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Retrospective observational study of the robustness of provider network structures to the systemic shock of COVID-19: a county level analysis of COVID-19 outcomes

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ABSTRACT

Objective To evaluate whether certain healthcare provider network structures are more robust to systemic shocks such as those presented by the current COVID-19 pandemic.

Design Using multivariable regression analysis, we measure the effect that provider network structure, derived from Medicare patient sharing data, has on county level COVID-19 outcomes (across mortality and case rates). Our adjusted analysis includes county level socioeconomic and demographic controls, state fixed effects, and uses lagged network measures in order to address concerns of reverse causality.

Setting US county level COVID-19 population outcomes by 3 September 2020.

Participants Healthcare provider patient sharing network statistics were measured at the county level (with n=2541–2573 counties, depending on the network measure used).

Primary and secondary outcome measures COVID-19 mortality rate at the population level, COVID-19 mortality rate at the case level and the COVID-19 positive case rate.

Results We find that provider network structures where primary care physicians (PCPs) are relatively central, or that have greater betweenness or eigenvector centralisation, are associated with lower county level COVID-19 death rates. For the adjusted analysis, our results show that increasing either the relative centrality of PCPs (p value<0.05), or the network centralisation (p value<0.05 or p value<0.01), by 1 SD is associated with a COVID-19 death reduction of 1.0–1.8 per 100 000 individuals (or a death rate reduction of 2.7%–5.0%). We also find some suggestive evidence of an association between provider network structure and COVID-19 case rates.

Conclusions Provider network structures with greater relative centrality for PCPs when compared with other providers appear more robust to the systemic shock of COVID-19, as do network structures with greater betweenness and eigenvector centralisation. These findings suggest that how we organise our health systems may affect our ability to respond to systemic shocks such as the COVID-19 pandemic.

STRENGTHS AND LIMITATIONS OF THIS STUDY

- ⇒ Use recent COVID-19 mortality rate and case rate data together with provider patient sharing networks data at the US county level.
- ⇒ Observational study design.
- ⇒ Use multivariable regression models to analyse association between provider network structure and COVID-19 mortality and case rates.
- ⇒ Estimates are adjusted for county level socioeconomic and demographic controls, as well as state fixed effects.
- ⇒ Use temporally lagged network measures to address concerns of reverse causality.

INTRODUCTION

The notion that provider networks, derived from patient sharing data, can lend insights into how our health systems are organised, and that these structures further affect outcomes such as costs, utilisation and care is becoming increasingly well documented.[1–8] Beyond providing us with a blueprint for how patient care is organised, provider networks encode information about professional patient sharing relationships between healthcare providers, and as such, the potential diffusion of provider-to-provider information on new treatment innovations and best practices.[9–11]

While the organisation, collaboration and information transmission that lay latent within these provider networks matters for care provision during normal times, its significance may likely be further elevated during times of systemic shocks such as that from COVID-19 as care providers may rely more heavily on their provider networks when searching for information that is so recent, and when seeking to triage and treat complex patient cases. As such, our study sets out to assess the relationship between

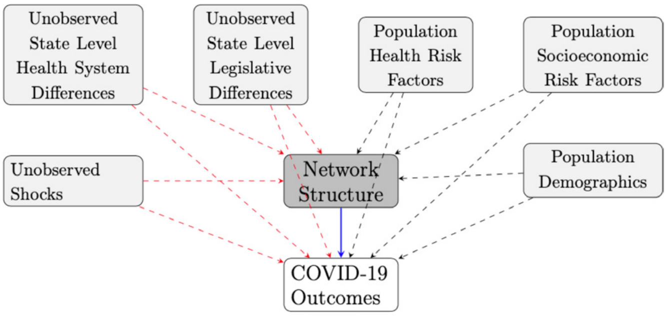

Figure 1 Directed acyclic graph diagram. Categories of observable variables, as well as unobserved characteristics, might have a causal effect on both network structure and COVID-19 outcomes. Red dashed lines capture the potential effects due to unobserved characteristics, while the black dashed lines capture the potential effects due to observable features within our data. The blue solid line captures the sought potential effect that network structure has on COVID-19 outcomes.

provider network structures and robustness to systemic shocks such as those presented by the current COVID-19 pandemic. We hypothesise that counties where primary care providers serve a more central role within the provider network structure are more robust to systemic shocks, and therefore experience lower mortality and case rates from COVID-19. As such, we hypothesise that provider patient sharing network structure matters for COVID-19 outcomes.

