Article

Predicting COVID-19 Infections in Eswatini Using the Maximum Likelihood Estimation Method

Sabelo Nick Dlamini ^{1,} *, Wisdom Mdumiseni Dlamini ¹ and Ibrahima Socé Fall²

¹University of Eswatini, Department of Geography, Kwaluseni, Manzini, Eswatini ²World Health Organization, Geneva, Switzerland

* Correspondence: sabelodlamini2004@yahoo.com ORCID: 0000-0002-4165-580X

Abstract: COVID-19 national spikes had been reported at varying temporal scales as a result of differences in the driving factors. Factors affecting case load and mortality rates have varied between countries and regions. We investigated the association between various socio-economic, demographic and health variables with the spread on COVID-19 cases in Eswatini using the maximum likelihood estimation method for count data. A generalized Poisson regression (GPR) model was fitted with the data comprising of fifteen covariates to predict COVID-19 risk in Eswatini. The results showed that variables that were key determinants in the spread of the disease were those that included the proportion of elderly above 55 years at 98% (95% CI: 97%-99%) and the proportion of youth below 35 years at 0.08% (95% CI: 0.017%-38%) with a pseudo R-square of 0.72. However, in the early phase of the virus when cases were fewer, results from the Poisson regression showed that household size, household density and poverty index were associated with COVID-19. We produced a risk map of predicted COVID-19 in Eswatini using the variables that were selected at 5% significance level. The map could be used by the country to plan and prioritize health interventions against COVID-19. The identified areas of high risk may be further investigated in order to find out the risk amplifiers and assess what could be done to prevent them.

Keywords: COVID-19; Eswatini; risk mapping; Poisson

1. Introduction

COVID-19 has spread dramatically since it was first discovered in China in December 2019 (1). In as much as the spread resulted in a global pandemic (2), countries continued to see national spikes of infections at different temporal scales as dominant strains of the virus took their toll on the population. There were various determinants of national spikes and they included factors such as population density, adherence to preventive measures and a host of typical socio-economic factors (3). The disease spreads through direct and effective contact of infected persons and as a result mechanical barriers limiting population interactions and mixing such as social distancing had been enforced by many countries (4). Understanding the environmental risk factors as well as the socio-economic and demographic factors associated with the spread of COVID-19 is crucial for effective prevention efforts (5). Often, the underlying factors would not always be exactly the same between affected countries as population behavior and structure and socio-economic activities may vary from country to country (6). For instance, the onset and severity of the disease and its national spikes had often been seen by disproportionate case load and mortality numbers between countries (7). The factors affecting the spread of the pandemic, case load and mortality rates had been studied at national and subnational levels and the identified key drivers varied between countries and regions. COVID-19 age mortality curves had shown that the spread of COVID-19 was different for High Income Countries (HIMs) and Low Middle Income Countries (LMICs) (8). A study by Peters, (2020) found that there were different susceptibilities and vulnerabilities to COVID-19 in urban and rural populations in the United States.



Eswatini (formerly known by its English name as Swaziland), a country in southern eastern Africa with a population of about 1.1 million had not been spared by the pandemic. According to the Ministry of Health, this lower-middle-income country had reported cumulative cases of about 69 000 and a total deaths of about 1 400 by February 2022. The Government of Eswatini had also implemented strict lockdowns and travel restrictions during the peaks of the pandemic in 2020 and 2021 (10). However cases continued to soar in the midst of these restrictions and in this study we were interested in determining the factors that were potential drivers of infections during the peak of the disease in Eswatini. For instance, Eswatini is known to have high poverty proportions at 58.9 % where 20% is considered to be extremely poor, high HIV infections at 26% (11) and high tuberculosis rates which could have increased susceptibility to the disease due to co-morbidities and other demographic factors.

