ECONSTOR
Make Your Publications Visible.

A Service of

ZBW Leibniz-Informationszentrum Wirtschaft
Leibniz Information Centre for Economics

Kuebart, Andreas; Stabler, Martin

Article — Published Version

Infectious Diseases as Socio-Spatial Processes: The COVID-19 Outbreak In Germany

Tijdschrift voor economische en sociale geografie

Provided in Cooperation with:
John Wiley & Sons

Suggested Citation: Kuebart, Andreas; Stabler, Martin (2020) : Infectious Diseases as Socio-Spatial Processes: The COVID-19 Outbreak In Germany, Tijdschrift voor economische en sociale geografie, ISSN 1467-9663, Wiley, Hoboken, NJ, Vol. 111, Iss. 3, pp. 482-496, https://doi.org/10.1111/tesg.12429

This Version is available at:
https://hdl.handle.net/10419/230219

Standard-Nutzungsbedingungen:

Die Dokumente auf EconStor dürfen zu eigenen wissenschaftlichen Zwecken und zum Privatgebrauch gespeichert und kopiert werden.

Sie dürfen die Dokumente nicht für öffentliche oder kommerzielle Zwecke vervielfältigen, öffentlich ausstellen, öffentlich zugänglich machen, vertreiben oder anderweitig nutzen.

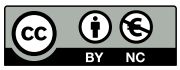
Sofern die Verfasser die Dokumente unter Open-Content-Lizenzen (insbesondere CC-Lizenzen) zur Verfügung gestellt haben sollten, gelten abweichend von diesen Nutzungsbedingungen die in der dort genannten Lizenz gewährten Nutzungsrechte.

Terms of use:

Documents in EconStor may be saved and copied for your personal and scholarly purposes.

You are not to copy documents for public or commercial purposes, to exhibit the documents publicly, to make them publicly available on the internet, or to distribute or otherwise use the documents in public.

If the documents have been made available under an Open Content Licence (especially Creative Commons Licences), you may exercise further usage rights as specified in the indicated licence.



http://creativecommons.org/licenses/by-nc/4.0/

WWW.ECONSTOR.EU

Mitglied der Leibniz-Gemeinschaft

INFECTIOUS DISEASES AS SOCIO-SPATIAL PROCESSES: THE COVID-19 OUTBREAK IN GERMANY

ANDREAS KUEBART* & MARTIN STABLER**

**Leibniz Institute on Research on Society and Space, Flakenstr. 29-31, Erkner, 15537, Germany; Brandenburg Technical University Cottbus-Senftenberg, Platz der Deutschen Einheit 1, Cottbus, 03013, Germany. E-mail: andreas.kuebart@leibniz-irs.de*
***Freie Universität Berlin, Centre for Development Studies - Geographic Sciences, Malteserstr. 74-100, Berlin, 12249, Germany. E-mail: martin.stabler@fu-berlin.de*

Received: April 2020; accepted May 2020

ABSTRACT

This paper argues that outbreaks of infectious diseases should be understood as socio-spatial processes with complex geographies. Considering the different dimensions of space through which an outbreak unfolds, facilitates analysing spatial diffusion of infectious disease in contemporary societies. We attempt to highlight four relevant dimensions of space by applying the TPSN framework to the case of the recent COVID-19 outbreak in Germany. By identifying key processes of disease diffusion in space, we can explain the spatial patterns of the COVID-19 outbreak in Germany, which did not feature the well-known patterns of spatially contagious as in or hierarchical diffusion. In contrast, we find superspreading events and especially relocation diffusion based on existing networks, on which the pathogen travelled like a blind passenger, to be more relevant. For us, these findings prove the value of combining relational thinking with geographic analysis for understanding epidemic outbreaks in contemporary societies.