Conceptual model

Figure 1 provides a directed acyclic graph (DAG) diagram that outlines our conceptual model representation of how provider network structure may influence county level COVID-19 outcomes. This model highlights a number of factors that may influence both our outcome and network measures, and therethrough present a confounding problem. Each of these factors are now discussed. First, it has been documented that individuals with chronic disease, such as diabetes, are at increased risk of mortality from COVID-19.[12 13] At a population level, the proportions of underlying health risk factors may influence how providers collaborate on patient care—confounding analysis of network structure effects on COVID-19 outcomes unless we are able to control for state and county level differences in the underlying population health. Similarly, other studies have shown that patient socioeconomic status and demographics may correlate with both COVID-19 spread and death.[14 15] This introduces two other channels that we need to consider and control for in order to avoid confounding the effect due to these features and the effect due to the provider network structure. Given that we have county level controls for these features within our data, we denote the effect of these features on our network structure measure and the COVID-19 outcome using black dashed lines within figure 1, that is, black dashed lines indicate effects due to features that are observable within our data.

Additionally, there may be a number of county and state level confounders that are unobserved within our data, but which may still influence both our network structure variable and our COVID-19 outcome. First, there may exist unobserved legislative and health system differences across states that cause systematic differences across states both pertaining to provider network structure and COVID-19 outcomes. As we explain further within the Methods section, we include state indicator variables in order to capture such state level latent influences, and as such, we are able to control for these latent factors within our analyses.

Lastly, even with the inclusion of state fixed effects, there may be local market (county level) shocks that are unobserved within our data, but which nevertheless may influence both the network structure and COVID-19 outcomes. In order to avoid confounding from such shocks, and the possibility of reverse causality of COVID-19 outcomes causing the observed network structure, we use a lagged network structure measure that predates the COVID-19 outbreak. These sources of potentially unobserved confounders are visually depicted within figure 1 using red dashed lines. Additional details regarding how our analysis adjusts for latent confounders are provided within the statistical analysis subsection of the Methods section.

METHODS

Study sample

We use county level case and mortality data as reported in the *New York Times*' historic data files on 3 September 2020. These data define cases and deaths based on both confirmed (based on laboratory testing) and probable (based on adherence to the April 5th Council of State and Territorial Epidemiologists issued recommendation on identification via specific criteria for symptoms and exposure) cases.[16] These data were combined with county level provider network data that were constructed based on Medicare claims data from 2016 by CareSet Systems (additional details are also provided within the online supplemental figure S1).[17] These data define a patient sharing link on the basis of two providers having at least 11 common patients. Such a cut-off helps ensure the omission of potentially spurious network links and is aligned with prior work in this area which has validated the use of such linkages as proxies for professional patient sharing relationships among providers.[18 19] Using the National Provider Identifiers within the Medicare patient sharing data, we linked providers to the Medicare physician compare dataset in order to extract each provider's specialty and county identifier, which we used for the purpose of constructing our county-specific provider network measures.

In addition to our COVID-19 and Medicare provider network data, we also sourced a number of county level covariates from the 2020 County Health Rankings Dataset, who in turn sources its data from a wide number of established data sources (described below). These variables were sourced in order to account for factors that have recently been identified as important in explaining regional heterogeneities in COVID-19 outcomes.[12–15 20 21] This study is based on publicly available deidentified data and it did not constitute human subjects research as defined by 45 CFR 46.102. This study follows the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) reporting guidelines.

Patient and public involvement

No patients involved.

