



## Perspective

## Visualizing COVID-19 pandemic risk through network connectedness

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## ABSTRACT

With the domestic and international spread of the coronavirus disease 2019 (COVID-19), much attention has been given to estimating pandemic risk. We propose the novel application of a well-established scientific approach – the network analysis – to provide a direct visualization of the COVID-19 pandemic risk; infographics are provided in the figures. By showing visually the degree of connectedness between different regions based on reported confirmed cases of COVID-19, we demonstrate that network analysis provides a relatively simple yet powerful way to estimate the pandemic risk.

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## 1. Introduction

With the domestic and international spread of the coronavirus disease 2019 (COVID-19), much attention has been given to estimating pandemic risk (Wu et al., 2020; Verity et al., 2020). We propose the novel application of a well-established scientific approach – network analysis (Loscalzo, 2017; Newman, 2018; Kim et al., 2015; Bennett et al., 2006; Newman, 2004; Horvath and Dong, 2008; Danon et al., 2011; Billio et al., 2012) – to provide a direct visualization of the COVID-19 pandemic risk. By showing visually the degree of connectedness between different regions based on data that are readily available (such as reported confirmed cases of COVID-19), network analysis offers a relatively simple yet powerful way to estimate the pandemic risk.

## 2. Network analysis

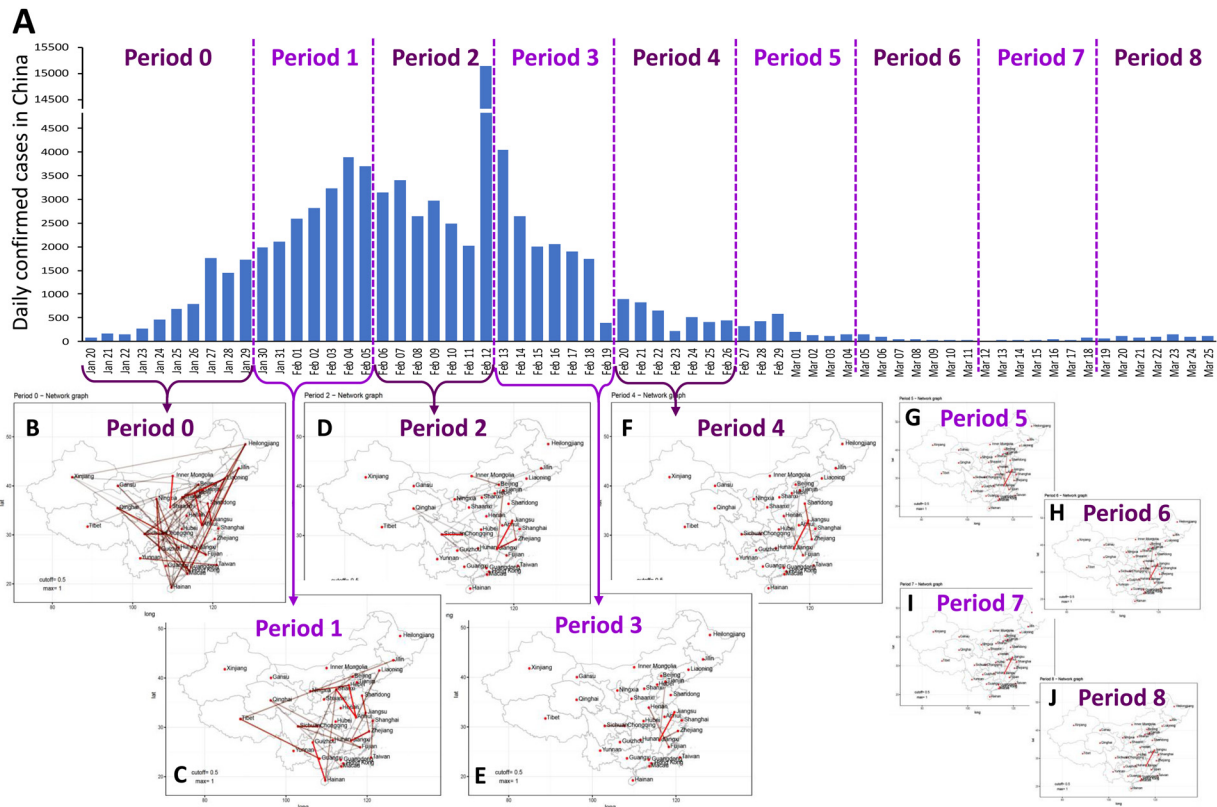
Network analysis has been used for many decades to assess connectedness and systemic risk in the financial and banking