Key words: Infectious Disease; COVID-19; Health Geography; TPSN; Disease Diffusion; Germany

INTRODUCTION

Amid the unprecedented amount of media coverage about the pandemic outbreak of the new coronavirus-induced respiratory disease (COVID-19) maps were from the onset of the illness at the centre of the public perception. Starting with the ubiquitous world map published and constantly updated by a team of researchers of the US-based Johns Hopkins University (Dong *et al.* 2020), interactive maps covering epidemiological numbers were used by numerous media outlets and public authorities to report on countries or regions. What most of these geovisualisations have in common is a territorial depiction of space: reported cases are counted and visualised on the level of countries, states, provinces, cities, or regions, but always based on a territorial logic.

Against this background of insufficient spatialisation of the outbreak, this paper seeks a broader perspective on the spatial diffusion of COVID-19 in Germany by analysing how it is shaped by different dimensions of space. The outbreak in Germany was characterised by a somewhat surprising pattern. Instead of an outbreak radiating out of a centre through spatially contagious diffusion, as observed in Italy, or an outbreak following existing patterns of centrality, as observed for the SARS outbreak in 2002 (Ali & Keil 2008), COVID-19

Tijdschrift voor Economische en Sociale Geografie – 2020, DOI:10.1111/tesg.12429, Vol. 111, No. 3, pp. 482–496.
© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig
This is an open access article under the terms of the Creative Commons Attribution-NonCommercial License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited and is not used for commercial purposes.

appeared very quickly all over Germany, without following these well-known patterns. To explain this process, we consider a multi-dimensional approach to space helpful to integrate the complex relations between infected (and infectious) people and places (Cummins *et al.* 2007) into one analytical framework. We argue that only a multi-dimensional approach can reveal insights on the complex processes of epidemic spread in contemporary societies. Following Jessop *et al.* (2008), we chose to implement this multi-dimensional perspective on socio-spatial processes by investigating the COVID-19 outbreak through the lens of the TPSN framework. This approach highlights the interconnectedness of the spatial categories of (T)erritory, (P)lace, (S)cale, and (N)etwork. Combined with a process perspective, this allows for a more balanced understanding of how disease outbreaks unfold in space.

By analysing context data on transmissions of COVID-19 between most of the first 1,500 registered cases in Germany, we can identify three common socio-spatial processes of disease transmission, through which COVID-19 spread through Germany. Each of these three processes is determined by the interaction of spatial dimensions in a distinct combination. We find complex topologies of interconnected outbreaks, moving along the paths of a rather mobile society through many different layers of networks (Castells 1996). Consequently, this paper has two aims: first, we explain the spatial diffusion of COVID-19 during the early weeks of the epidemic in Germany. Second, on a conceptual level, we want to argue for a multi-dimensional perspective on space to analyse outbreaks of infectious diseases as socio-spatial processes. Only through combining insights on how outbreaks move in networks, are impacted by characteristics of places, are scaled and territorialised, it becomes possible to understand contemporary outbreaks of infectious diseases.

The paper is structured as follows: in the next section, we outline the TPSN framework and define how each of the four categories is relevant to analyse the outbreak process of infectious diseases. After specifying our methodological and analytical approach, we provide some details on the characteristics of the early weeks of the COVID-19 epidemic in Germany. Finally, we highlight three common instances of socio-spatial processes we derived from the data and analyse how the spatial categories of TPSN intersect in them.

THEORISING THE SPREAD: THE COVID-19 OUTBREAK AS A SPATIAL PROCESS

Fundamental for understanding the geography of communicable diseases transmitted via human-to-human transmission is that the physical co-presence of an infected, and thus contagious individual, and a previously not-infected individual is necessary (van Loon 2005; Meade & Emch 2010). The transmission of such diseases, therefore, is a complex socio-spatial process, determined by multiple factors including physical characteristics of the pathogen, patterns of contagiousness and immunity of bodies, and social interactions. Among the latter, the convening of groups for socio-cultural events, the behaviour of individuals in such groups, and societal responses to diseases are most relevant (Koopman 2005). The multi-factorial and non-linear causality for transmission processes implies that applying a process ontology is beneficial to analyse the spread of infectious diseases (Lee 2019). In a process ontology, processes are the principal category of analysis, because they carry primacy over things (Rescher 2007). Therefore, aspects like change and activity are central in making sense of an empirical phenomenon, and temporality is the most important connector since processes can be causal but must be successive (Rescher 2007).