Study variables

COVID-19 mortality and case rates

We compute two mortality rates and one case rate—all on a 'per 100 000 individuals" basis—for the purpose of our analysis. Our first COVID-19 mortality rate is based on the total county level population estimates (where our county population numbers come from the 2018 Census Population Estimates) and is defined as: $\frac{TotalCOVID-19\ Deaths}{Total\ Population} * 100,000$. The second COVID-19 mortality rate is instead based on the total of positive COVID-19 cases and is defined as: $\frac{Total\ COVID-19\ Deaths}{Total\ COVID-19\ Cases} * 100,000$. Lastly, the case rate is defined on the basis of the total county population: $\frac{Total\ COVID-19\ Cases}{Total\ Population} * 100,000.$[22]

Network measures

We draw on two types of network measures—relative centrality and centralisation. The first of these is given by computing the average degree centrality for primary care physicians (PCPs) and all non-PCP providers, and then by taking the ratio of these two values. In following with prior work, provider degrees are based on the hospital referral region,[8 23] and county-specific measures are obtained by taking the county specific ratio of the average PCP and non-PCP degree values. As such, the resulting relative PCP to non-PCP centrality ratio will be higher in areas where the degree centrality of PCPs is higher relative to that of non-PCPs, which indicates that PCPs are relatively more central within these local areas.

Second, we use two network statistics based on the overall, local county level, network structures—this is done using betweenness centralisation and eigenvector centralisation. These centralisation measures will be zero for networks where all providers occupy identical positions within the network (based on betweenness or eigenvector centrality), and it will increase with the level of global inequality within the specified network centrality measure. As such, it is important to note that betweenness centrality (at the individual provider level) informs us about how important a provider is in terms of their ability to connect other providers; while a provider's eigenvector centrality is inferred from the relative importance (or centrality) of that provider's direct patient sharing connections (ie, from their colleagues).[24 25]

Additional details on the mathematical definitions, and construction, of each of these measures are provided within the online supplemental table S1.

Covariates

The median household income variable is based on the median of total income and it is sourced from the US Census Bureau's Small Area Income and Poverty Estimates (SAIPE) programme 2018 data.[26] Our unemployment rate variable is sourced from 2018 Bureau of Labor Statistics data and captures the percentage of the county's civilian labour force, ages 16 and older, that is unemployed but seeking work.[27] The diabetes prevalence measure comes from the Centers for Disease Control and Prevention Diabetes Interactive Atlas 2016 data, and denotes the percentage of adults aged 20 and above with a diagnosis of diabetes.[28] Lastly, we also use Census Bureau's 2018 Population Estimates data for county measures on the per cent 65 and older, per cent non-Hispanic African–American and per cent females.[29]

Statistical analysis

To obtain estimates of the effect of provider network structure on COVID-19 outcomes, we use multivariable regression methods. As with any observational study design, obtaining unbiased network effects is complicated by the potential confounding of unmeasured determinants (see conceptual model for additional details). To ameliorate such concerns, our study takes three steps. First, we include a rich set of county level covariates that have been identified as important for explaining regional variations in population level COVID-19 outcomes (which we also outlined within our conceptual model, figure 1). Second, we include state level fixed effects within all of our analysis in order to account for and avoid confounding from potentially unobserved state level differences that may influence both how providers collaborate on care, as well as the resulting COVID-19 outcomes. Lastly, since county level shocks may possibly influence both our network measures and COVID-19 outcomes, and given the potential of reverse causality with COVID-19 outcomes causing the contemporaneous provider network structure, we use lagged network measures (from 2016) in order to avoid these issues.

In summary, for each mortality and case rate outcome (Y_i), we fit the following regression model:

$$Y_i = \alpha + \tau NetworkMeasure_i + \boldsymbol{\beta X} + \boldsymbol{\phi_s} + \epsilon_i \qquad (2)$$

where, $NetworkMeasure_i$ denotes the network measure of interest; $\boldsymbol{X}$ denotes a vector of covariates consisting of median household income, unemployment rate, diabetes prevalence, percent 65 and older, percent non-Hispanic African–American and percent females; and lastly, ϕ_s captures state fixed effects. As such, the network effect (τ) is identified using within state variation conditional on the noted controls. This approach controls for all the potentially confounding channels outlined within figure 1 (of the conceptual model) either directly (via

Table 1 Summary statistics for outcome measures, network measures and county level control variables