sectors (Billio et al., 2012; Avdjiev et al., 2019; Bricco and Xu, 2019). In the financial system, a collection of interconnected institutions with mutually beneficial business relationships (e.g., commercial banks) can quickly collapse through rapid propagation of illiquidity, insolvency, and losses during financial crises. The demise of Lehman Brothers in 2008 and the European sovereign debt crisis of 2011–2012, for example, demonstrate how business ties among financial institutions, when conducted on a large enough scale, can significantly contribute to systemic risk. Our analysis on pandemic networks is different from that on epidemiological networks for disease transmission. A main contribution is to construct a pandemic network for studying the relationship of changes in the numbers of confirmed cases. We also argue that when applying network analysis to a pandemic situation, the degree of connectedness between the regions can help visualize the pandemic risk.

## 3. Methods and results

Network analysis has been used in medical research to study gene co-expression, disease co-occurrence, and the topological dynamics of the spread of infectious disease (Horvath and Dong, 2008; Jiang et al., 2018; Yang and Jung, 2020; Forster et al., 2020). Network analysis is relatively easy to execute, as it uses data that are readily accessible, such as publicly available confirmed

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**Figure 1.** Daily confirmed cases in China and the network graphs.

numbers of cases in databases (Dong et al., 2020). In the present study, the number of confirmed COVID-19 cases in China from late January to March 2020 were retrieved, and plots of confirmed cases were constructed for nine time periods (periods 0–8) (Figure 1A) (China, 2020; National Health Commission of the PRC, 2020). The numbers of confirmed cases worldwide (excluding China) were also retrieved for the same time periods and the plots constructed (Figure 2A) (WHO, 2020). Next, network graphs were constructed based on the correlation of changes in the numbers of confirmed cases between two geographical areas (e.g., provinces). If the correlation is  $>0.5$ , the two areas are connected in a network. Below are the summary steps in constructing the network graphs, as shown in Figure 1B–J and Figure 2B–J.

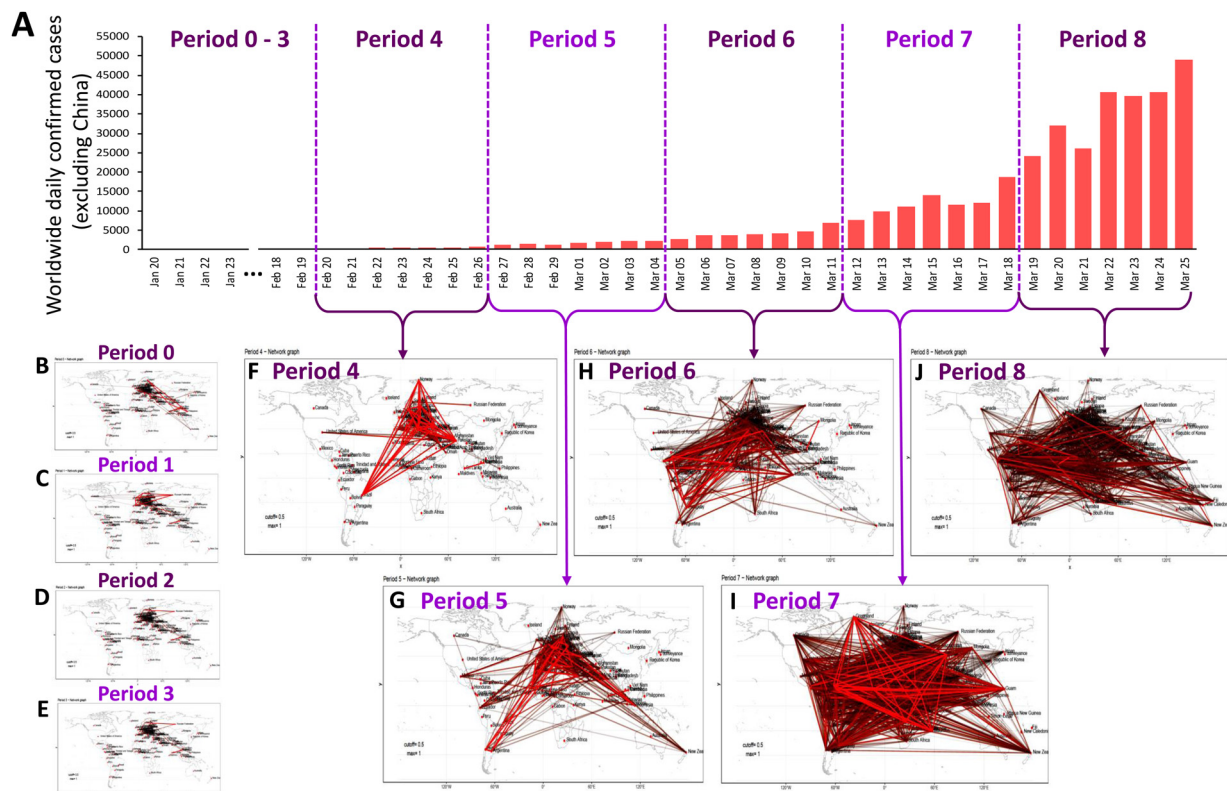
- (1) Define  $X_{it}$  as the number of confirmed cases in province/country  $i$  on day  $t$ . Calculate the daily changes in the square-root of newly confirmed cases, i.e.  $X_{it} = \sqrt{X_{it}} - \sqrt{X_{it-1}}$  (Bartlett, 1936; Bartlett, 1947). Statistically, the ‘square-root transformation’ is to make the transformed counts more stable.
- (2) In a particular period, calculate the correlation of  $Y_{it}$  and  $Y_{jt}$  (representing changes in province/country  $i$  and province/country  $j$ ) using the accumulated data up to the end of that period.
- (3) Construct the network graphs in a particular period by linking the provinces/countries if the correlation is  $>0.5$ .