COVID-19 predictors and case load forecasting include a host of clinical, epidemiological, demographic, and socio-economic factors ((12–14). In this study, we explored the association between various socio-economic, demographic and health variables with the distribution and spread on COVID-19 cases in Eswatini using the maximum likelihood estimation method for count data. Count data are dispersed data that involves discrete variables and requires discrete analysis methods to estimate the parameters.. We mapped and predicted the risk of COVID-19 for the whole of Eswatini using those variables that were significantly associated with the disease. We hope that the mapping products produced will not only help in the ongoing health intervention efforts against COVID-19 but will also help in identifying the risk amplifiers of the disease in those areas. This work is a continuation from our previous work which used a similar set of predictors to perform a spatial risk assessment and identified epidemic risk prone areas based on susceptibility risk, transmission risk and exposure risk (15).

2. Materials and Methods

2.1. Study area and data sources

Eswatini is a southern African country bordered by South Africa all around except on the north eastern side where it is bordered by Mozambique. COVID-19 had spread throughout the entire country and its severity had varied between the four districts comprising of Hhohho, Manzini, Shiselweni and Lubombo. Figure 1 shows the geographic location and distribution of COVID-19 reported cases in Eswatini while Figure 2 shows the incidence of cases per 1000 population. As can be seen in the maps COVID-19 had spread throughout the entire country since the first case was introduced in March, 2020, affecting both rural and urban populations but risk severity varied from locality to locality. The country is landlocked and travel within and outside Eswatini is mostly by road. Informal crossings (mainly to South Africa and Mozambique) are also common along the borders especially for the local communities along the borders.



Figure 1. Distribution of reported COVID-19 infections in Eswatini.



Figure 2. Distribution of COVID-19 per 1000 population in Eswatini.

To map and predict the distribution of COVID-19 in the country we used data ranging from communication data, internet connectivity, traffic density, health and demographic as well as socio-economic variables. The data was made up of a list of fifteen covariates which were used as predictors and regressed with georeferenced case data via a generalized Poisson regression (GPR) model (16). Data variables on location such as supermarket, shopping and church distance were extracted from Google earth. Health, demographic and socio-economic data used was obtained from the central statistics office (CSO). The CSO data included household density, household size, HIV prevalence, population density, youth proportion and proportion of elderly above 55 years. Details of the data used had been provided in our previous work (15). COVID-19 data comprising of reported cases ranging from the first case in March 2020 until December 2021 were obtained from the Ministry of Health (Government of Eswatini, 2022). The COVID-19 data comprised of cases sex, age, case locality, clinical severity and date of hospital presentation and it was made of about 12986 individual cases. The data were summed at enumeration area (EA) level (made up of a total of 2326 EAs) which serves as the smallest census unit in the country ranging from an area of about 0.013 km² to about 194 km². The data used in this study is described and presented in Table 2.1.

No.	Variable	Variable Short name	Format	Description	
1.	Cellphone usage	Cellphone	Values ranging from 0 to 1	Proportion of cellphone users per EA	
2.	Church-distance	Church_dis	Distance (km)	Distance between EA and church	
3.	Elderly above 55 years	Elderly_55	Values ranging from 0 to 100	Percentage or number of people above 55 years of age per 1000 people in each EA	
4.	Household density	Hhld_dens	Number of buildings per unit area (km²)	Numerical quantities of the built up surface area in each EA	
5.	Household size	Hhld_size			
6.	HIV Prevalence	HIV_prev	Values ranging from 0 to 100	Percentage of people living with HIV in each EA	
7.	Internet connectivity	Internet			
8.	Poverty index	Po_index	Values ranging from 0 to 100	Percentage of people living below USD 2 per day in each EA.	
9.	Building density	People_bld	Values ranging from 0 to 100	Proportion of built up area in each EA	
10.	Youth proportion	Youth_prop	Values ranging from 0 to 100	Percentage or rate of people below 35 years per 1000 people of age in each EA.	
11.	Shopping distance	Shop_dist	Distance (km)	Distance between EA and shopping area	
12.	Supermarket distance	Supmkt_dis	Distance (km)	Distance between EA and supermarket	
13.	Temperature	Temp	Degrees celcius	Heat/cold	
14.	Traffic mean	Traff_mean	Number of vehicles moving through an area per day per unit area (km²)	Numerical quantities of average traffic moving through each EA approximated as a surface area of that EA	
15.	Population density	Pop_dens	Number of people/ per unit area (km²)	Numerical quantities of the populated surface area in each EA.	
16.	Total population		Number of people	Number of people in the entire country obtained by summing up the number of people recorded in each EA	