Variable	Mean	Std. dev.	Observations
Outcome measures			
COVID-19 mortality rate—population level	34.76	46.13	3120
COVID-19 mortality rate—case level	2121.57	2414.12	3203
COVID-19 positive case rate	1496.86	1298.21	3120
Network measures			
Number of nodes*	3292.45	2893.42	2806
Number of links*	154 797.99	152 230.05	2806
PCP/nonPCP degree centrality ratio	1.7	4.3	2582
Betweenness centralisation	0.01	0.05	2549
Eigenvector centralisation	0.22	0.15	2549
County level controls			
Mean household income	32 870	6979.48	3131
Unemployment rate	0.05	0.02	3131
Diabetes prevalence	0.12	0.04	3142
% 65 and older	0.19	0.05	3142
% females	0.5	0.02	3142
% non-Hispanic black	0.09	0.14	3142

*Numbers based on county averages from hospital referral region networks.
non-PCP, non-primary care provider; PCP, primary care provider.

inclusion of controls) or indirectly (via inclusion of state fixed effects and the use of a lagged network measure).

RESULTS

County characteristics and between-county variation

Table 1 provides summary statistics across our outcome, network and control variables. From this, we note a mean COVID-19 death rate of 34.8 (SD=46.1) per 100 000 people in the population, and a corresponding case rate of 2121.6 (SD=2414.1) per 100 000 individuals. For the network measures, we note that PCPs on average have a higher network degree by a factor of 1.7 (SD=4.3) than non-PCP providers, which indicates their relatively higher centrality. As for the centralisation measures, both of these indicate centralisation distributions with significant inequality in provider centralities (p value<0.001 for a two-sided t-test where the null hypothesis is that of a centralisation equal to 0). Additional descriptive statistics are also provided within the online supplemental figure S2 and tables S2–S9.

Figure 2 provides county level map plots of county-to-county variation across our outcome and network measures. Starting with figure 2A, this showcases the COVID-19 population level mortality rate per 100 000 individuals. Looking at the PCP to non-PCP degree centrality ratio in figure 2B. We note some visible overlap with the COVID-19 mortality trends presented in figure 2A. Areas with lower relative PCP to non-PCP centrality appear to have higher levels of COVID-19 population mortality. Similar trends are observed for the centralisation measures in figure 2C. and figure 2D, indicating that more heterogeneities in terms of the centrality of providers appears to be associated with lower mortality outcomes. Additional maps that further showcase these geographic correlation patterns can be seen in the online supplemental figures S3–S5.

Provider network structure and systemic shock robustness

Table 2 shows adjusted regression results controlling for median household income, unemployment rate, diabetes prevalence, as well as for county level demographics, in addition to state-specific fixed effects. Details on unadjusted results—which are qualitatively very similar to the adjusted results are available in online supplemental appendix and tables. Looking at panel A, our outcome measure is the COVID-19 mortality rate computed at the county population level. For the relative average PCP to non-PCP degree centrality ratio, we find a negative point estimate of −0.254 (95% CI −0.487 to −0.022; p value<0.05). It should be noted that all p values are reported based on a null hypothesis of the marginal effect estimate being equal to a zero effect. For a 1 SD increase in this network measure, we observe a decrease of 1.1 deaths per 100 000 (or a mortality rate reduction of 3.1%) from COVID-19. Similar effects are observed for the two network centralisation measures.

For the betweenness centralisation, we find a negative point estimate of −19.19 (95% CI −36.310 to −2.070; p value<0.05). A 1 SD increase in this measure corresponds to a reduction of 1.0 death per 100 000 (or a 2.8% mortality rate reduction) from COVID-19. For the eigenvector centralisation, we find a negative point estimate of −11.17 (95% CI −19.050 to −3.293; p value<0.01). For this network measure a 1 SD increase indicates a 1.8 deaths per 100 000 reduction (or a 5% rate decrease) in COVID-19 deaths. In summary, the effect due to a 1 SD increase, depending on the network measure considered, ranges between a 1.0 and 1.8 deaths per 100 000 reduction in COVID-19 mortality (or a 2.7% to 5.0% decrease in the COVID-19 mortality rate).