Pandemic risk can be visualized based on how frequently different regions are connected in the network graphs. Thus, the more frequently the regions are connected, the higher the density of the lines in the network graphs and the stronger the tendency of co-evolution of virus propagation among the regions – and an increase in pandemic risk is suggested (see for example, Figure 2H, the network graph for worldwide excluding China in the second

week of March). Conversely, the less frequently the regions are connected, the lower the density of the lines in the network graphs and the less the tendency of co-evolution of virus propagation among the regions – and a decrease in pandemic risk is suggested (see for example, Figure 1H, the network graph for China provinces in the second week of March).

Network connectedness provides a more timely prediction of pandemic risk than relying on the raw data of daily confirmed cases. In Figure 1B, period 0 (January 20–29), the number of confirmed cases was low and had just begun to rise in China. Despite this, the network graph for period 0 already showed a high connectedness between provinces (Figure 1B), indicating the imminence of an epidemic in China. Further, although the number of daily confirmed cases continued to rise exponentially in China in period 1 (January 30 to February 5) (Figure 1A), the network graph (Figure 1C) already showed a significant decrease in connectedness compared with that in period 0. The decrease in connectedness provided an early sign of an improvement in the epidemic, probably due to the lockdown of Wuhan and another 15 cities to reduce social interaction. Similarly, a slight decrease in daily confirmed cases in China was first recognized in period 2 (February 6–12) and period 3 (February 13–19), but the trend of decline was not obvious until period 4 (February 20–26) (Figure 1A). The network graphs, however, provided a clearer visualization of the significant decrease in connectedness from period 1 to period 4 (Figure 1C–F), signalling the trend of decline as early as from period 1.

Also, for the other countries in the same time periods (periods 0–8) (see Figure 2), the network graphs provided powerful visualization of the pandemic risk, more so than that revealed by the daily confirmed COVID-19 cases. For example, there was a marked increase in connectedness between European, American, and other countries in period 4 (February 20–26) (Figure 2F),



**Figure 2.** Worldwide daily confirmed cases (excluding China) and the network graphs.

indicating an increasing pandemic risk even though the number of daily confirmed cases in Europe was still low in period 4 (Figure 2A). This phenomenon was similar to that observed in China in period 0 (Figure 1B). The connectedness of European and American countries continued to rise and intensify from period 5 to period 7 (February 27 to March 18) (Figure 2G–I), suggesting that the situation in Europe and America was getting worse. There is a sign of a decrease in connectedness in period 8 (March 19–25) (Figure 2J), although the number of daily confirmed cases did not soar until period 8 (Figure 2A).

