted and population compliance over time[6]. Model results should be interpreted with caution in view of potential temporal variations in the relationship between GSI and disease transmission. Third, although the model could reproduce the epidemic curves from the early phase of the pandemic, more data are required to parameterize the model if it were to be applied for forecasting later stages of the pandemic, given heterogeneities in vaccination coverage, infection history and circulating variants in different populations.

Despite these limitations, the authors are among the first to develop explainable models of great potential for studies of social structure and population mixing in infectious disease modeling[4]. Future research on this stream may develop models based on other network distribution assumptions and investigate the impact of network structural features beyond network size and contact frequency. In particular, higher-order network interactions and topographies (for instance, network motifs and embeddedness structure) may be used to capture otherwise unobservable indirect relationships within specific social structures (for instance, families, nursing homes, schools and so forth) and provide epidemiological insights beyond what traditional contact-tracing methods achieve. The interactions among social demographics, population mixing, vaccine coverage, past waves of outbreaks and characteristics of circulating variants could also be potentially integrated to the model by modifying the degree of connectivity of the networks (Fig. 1), thus bringing more insights into epidemic spread. ❑

Kathy Leung [iD] [1,2 ✉], Jayson S. Jia[3] and Joseph T. Wu[1,2]

[1]*WHO Collaborating Centre for Infectious Disease Epidemiology and Control, School of Public Health, LKS Faculty of Medicine, The University of Hong Kong, Hong Kong SAR, China.* [2]*Laboratory of Data Discovery for Health (D24H), Hong Kong Science Park, New Territories, Hong Kong SAR, China.* [3]*Faculty of Business and Economics, The University of Hong Kong, Hong Kong SAR, China.*
✉e-mail: ksmleung@hku.hk

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Competing interests
The authors declare no competing interests.