Panel B reports the estimation results for when the outcome measure is instead the COVID-19 mortality rate computed based on the county level case counts. Again, we find negative significant effects across all three network measures (p value<0.05, p value<0.05, p value<0.05). In terms of the overall effect sizes (due to a 1 SD increase in the network measure), we find that these range between a 55.1 and 89.4 deaths per 100 000 reduction in COVID-19

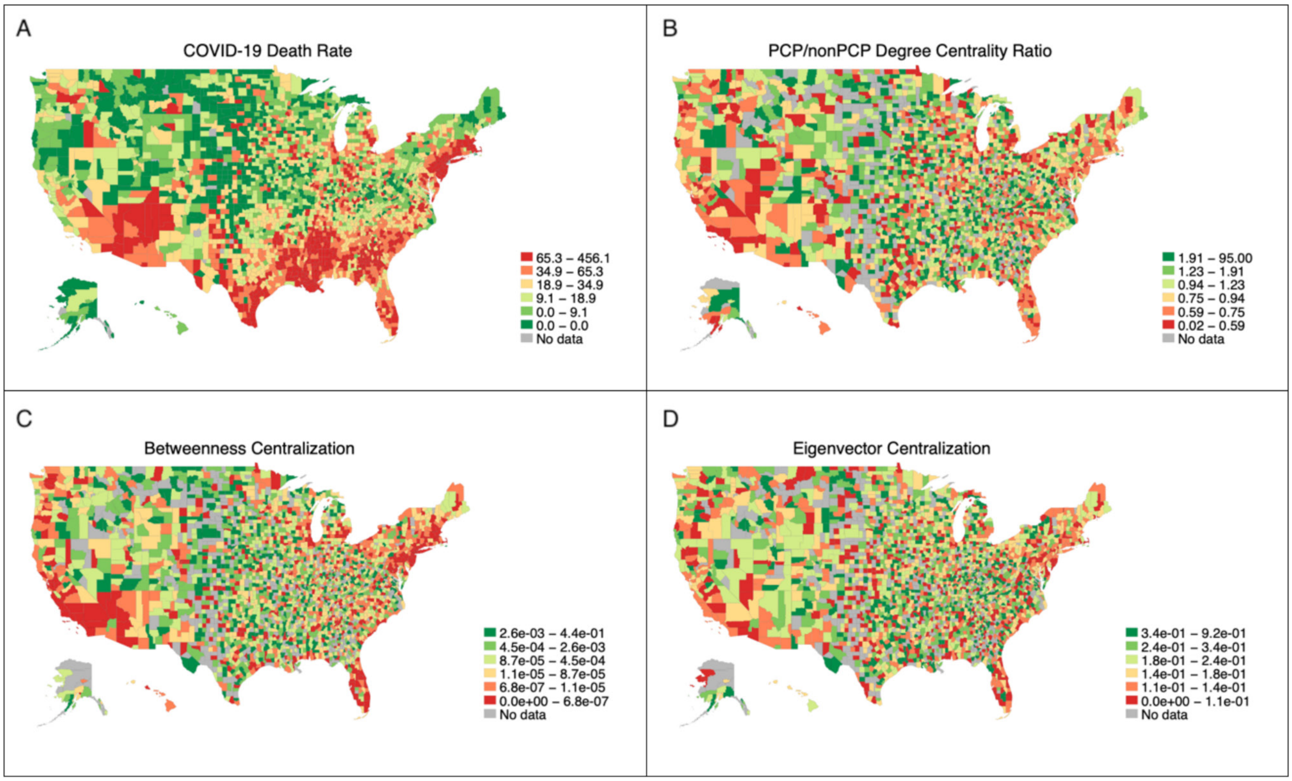

Figure 2 US between-county variation maps. (A) Shows the COVID-19 deaths per 100 000, with red indicating higher, and green indicating lower, death rates. (B) Shows the primary care physician (PCP) to non-PCP degree centrality ratios. (C) The betweenness centralisation and (D) the eigenvector centralisation. For all of the network measures, red indicates lower values, while green indicates higher values.

deaths among the COVID-19 positive case population (or a 2.6% to 4.2% case-based mortality rate decrease).

Lastly, panel C presents estimates for the county population level COVID-19 case counts per 100 000 individuals. Here we note results that are qualitatively similar to our unadjusted results (see online supplemental appendix and tables); however, there is a loss of significance with the exception of our eigenvector centralisation network measure (p value<0.1), which retains weak significance. For the eigenvector centralisation measure, the effect due to a 1 SD increase in this network measure implies a 28.9 cases per 100 000 reduction in confirmed COVID-19 cases (or a 1.9% case rate decrease).