2.2. Statistical modeling

In the first stage of the model we conducted a bivariate stepwise regression to select the set of variables that were associated with COVID-19 at 5% significance level and then we fitted the selected variables into the GPR model to estimate the Incidence Rate Ratio (IRR) of the virus in Eswatini. The stepwise regression method allows the user to evaluate

variables according to their order of importance (17). This way we were able to select useful or significant subsets of the regressed variables in addition to identifying any variable enhancement or suppression (18) by adding or removing different single variables or combination of variables in the model. In the final stage we used the variables selected in the second stage of the model to predict COVID-19 cases in the entire country using the maximum likelihood estimation method. Association of COVID-19 symptoms with age was also assessed by categorizing individual age into different groups. Before selecting the model we first investigated which model would be suitable for fitting the data between two more or less similar models involving the Poisson model and the Negative binomial model (19) by assessing the presence of over-dispersion in the data. We checked for excess variation in the model by assessing whether the deviance of the model was greater than its degree of freedom. We also wanted to find out if any excess variation was due to overdispersion or it was due to excess zeros (20). Since the Negative binomial model is suitable in cases where there is over-dispersion, in our case we proceeded with the Poisson model as the deviance was not greater than its degree of freedom. We then developed a Poisson regression model which was first fitted with all the covariates using STATA software in order to select the most parsimonious set of variables that were associated with COVID-19. Variables that were selected at 5% significance level were then added into the GPR model in order to predict the risk of COVID-19 in the whole of Eswatini. The Poisson model has only one parameter, μ (mean), which corresponds to the mean of the count. In the GPR model we used the maximum likelihood method to estimate the outcome of

Let μ_{ij} be the mean count of Y_{ij} COVID-19 cases *i* on a particular date *j* and $Xi \sim P(\mu_i)$ with likelihood:

$$P(Y;\mu) = \frac{\mu^{\gamma}}{Y!} e^{-\mu}$$
⁽¹⁾

The model was linearized as:

the counts of COVID-19 cases as follows:

$$\log(\mu_i) = \log(N_i) + \sum_{k=1}^{14} \beta X_i$$
 (2)

Where N_i is the population in each EA used here as an offset in order to scale the modeling of μ_i and βX are the regression coefficients corresponding to the 14 covariates. The maximum likelihood estimation method determines the values for the parameters in the model by maximizing. The parameter values under investigation are found by maximizing the likelihood that the process described by the model produced the data that were actually observed. The model maximizes the probability of obtaining the data we observed by estimating the mean outcome of cases and assuming that the counts are independent of each other. In our model, we assumed that the mean counts of COVID-19 cases followed a Poisson distribution. The second model involved the fitting of the data into the same Possion model but with only the variables that were selected at 5% significane level in the first run. The selected variables were used to predict the risk of COVID-19 in the whole country.

3. Results and discussion

3.1. Generalized Poisson Regression model

The results from the Poisson modeling with all fifteen predictors showed that two variables were associated with COVID-19 at 5% significance level. This was partly due to the fact that the rest of the socio-economic variables did not vary in space as the virus became indiscriminate as it spread throughout the entire country. Therefore variation by these variables did not hold and they became insignificant. The selected variables included the proportion of elderly above 55 years at 98% (95% CI: 97%-99%) and the proportion of youth below 35 years at 0.08% (95% CI: 0.017%-38%) with a pseudo R-square

of 0.72 (Table 2). This finding confirms what was found by Farshbafnadi et al., (2021) on the clinical manifestations of the disease by age which was that older people (age > 60) were at greater risk of developing severe symptoms from COVID-19. Age remained a key mortality risk factor in a study by (22), while another study by (23) found that elderly people aged over 60 years exhibited more severe symptoms and higher mortality among patients infected with COVID-19. Indeed the difference in the proportion of elderly compared to the youth may also be explained by the fact that a greater percentage of the elderly were likely to present with symptoms at health facilities and get tested compared to the youth who were found to be mostly asymptomatic. Other studies have found that COVID-19 infections can be driven by asymptomatic young people (24,25).