To make sense of the interrelated factors that form the 'intrinsically spatial and temporal' (Bian & Liebner 2007, p. 155) process of epidemic spread, we have to theorise how people (and with them the pathogen) move and engage within society and space (van Loon 2005). Informed by general concepts from the field of health geography and especially the body of literature that emerged out of the empirical findings from the SARS outbreak in 2003 (Fidler 2003; van Loon 2005; Cummins *et al.* 2007; Ali & Keil 2008; Van Wagner 2008), we intend to analyse the geographies of the spread of COVID-19 by considering space as a

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

lens, through which we observe the unfolding of the outbreak as a process. For such a perspective, the understanding of space is crucial, in that socio-spatial processes should be studied with attention to several dimensions of space (Jessop *et al.* 2008).

As described in the Introduction, the territorial dimension dominates the discourse on the epidemic outbreak of COVID-19. However, among the four dimensions of space, previous studies on infectious diseases in the fields of medical and health geography and epidemiology have especially emphasised the relevance of networks of infections (e.g. Bian 2004; Lloyd-Smith *et al.* 2005; van Loon 2005; Bian & Liebner 2007; Ali & Keil 2008) and places as the environment of infections (e.g. Meade 1977, Yu *et al.* 2004, Cummins *et al.* 2007, Stein 2011). Considering this contrast, we suggest that a purely territorial lens is not sufficient and arguably even harmful to understand the geographies of disease transmission. Therefore, this paper aims to integrate different dimensions of space to analyse infectious disease outbreaks from a process perspective. Consequently, we chose to apply the TPSN framework to analyse the spatial diffusion of the COVID-19 epidemic in Germany since it enables us to grasp the complex geographies of socio-spatial processes.

The TPSN framework combines the four well-established spatial categories of 'Territory', 'Place', 'Scale' and 'Network' in a suitable tool for empirical research engaged with questions on societal phenomena unfolding in space. Since each of the four categories is well theorised and conceptualised on its own, the TPSN framework enables analysis based on combinations of and relations between different spatial categories. Instead of a formulaic interpretation scheme, the TPSN framework can be applied rather heuristically to explain how socio-spatial processes are structured (Jessop *et al.* 2008). Criticising previous inquiries under only one spatial category as centrism and 'overontologising' (Jessop *et al.* 2008, p. 391) of a single spatial dimension TPSN considers the categories as permanently intertwined. Developing a classification where every dimension can be interpreted as both a 'structuring principle' and a 'structured field' puts special emphasis on studying the connectedness between them. However, to provide a framework that encourages explorative studies the four provided dimensions are only briefly introduced but not defined by the authors into detail (Gailing *et al.* 2019). This creates a site for criticism as it disregards other important spatial categories (Paasi & Metzger 2017). It is also questionable how far the chosen categories can be seen as equally qualified for the generation of space (Casey 2008). Further, the framework could be interpreted as structuralist while it enforces its four categories instead of encouraging an individual exploration of socio-spatial relations (Tan 2016).

When considering space from a relational perspective, it is constituted by social actors and their relationships, while space also conversely constitutes and shapes these relationships (Cummins *et al.* 2007; Massey 2007). Following the above-mentioned ideas consequently would mean that getting infected with COVID-19 may directly depend on the obvious geographical proximity to individuals infected with SARS-CoV2. However, how individuals are embedded in specific social networks, relate to territories and places, and how scalar differences determine relational pathways is also important to understand who gets close to infected individuals in the first place. In the following, we relate each of the four spatial dimensions of TPSN to basic epidemiologic concepts of pathogen transmission.