#### 4. Conclusions

This study has demonstrated that, compared to just relying on reported confirmed cases of COVID-19, network analysis can provide a powerful and clearer visualization of the pandemic risk through the degree of connectedness in pandemic network graphs. Being data-driven and based on data that are readily accessible, network analysis can supplement traditional modelling techniques to enhance the estimation of pandemic risk and provide more timely evidence to inform preparedness plans. Future works on quantifying the network connectedness are worthy of investigation.

#### Declarations

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**Ethical approval:** No human or animal subject was involved in the study. Therefore, ethical approval is not applicable.

**Conflict of interest:** All authors have no conflict of interest to declare.

#### Author contributions

MKPS and AMYC conceptualized the study. MKPS and JNLC collected and analyzed the data. MKPS, AT, AMYC, and JTYT interpreted the results. AMYC and JTYT drafted the manuscript. MKPS and AT finalized the manuscript. All authors read and approved the final version of the manuscript.

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#### References

- Avdjiev S, Giudici P, Spelta A. Measuring contagion risk in international banking. *J Finan Stab* 2019;42:36–51.
- Bartlett MS. The square root transformation in analysis of variance. *Suppl J R Stat Soc* 1936;3(1):68–78.
- Bartlett MS. The use of transformations. *Biometrics* 1947;3(1):39–52.
- Bennett DA, Schneider JA, Tang Y, Arnold SE, Wilson RS. The effect of social networks on the relation between Alzheimer's disease pathology and level of cognitive function in old people: a longitudinal cohort study. *Lancet Neurol* 2006;5:406–12.
- Billio M, Getmansky M, Lo AW, Pelizzon L. Econometric measures of connectedness and systemic risk in the finance and insurance sectors. *J Finan Econ* 2012;104:535–59.
- Bricco J, Xu T. *Interconnectedness and Contagion Analysis: A Practical Framework*. International Monetary Fund; 2019.

- China CDC. Official press releases. 2020 <http://www.chinacdc.cn/> [accessed 1.4.20].
- Danon L, Ford AP, House T, Jewell CP, Keeling MJ, Roberts GO, et al. Networks and the epidemiology of infectious disease. *Interdiscip Perspect Infect Dis* 2011;2011:284909.
- Dong E, Du H, Gardner L. An interactive web-based dashboard to track COVID-19 in real time. *Lancet Infect Dis* 2020;. doi:[http://dx.doi.org/10.1016/S1473-3099\(20\)30120-1](http://dx.doi.org/10.1016/S1473-3099(20)30120-1).
- Forster P, Forster L, Renfrew C, Forster M. Phylogenetic network analysis of SARS-CoV-2 genomes. *Proc Natl Acad Sci* 2020;. doi:<http://dx.doi.org/10.1073/pnas.2004999117>.
- Horvath S, Dong J. Geometric interpretation of gene coexpression network analysis. *PLoS Comput Biol* 2008;4:e1000117.
- Jiang Y, Ma S, Shia B-C, Lee T-S. An epidemiological human disease network derived from disease co-occurrence in Taiwan. *Sci Rep* 2018;8:1–12.
- Kim DA, Hwang AR, Stafford D, Hughes DA, O'Malley AJ, Fowler JH, et al. Social network targeting to maximise population behaviour change: a cluster randomised controlled trial. *Lancet* 2015;386:145–53.
- Loscalzo J, editor. *Network Medicine*. Harvard University Press; 2017.
- National Health Commission of the PRC. List of Health Commission of the People's Republic of China sites. 2020 <http://www.nhc.gov.cn/wjw/dfzfwz/list.shtml> [accessed 1.4.20].
- Newman ME. Coauthorship networks and patterns of scientific collaboration. *Proc Natl Acad Sci USA* 2004;101:5200–5.
- Newman M. *Networks*. [56\_TD\$DIFF]Oxford: Oxford University Press; 2018.
- Verity R, Okell LC, Dorigatti I, Winskill P, Whittaker C, Imai N, et al. Estimates of the severity of coronavirus disease 2019: a model-based analysis. *Lancet Infect Dis* 2020;30243–7. doi:[http://dx.doi.org/10.1016/S1473-3099\(20\)30120-1](http://dx.doi.org/10.1016/S1473-3099(20)30120-1).
- WHO. Coronavirus disease (COVID-2019) situation reports. 2020 <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports> [accessed 2.4.20].
- Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *Lancet* 2020;395:689–97.
- Yang CH, Jung H. Topological dynamics of the 2015 South Korea MERS-CoV spread-on-contact networks. *Sci Rep* 2020;10:1–11.