In this study, a bivariate analysis of the clinical symptoms by age of COVID-19 patients showed that an average of 33 years old patients had no symptoms (Table 3). A study by (26) found that the median age of COVID-19 patients with mild or moderate symptoms was 28 years. This finding proved that a greater proportion of the youth who were infected with COVID-19 did not have any symptoms and thereby were less likely to get tested as government testing strategy tended to be more reactive especially in the earlier phase of the pandemic when testing kits were embarrassingly scarce. Furthermore, in the early stages of the pandemic, medical attention was on the screening and management of symptomatic patients, and asymptomatic patients were only attended much later as clinical understating of the transmission of the virus improved.

Other variables such as church distance, shopping distance and supermarket distance were not significantly associated with COVID-19 infections and this was because most of these centers were closed and visiting these centers was severely restricted during the government strict lockdown measures (27). Surprisingly, household size, household density and poverty index were not associated with COVID-19. However other studies have found that households size and population density were associated with COVID-19 (28–31). We wish to clarify that in the initial phase of the virus when cases were fewer and emerging, preliminary results from the Poisson regression showed that these variables were associated with COVID-19. Similarly studies using early COVID-19 data until December 2020 mostly had the same finding (32). In Eswatini, this was mostly because it was highly likely to find a positive case within the household of an index case as the Ministry of Health was conducting contact tracing following a positive case. Moreover, cases were spreading faster within the low costs housing and poorer but congested communities who had little or no room to self-isolate in the country and this finding was similar to what (33) found in Africa and Latin America. But as infections had spread country wide affecting both rich and poor communities, the association of these variables with COVID-19 had been confounded. Also, the information, technology and communication variables such as internet connectivity and cellphone usage were also not associated with COVID-19. Some studies have shown that reduction in cellphone activity at work and retail locations was associated with lesser growth in COVID-19 cases (34). Clearly, the spread of the virus was indiscriminate as it attacked the rest of the country.

Individual	IRR	Std Err.	Z	P>z	95% CI		
cellphone	3.336945	2.693032	1.49	0.135	0.6861192	16.229	
church_dis	0.991159	0.016569	-0.53	0.595	0.9592107	1.0242	
elderly_55	0.984678	0.0025786	-5.9	0.000	0.979637	0.9897	
hhld_dens	1.000045	0.0001841	0.25	0.806	0.9996845	1.0004	
hhld_size	0.9565653	0.0408021	-1.04	0.298	0.8798463	1.04	
hiv_prev	0.3712601	0.3929613	-0.94	0.349	0.046636	2.9555	
internet	0.936553	0.4262686	-0.14	0.885	0.3838055	2.2854	
p0_index	1.00156	0.0044225	0.35	0.724	0.99293	1.0103	
people_bld	0.9836968	0.0358074	-0.45	0.652	0.9159606	1.0564	
pop_dens	1.000002	0.0000865	0.03	0.977	0.999833	1.0002	
youth_prop	0.0816543	0.0646422	-3.16	0.002	0.0173029	0.3853	
shop_dist	0.9976175	0.0178658	-0.13	0.894	0.9632086	1.0333	
supmkt_dis	1.002583	0.0159068	0.16	0.871	0.9718864	1.0343	
temp	0.9545037	0.0276899	-1.61	0.108	0.9017466	1.0103	
traff_mean	0.9999643	0.0000665	-0.54	0.591	0.9998339	1.0001	
*Selected variables at	elected variables at 5% significance leve.						