Territorialisation and infectious diseases – Even the World Health Organization usually communicates the proliferation of pandemics by counting infections via territorial world maps (Keeler & Emch 2018; WHO 2020). Thus, the territorial dimension remains vital for the public sensemaking of an epidemic outbreak. However, we argue for a more nuanced understanding: especially in the early stages of epidemic outbreaks, a territorial perspective falls short of explaining the geographies of infectious disease outbreaks. Instead, network and place dimensions of space are better suited to explain the process of an outbreak.

This is not to say that territory, understood as explicit demarcated physical spaces characterised by certain types of governance and institutional settings (Elden 2010), is irrelevant to understand outbreaks. Territories execute means of control over their lands, such as laws and borders.

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

Respectively, asserting control over people, objects, and relationships by authorities as well as the strategies that form, change, and obtain given territories should be understood as territorialisation (Sack 1983). Concerning infectious diseases spread, territorialisation makes two relevant implications on a macro level. First, it presents general conditions for human mobility, and second, it provides a health system as well as surveillance mechanisms and counter-strategies to disease spread. Former pathogens and viruses such as SARS or MERS-CoV have been analysed and due to political actions, they have been named and became part of a national and international surveillance system (Wolf 2016). However, new pathogens and consequent diseases are in the essence of the matter underexplored and thus cannot be classified as an appropriate threat while entering territories. In the early stage of a newly emerging disease it is especially true that 'microbes live in a borderless world' (Wolf 2016, p. 973). In the particular case of a highly efficient person-to-person infection—as witnessed with COVID-19—a pathogen can bypass common measures and emerge into territories almost unhindered. An outbreak must be recognised as such by territorial institutions in order to become visible. Under these circumstances, Fidler (2003, p. 485) already called the earlier generation of the SARS pathogen 'the first post-Westphalian pathogen' by dryly noting that the virus took no notice of the governance framework that defined international public health from the mid-nineteenth century. Therefore, 'territorialising' is relevant mostly on the macrolevel of response to an outbreak but does not necessarily influence the microlevel of disease diffusion. Most relevant processes in shaping the spatial spread of infectious diseases are then networking, impacting by places, and scaling.

Networking as the mechanism of outbreaks – Networks are arguably most important to conceptualise the geographies of disease outbreaks because the '*networking*' of communicable diseases necessarily occurs via ties of personal contacts or 'infection pathways' (Bian 2004). From a process perspective, 'networking' thus refers to the diffusion of a disease vie personal ties.

Due to network patterns, infectious diseases hardly spread evenly in space. Therefore, a relational focus must consider behavioural patterns of humans that interact with their built environment (Keeler & Emch 2018). Since in modern societies people have individual and complex spatial routines in their everyday lives (Kwan & Lee 2004; Kwan *et al.* 2003), it has to be considered that people tend to pass through a variety of places over time. Considering for example family and friends, employment, and leisure activities, most people have different network structures they interact with at different times of the day, so that a tempo-spatial perspective is necessary to understand outbreaks of infectious diseases (Bian 2003). This reasoning is followed in this study by explicitly taking up a process perspective.

The multifaceted layers of networks in contemporary societies (Castells 1996) imply the pre-dominance of open networking of infection paths, which include interactions between different network structures, over closed infection paths, which only involve a closed group of individuals (Bian 2003). With open infection paths, 'infectious diseases are not contained by office buildings or gated communities' (van Wagner 2008, p. 25). Aside from direct ties between individuals being a necessary condition for infections, the quality of ties matters as well. Social proximity between individuals enhances the likelihood of close personal contact, which in turn enhances the likelihood of a respiratory infection (Lloyd-Smith *et al.* 2005).

Evidence from previous epidemic outbreaks shows the network structures of infection paths to be relatively uneven. Not every infected individual also causes further infections, but a small number of highly contagious individuals cause most infections. The often-cited 20/80 rule (Woolhouse *et al.* 1997; Stein 2011) suggests that just 20% of individual infected bodies contribute to 80% of infections by acting as 'superspreaders'.