DISCUSSION

This study shows there is a significant relationship between the structure of regional provider networks (ie, how we organise and provide care) and the robustness of response to systemic shock such as those from the COVID-19 pandemic. As such, our findings contribute to a growing literature on the topic of COVID-19 as well as regional variations in healthcare outcomes.[30–34] For COVID-19 mortality rates that are based on county population estimates, our adjusted regression results indicate that the effect due to a 1 SD increase, depending on the network measure considered, ranges between 1.0 and 1.8 avoided deaths per 100 000. Extrapolated to the full US population of 331 million in 2020,[35] this would equate to a potential range of 3310 to 5809 saved lives. Thus, it appears that provider network structure is important for ensuring better population health outcomes pertaining to the system wide shock of COIVD-19.

In addition, we find that higher levels of betweenness centralisation (ie, higher levels of global inequity in terms of betweenness centrality) correlates with lower COVID-19 mortality rates. This suggests that not all providers ought to occupy the same role within our health system networks; that is, we may want to have specific providers serve in the role of broader 'network connectors' (providers that connect otherwise underconnected provider groups). A natural 'network connector' would be primary care physicians that help occupy a central role within these networks. We also find that provider networks where primary care physicians hold greater relative centrality compared with other providers correlate with lower COVID-19 deaths per 100 000 individuals. As such, this finding further stresses the potential importance that primary care physician centric care networks/models may play in ensuring not only greater care coordination and patient outcomes,[20 36 37] but also in ensuring provider network structures that are robust to systemic shocks such as that presented by the COVID-19 pandemic.

Table 2 Regression estimates across outcome and network measure models

	Model (1)	Model (2)	Model (3)
Panel A: COVID-19 mortality rate—population level			
Network measures			
PCP/non-PCP degree centrality ratio	–0.254** (–0.487 to –0.022)		
Betweenness centralisation		–19.19** (–36.31 to –2.070)	
Eigenvector centralisation			–11.17*** (–19.05 to –3.293)
County level controls			
Mean household income	0.0003* (–0.0000 to 0.0006)	0.0003** (0.0000 to 0.0006)	0.0003** (0.0000 to 0.0006)
Unemployment rate	447.4*** (295.0 to 599.7)	461.5*** (306.9 to 616.2)	462.3*** (308.5 to 616.2)
Diabetes prevalence	6.575 (–41.85 to 55.00)	18.13 (–31.07 to 67.32)	19.79 (–29.23 to 68.82)
% 65 and older	–72.12*** (–107.9 to –36.32)	–77.66*** (–114.0 to –41.29)	–78.50*** (–114.6 to –42.44)
% females	158.5*** (52.39 to 264.6)	150.6*** (43.49 to 257.7)	142.7*** (35.79 to 249.6)
% non-Hispanic black	84.68*** (62.31 to 107.0)	81.32*** (58.50 to 104.1)	80.28*** (57.41 to 103.2)
Fixed effects	Yes	Yes	Yes
N	2573	2541	2541
R^2	0.434	0.426	0.427
Panel B: COVID-19 mortality rate—case level			
Network measures			
PCP/non-PCP degree centrality ratio	–12.82** (–25.05 to –0.591)		
Betweenness centralisation		–1642.6** (–3085.7 to –199.4)	
Eigenvector centralisation			–595.8** (–1155.3 to –36.20)
County level controls			
Mean household income	0.019** (0.0011 to 0.0369)	0.0244*** (0.0080 to 0.0408)	0.0242*** (0.0078 to 0.0407)
Unemployment rate	6802.6* (–483.7 to 14089.0)	9376.3*** (2753.4 to 15999.2)	9506.0*** (2878.1 to 16134.0)
Diabetes prevalence	849.7 (–2226.4 to 3925.7)	2518.7** (32.67 to 5004.7)	2632.3** (156.8 to 5107.8)
% 65 and older	3250.5** (424.5 to 6076.5)	2006.8** (73.35 to 3940.2)	1877.3* (–49.95 to 3804.6)
% females	11083.2*** (5455.8 to 16710.6)	8697.4*** (4215.6 to 13179.2)	8308.9*** (3769.8 to 12848.0)
% non-Hispanic black	1353.3*** (666.6 to 2040.0)	1249.9*** (555.2 to 1944.5)	1188.1*** (493.9 to 1882.3)
Fixed effects	Yes	Yes	Yes
N	2573	2541	2541
R^2	0.260	0.285	0.285
Panel C: COVID-19 case rate—population level			
Network measures			
PCP/non-PCP degree centrality ratio	–2.278 (–12.10 to 7.539)		
Betweenness centralisation		–211.7 (–798.8 to 375.5)	
Eigenvector centralisation			–192.9* (–405.7 to 19.88)
County level controls			
Mean household income	–0.0003 (–0.0081 to 0.0075)	0.0014 (–0.0062 to 0.0090)	0.0012 (–0.0063 to 0.0088)
Unemployment rate	11176.1*** (7112.5 to 15239.7)	11696.9*** (7622.2 to 15771.6)	11693.3*** (7633.5 to 15753.2)
Diabetes prevalence	–408.6 (–1756.3 to 939.1)	–502.9 (–1859.0 to 853.2)	–478.9 (–1832.8 to 875.0)
% 65 and older	–7080.3*** (-8109.5 to –6051.1)	–6842.0*** (–7852.7 to –5831.3)	–6840.1*** (–7846.1 to –5834.2)
% females	–6962.7*** (–11960 to –1965.4)	–6082.0** (–11061.0 to –1103.0)	–6225.1** (–11250.6 to –1199.6)
% non-Hispanic black	2407.9*** (1856.5 to 2959.3)	2358.2*** (1791.2 to 2925.2)	2341.7*** (1775.7 to 2907.7)
Fixed effects	Yes	Yes	Yes
N	2573	2541	2541
R^2	0.497	0.504	0.504