3.2. Age and COVID-19 infections

The results of the bivariate analysis of the distribution of symptoms by age revealed that younger people of age >35 years were less likely to present with symptoms. It is possible that a majority of infected young people did not get tested and may have recovered without being reported anywhere. Table 3 presents the results of the bivariate analysis between clinical symptoms severity and age of COVID-19 patients.

Mean age by symptoms								
Symptoms	mean	sd	Ν	% N				
No symptoms	33.4	13.75395	5566	42.86				
Mild	34.8	11.23121	4681	36.05				
Moderate to severe	48.0	16.97056	177	1.36				
Severe	29.0	12.346	88	0.68				
Recovered	36.0	10.7846	1236	9.52				
Deceased	58.0	1.414214	177	1.36				
Unknown	36.2	9.388904	1060	8.16				
Total	34.9	12.46639	12986	100				

Table 3. Mean age by symptoms.

Variables that were selected at 5% significance level were used in the GPR model in order to predict the risk of COVID-19 infections and Figure 3 shows the predicted risk of COVID-19 in the country. The risk of COVID-19 was found to be higher (180 cases per 1000 population) in the surrounding urban and peri-urban areas of main towns and industrial complexes of the country comprising of Piggs Peak, Manzini, Mbabane, Nhlangano, Bhunya, Mankayane, Matsapha, Siphofaneni and Big Bend. This was followed by rural and agricultural towns and main places at 110 cases per 1000 population and these comprised of Tshaneni, Simunye, Ngwenya and Sidvokodvo. The remainder of rural areas and other sparse settlements in the countryside had less than 34 cases per 1000 population. A study by Shekhar et al., (2022) also found that urban centers of the global south were highly likely to be predisposed to global risks such as COVID-19 due to their vulnerability and exposure, exacerbated by the process of urbanization in those centers.

In Eswatini, urban centers are the backbone of daily activities and daily commuting between rural and urban centers is not uncommon. Indeed cases reported in the earlier stages of the virus were mostly concentrated around urban and peri-urban areas and the daily contact between such places with rural commuters may have fueled the spread of the various to the rest of the country. The remaining areas with lower or zero cases were mainly private farms and rangelands with low population density and no residential areas.



Figure 3. Predicted risk of COVID-19 infections in Eswatini.

4. Conclusions

We implemented a maximum likelihood estimation method based on the GPR model to find out the set of socio-economic, demographic and health variables that were associated with COVID-19 in Eswatini. We found that the proportion of elderly population above the age of 55 years and the proportion of youth population less than 35 years of age were highly associated with the disease. Clearly, the virus had severe symptom manifestations among the elderly, prompting them to seek medical attention and subsequently get tested for the disease. Therefore the presence of higher population of elderly was an indicator for risk to the virus as they were more likely to fall sick compared to the youth who were found to be mostly asymptomatic. The association of the disease with other socio-economic variables gets confounded as the virus indiscriminately spread to the rest of the population in the country. While the first analysis of the disease done during the early stage of the disease when cases were fewer showed that it was associated with poverty, household size and household density, these associations did not hold as most of these variables were later not significant as cases spread. Caution must be taken when interpreting such results as they also depend on the stage of the virus and its level of spread in a country and confounding and interaction of variables must be investigated.

In this work, we mapped and predicted the risk of COVID-19 infections in Eswatini using socio-economic, demographic and health variables. The mapping products produced in this work could be used by the country to plan and prioritize health interventions for similar diseases in future. The areas of high risk may be further investigated in order to find out the risk amplifiers in those areas and to assess what could be done to prevent them. Our work contributes to the ongoing COVID-19 surveillance and response efforts in the country and to the rest of the global fight against the virus in areas with similar setting.

Conflicts of Interests: The authors have no competing interests to declare that are relevant to the content of this article.

Funding: The authors declare that there was no funding received for this work

Authors' contribution: SND conceived the article, conducted formal anylysis, investigation, methodology and wrote the manuscript. WMD and ISF reviewed and edited the manuscript. All authors approved the final manuscript.