Place impacting as the facilitator of outbreaks – Characteristics of places such as size, shape, and usage determine the sociodemographic configuration of the people most likely to be found at those places as well as the way they interact with each other. The relationship between places and people has been considered highly relevant for the

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

understanding of how infectious diseases spread for a long time already. For example, Melinda Mead's (1977) triangle of disease ecology conceptualises the geographies of infectious diseases as a function of human action and environmental aspects (Keeler & Emch 2018).

Taking the sub-family of Orthocoronaviridae as an example, the early infections in humans all occurred after close contact with host animals (Cui *et al.* 2019), such as cattle (HCoV-OC43), civets (SARS-CoV), and dromedaries (MERS-CoV). A similar zoonotic origin is also likely for the novel SARS-CoV2 (Andersen *et al.* 2020). After the virus mutated to a type relying on respiratory human-to-human transmission, the place conditions favouring a spread of infections changed as COVID-19 is highly transmissible (Wilder-Smith *et al.* 2020) and therefore not bound to specific environments. However, specific conditions might favour super-spreading events.

The case of Amoy gardens during the 2003 SARS outbreak in Hong Kong showed how built structures facilitate the spread of pathogens. Constructional features like air shafts and plumbing systems favoured the diffusion of aerosols within the building site (Yu *et al.* 2004; McKinney *et al.* 2006). Although the transmission requires physical co-presence of individuals, the place impacts how and at what scale infections can happen and specific places can be 'high-risk transmission settings' (Shannon & Willoughby 2004, p. 362).

Places and networks are closely inter-related in the process of transmittable disease outbreaks (Wolf 2016; Brinks & Ibert 2020). This notion is especially relevant since 'superspreading events' in which specific individuals carrying a pathogen cause an unusually large number of infections in a specific place (Lloyd-Smith *et al.* 2005). Super-spreading is not just bound to specific individuals, but also requires specific places, in which environmental conditions such as crowding or poor ventilation is met (Stein 2011). For a superspreading event to occur, both the relational set-up, such as at least one highly infectious patient and a large number of receptive individuals and the conditions of the place, such as a crowded space with close personal contact, must overlap. For the previous epidemic outbreaks caused by Orthocoronaviridae, highly uneven patterns have been described: for SARS, superspreading events have been documented during the local outbreaks in Singapore (Lipsitch *et al.* 2003, Lloyd-Smith *et al.* 2005) and Beijing (Stein 2011) and in the case of MERS, super-spreading occurred in a hospital in Seoul (Cho *et al.* 2016). Early findings on COVID-19 also report superspreading events to occur in crowded places with poor ventilation (Park *et al.* 2020).

Scaling as the accelerator of outbreaks – The SARS outbreak in 2003 illustrated how an unnoticed pathogen can rush through space via the same routes that usually just facilitate flows of people (Ali & Keil 2008; van Wagner 2008). A process that was magnified catastrophically with COVID-19. 'Scaling' implies a vertical differentiation of space and highlights the overlapping of places, networks, and territories (Jessop *et al.* 2008; Jessop 2018). For infectious diseases, scaling can be seen as the process of pathogen spread or diffusion of pathogens within and in-between social networks. Scales can be understood as an integral dimension of places, networks, and territories, and thus as the difference between a pathogen diffusing locally or globally.

The literature on medical geography differentiates three spatial diffusion (or 'scaling') processes (Meade & Emch 2010). Each of them is a socio-spatial process based on a different interaction of territorialising, impacting, networking, and scaling. Most typically, diseases can spread spatially contagious (SCD) in a relatively even diffusion process over space via everyday networks such as commuting. This process implies a distance decay pattern since the outbreak spreads first to places nearby and thus a scaling based on the characteristics of place and proximity. Second, hierarchical diffusion (HD) occurs along with established patterns such as the centrality of transport networks. This pattern was observed when the SARS outbreak in 2002 spread first from the Chinese countryside to Hong Kong and from there to other global cities (Litaker *et al.* 2003; Bowen & Laroe 2006; Ali & Keil 2008). Third, relocation diffusion (RD) occurs when diseases are introduced to new places and spread from there. Usually, the different diffusion processes occur intertwined, for example when SARS was transmitted from Hong Kong to Toronto