Significance is indicated as: *p<0.1, **p<0.05, ***p<0.01.
95% CIs are reported within the parentheses, and these are based on robust SEs.
PCP, primary care physician.

While our results appear robust to the use of different network measures, and the two different COVID-19 mortality rates used within this study, the analysis is not without limitations. First, due to data availability limitations, our provider network measures are based on Medicare patient sharing data and not patient sharing data for the population at large. As such, our analysis makes the assumption that patient sharing patterns for the Medicare population can serve as proxies for patient sharing patterns between providers within the population at large. This is an assumption that needs to be validated in future studies. Nevertheless, because we control for proportion of the population that is 65 or older within each county, we ameliorate concerns regarding confounding from variation in the prevalence of Medicare patients across counties.

A second data limitation is that our network measures are based on data from 2016. This lag may induce some noise into our analysis; however, it reduces concerns about endogeneity from the potential correlation between our network measure and the regression residual. As such, using a lagged network measures helps us ameliorate potential concerns of reverse causality between our network and outcome measures.[38]

A third limitation is that results based on networks may be sensitive to the choice of threshold used to define a shared patient relationship (or linkage) between providers. Pertaining to this, our chosen threshold of 11 shared patients is aligned with prior literature in this area[18 19]; however, this assumption is still important to note. Additionally, our PCP to non-PCP degree centrality ratio draws on degree centrality measures from the hospital referral region network for its construction. This choice was based on alignment with prior work in this area; however, this decision does not drive our results as using county level networks (instead) yields qualitatively similar results (see online supplemental appendix).

Finally, case rate and mortality rate that were computed based on positive COVID-19 cases may underestimate the true case count since the positive counts are based on confirmed cases. Furthermore, the mortality rates computed from these confirmed cases will likely suffer from selection bias. That is, if we believe that individuals with more severe COVID-19 symptoms are more likely to get tested, then the mortality rates based off of this population will overstate the actual population level mortality rate. As such, we have primarily focused our analysis and discussion on the results obtained for our COVID-19 mortality rates that we computed based on the overall county level population.

In summary, provider network structures are found to be associated with county level COVID-19 mortality, and to a weaker degree COVID-19 case prevalence. These findings suggest that how we organise our health systems may not only affect outcomes such as costs, utilisation and care, but may be important to how they respond to systemic shocks such as the COVID-19 pandemic.

Contributors SL and LEE designed the study. SL acquired and analysed the data. SL drafted the manuscript. LEE reviewed and revised the manuscript. All authors critically revised for intellectual content and approved the final manuscript. SL and LEE are guarantors of the work.

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Competing interests None declared.

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Patient consent for publication Not applicable.

Ethics approval Not applicable.

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Data availability statement Data are available upon reasonable request.

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