Institutional Review Board Statement: not applicable

References

- 1. Chen X, Yu B. First two months of the 2019 Coronavirus Disease (COVID-19) epidemic in China: real-time surveillance and evaluation with a second derivative model. Glob Health Res Policy. 2020 Mar 2;5(1):7.
- Khanna RC, Cicinelli MV, Gilbert SS, Honavar SG, Murthy GVS. COVID-19 pandemic: Lessons learned and future directions. Indian J Ophthalmol. 2020 May;68(5):703–10.
- 3. Chaudhry R, Dranitsaris G, Mubashir T, Bartoszko J, Riazi S. A country level analysis measuring the impact of government actions, country preparedness and socioeconomic factors on COVID-19 mortality and related health outcomes. EClinicalMedicine. 2020 Aug 1;25:100464.
- 4. Qian M, Jiang J. COVID-19 and social distancing. J Public Health. 2022 Jan 1;30(1):259–61.
- 5. Pradhan D, Biswasroy P, Kumar Naik P, Ghosh G, Rath G. A Review of Current Interventions for COVID-19 Prevention. Arch Med Res. 2020 Jul 1;51(5):363–74.
- Hashim MJ, Alsuwaidi AR, Khan G. Population Risk Factors for COVID-19 Mortality in 93 Countries. J Epidemiol Glob Health. 2020 Sep;10(3):204–8.
- 7. Sorci G, Faivre B, Morand S. Explaining among-country variation in COVID-19 case fatality rate. Sci Rep. 2020 Nov 3;10(1):18909.
- 8. Demombynes G. COVID-19 Age-Mortality Curves Are Flatter in Developing Countries [Internet]. Washington, DC: World Bank; 2020 Jul [cited 2022 Feb 22]. Available from: https://openknowledge.worldbank.org/handle/10986/34028
- Peters DJ. Community Susceptibility and Resiliency to COVID-19 Across the Rural-Urban Continuum in the United States. J Rural Health. 2020;36(3):446–56.
- Pasquali G, Godfrey S. Governance of Eswatini Apparel Regional Value Chains and the Implications of Covid-19. Eur J Dev Res. 2022 Feb 1;34(1):473–502.
- 11. Nhapi TG, Dhemba J. The conundrum of old age and COVID-19 responses in Eswatini and Zimbabwe. Int Soc Work. 2020 Nov 1;63(6):842–6.