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

(HD) and then spread there locally (SCD). It is the structuring principle of scales that turns a place into a global hub for the virus spread. Therefore, it is important to analyse the inter-relations between places and networks of infections also through the lens of scale (Wolf 2016). To sum up, we consider all four dimensions as relevant factors to understanding the geographies of epidemic outbreaks. However, the crucial strength of the TPSN approach is to combine the different dimensions of space.

METHODOLOGICAL APPROACH

Context: the COVID-19 outbreak in Germany – Before discussing our methodological approach, this section introduces context information about the COVID-19 outbreak in Germany, as seen through the (territorial) lens of the official epidemiological statistics.[1] From a tempo-spatial perspective, the COVID-19 outbreak can be separated into three phases: An early phase during which all cases had a direct link to China. This includes one cluster of about twenty infections in Southern Bavaria (27 January–11 February), where a Chinese participant in a business meeting infected several colleagues, who in turn infected some family members, as well as two distinct cases returnees from China (2 February) (Figure 1).

The second phase began around 23 February 2020 with several infections emerging especially in Western (cluster Heinsberg) and Southern Germany (multiple districts in Baden-Württemberg and Bavaria). Over the following three weeks, the epidemic proliferated rapidly until in mid-March cases were reported from all over Germany (from each of the 16 states on 10 March 2020, and each of the 401 German districts and cities two weeks later). Curiously, the spatial distribution is relatively even during this phase, whereas only the 'hotspot Heinsberg' continues to have a much higher share of infections, with adjacent territories being not more affected than other regions (RKI 2020a). Therefore, from a spatial perspective, the COVID-19 outbreak in