- 12. Gallo Marin B, Aghagoli G, Lavine K, Yang L, Siff EJ, Chiang SS, et al. Predictors of COVID-19 severity: A literature review. Rev Med Virol. 2021;31(1):e2146.
- 13. Sun Y, Koh V, Marimuthu K, Ng OT, Young B, Vasoo S, et al. Epidemiological and Clinical Predictors of COVID-19. Clin Infect Dis. 2020 Jul 28;71(15):786–92.
- 14. Moreira A, Chorath K, Rajasekaran K, Burmeister F, Ahmed M, Moreira A. Demographic predictors of hospitalization and mortality in US children with COVID-19. Eur J Pediatr. 2021 May 1;180(5):1659–63.
- 15. Dlamini WM, Dlamini SN, Mabaso SD, Simelane SP. Spatial risk assessment of an emerging pandemic under data scarcity: A case of COVID-19 in Eswatini. Appl Geogr. 2020 Dec 1;125:102358.
- 16. Consul PC, Famoye F. Generalized poisson regression model. Commun Stat Theory Methods. 1992 Jan 1;21(1):89–109.
- 17. Thompson B. Stepwise Regression and Stepwise Discriminant Analysis Need Not Apply here: A Guidelines Editorial. Educ Psychol Meas. 1995 Aug 1;55(4):525–34.
- 18. Currie I, Korabinski A. Some Comments on Bivariate Regression. J R Stat Soc Ser Stat. 1984;33(3):283-93.
- 19. Gardner W, Mulvey EP, Shaw EC. Regression analyses of counts and rates: Poisson, overdispersed Poisson, and negative binomial models. Psychol Bull. 1995;118(3):392–404.
- Greene WH. Accounting for Excess Zeros and Sample Selection in Poisson and Negative Binomial Regression Models [Internet]. Rochester, NY: Social Science Research Network; 1994 Mar [cited 2022 May 27]. Report No.: 1293115. Available from: https://papers.ssrn.com/abstract=1293115
- 21. Farshbafnadi M, Kamali Zonouzi S, Sabahi M, Dolatshahi M, Aarabi MH. Aging & COVID-19 susceptibility, disease severity, and clinical outcomes: The role of entangled risk factors. Exp Gerontol. 2021 Oct 15;154:111507.
- 22. Leung C. Risk factors for predicting mortality in elderly patients with COVID-19: A review of clinical data in China. Mech Ageing Dev. 2020 Jun 1;188:111255.
- 23. Wei C, Liu Y, Liu Y, Zhang K, Su D, Zhong M, et al. Clinical characteristics and manifestations in older patients with COVID-19. BMC Geriatr. 2020 Oct 8;20(1):395.
- 24. Han D, Li R, Han Y, Zhang R, Li J. COVID-19: Insight into the asymptomatic SARS-COV-2 infection and transmission. Int J Biol Sci. 2020 Aug 27;16(15):2803–11.
- 25. Balasubramanian S, Rao NM, Goenka A, Roderick M, Ramanan AV. Coronavirus Disease 2019 (COVID-19) in Children What We Know So Far and What We Do Not. Indian Pediatr. 2020 May 1;57(5):435–42.
- 26. Lu J, Peng J, Xiong Q, Liu Z, Lin H, Tan X, et al. Clinical, immunological and virological characterization of COVID-19 patients that test re-positive for SARS-CoV-2 by RT-PCR. eBioMedicine. 2020 Sep 1;59:102960.
- 27. Pillay J. COVID-19 Shows the Need to Make Church More Flexible. Transformation. 2020 Oct 1;37(4):266–75.
- 28. Sigler T, Mahmuda S, Kimpton A, Loginova J, Wohland P, Charles-Edwards E, et al. The socio-spatial determinants of COVID-19 diffusion: the impact of globalisation, settlement characteristics and population. Glob Health. 2021 May 20;17(1):56.
- 29. Liu P, McQuarrie L, Song Y, Colijn C. Modelling the impact of household size distribution on the transmission dynamics of COVID-19. J R Soc Interface. 18(177):20210036.
- 30. Hamidi S, Hamidi I. Subway Ridership, Crowding, or Population Density: Determinants of COVID-19 Infection Rates in New York City. Am J Prev Med. 2021 May 1;60(5):614–20.
- 31. Sugg MM, Spaulding TJ, Lane SJ, Runkle JD, Harden SR, Hege A, et al. Mapping community-level determinants of COVID-19 transmission in nursing homes: A multi-scale approach. Sci Total Environ. 2021 Jan 15;752:141946.
- 32. Gershengorn HB, Patel S, Shukla B, Warde PR, Bhatia M, Parekh D, et al. Association of Race and Ethnicity with COVID-19 Test Positivity and Hospitalization Is Mediated by Socioeconomic Factors. Ann Am Thorac Soc. 2021 Aug;18(8):1326–34.
- 33. Bargain O, Aminjonov U. Poverty and COVID-19 in Africa and Latin America. World Dev. 2021 Jun 1;142:105422.
- 34. Sehra ST, George M, Wiebe DJ, Fundin S, Baker JF. Cell Phone Activity in Categories of Places and Associations With Growth in Cases of COVID-19 in the US. JAMA Intern Med. 2020 Dec 1;180(12):1614–20.
- 35. Shekhar H, Rautela M, Maqsood M, Paris R, Flores de León RM, Romero-Aguirre MF, et al. Are leading urban centers predisposed to global risks- An analysis of the global south from COVID-19 perspective. Habitat Int. 2022 Mar 1;121:102517.