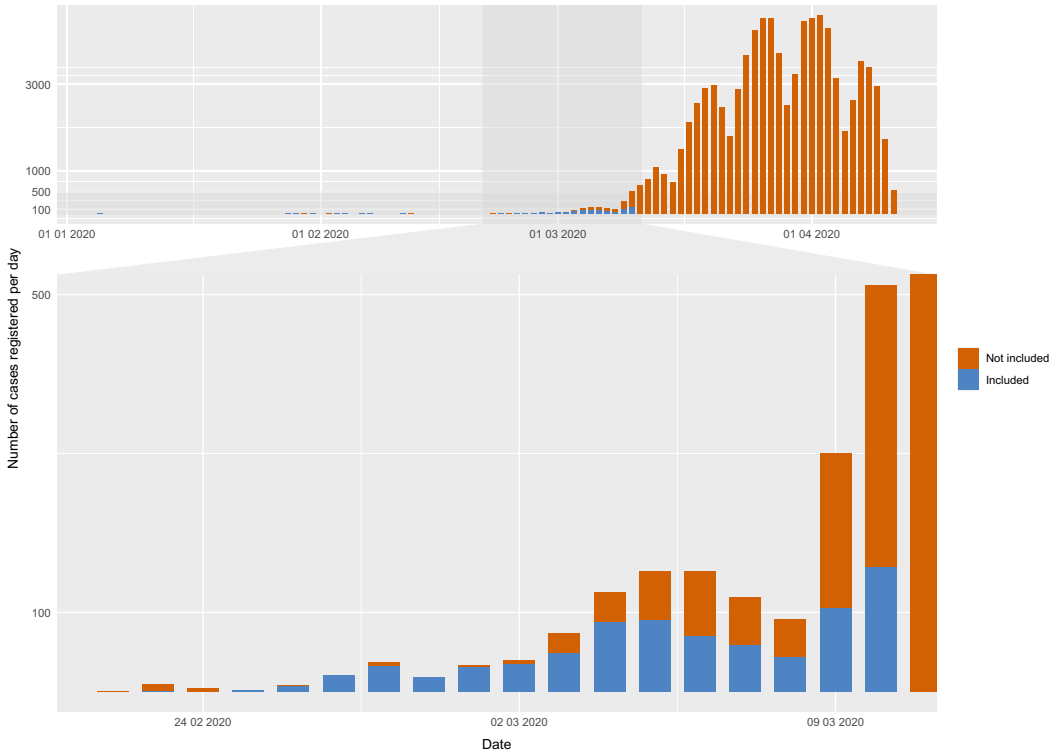


Figure 1. *Cases included in our dataset compared to the overall outbreak of COVID-19 in Germany as reported by RKI. [Colour figure can be viewed at wileyonlinelibrary.com]*

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

Germany resembles the opposite of the SCD epidemic model. Instead, the epidemic seems to start almost everywhere in Germany at the same time. A third phase can be distinguished, during which the number of infections grows exponentially in most regions, albeit at a different speed. New hotspots emerge, mostly in Southern Germany. Now, political action is implemented on unprecedented levels, including school closures and the shutdown of social activities to counter the outbreak.

Tracing socio-spatial processes – The remainder of this study will focus mostly on the second phase for two reasons: on the one hand, we consider the pattern of proliferation described above very interesting since it already indicates complex geographies of epidemic diffusion. On the other hand, from a methodological perspective, it remains possible to retain focus on individual socio-spatial processes of infections as the disease spreads rapidly, whereas it is hardly possible to trace networks of infections in an advanced stage and close attention to temporality and timeframe is necessary for spatial epidemiology (Chan & King 2011). Specifically, we confined our analysis to the period between the first documented super-spread event in Germany, which happened on 15 February 2020 in Heinsberg county in Western Germany, and the following 25 days up to 12 March 2020. While at the beginning of our study period, only ten districts reported COVID-19 infections, in total 1,567 infections were reported on 11 March 2020 in 277 of the 401 German districts, revised to 2,693, later (Schilling *et al.* 2020).[2]

During this period of the rapid proliferation of COVID-19, we reconstructed the socio-spatial processes causing the spread of infections as far as possible by combining different sources of information to a coherent data set. Our starting point for this endeavour was a dataset provided by the German Federal Institute for disease control (Robert Koch Institute or RKI). It includes location by district and date of registration along with some basic socio-demographic information for each case of COVID-19 in Germany known to the RKI on 10 April 2020. Since this dataset did not include information regarding the origin of infection or relation between cases, we decided to gather this information from other publicly available sources, which often provided much more comprehensive information on individual cases. The sources for this document analysis included additional publications of the RKI, authorities of the German states (Länder), and local health departments on the district level.[3] Further, we analysed the coverage of the nine regional public broadcast institutions but relied on official information wherever possible. Since we are researching an ongoing process, we consider it important to note that the data collection was concluded on 10 April 2020, about one month after the period we analyse. Any information published later was not considered. Although the final statistics on the outbreak might show some minor variations, we are confident our data draws a solid picture of the outbreak during this period.

For each case, we tried to establish the circumstances that led to the infection. We collected information on the place of infection, connections to other cases in the dataset, like personal ties or temporal co-location during an event, and other context information.[4] In total, we were able to collect meaningful data on 946 infected individuals out of the 2,693 known infections during our period of research. Although our dataset is far from complete, it does represent a fair sample both in space and time over our period of research (see Figure 2). The dataset was stored in a relational database, which then was analysed for common patterns. These common patterns of socio-spatial processes were analysed through the lens of TPSN by extracting how network, place, and scale were acting as structuration principles.

FINDINGS

Analysing the spread of COVID-19 in Germany between mid-February and mid-March 2020 reveals three broad patterns. First, a regional outbreak in Western Germany centred around Heinsberg district. Second, tourists returning to their home regions while carrying an infection. Third, infection networks based on specific focus places or events. The cases included in our sample suggest that the first two patterns dominate the outbreak during the period we analysed. In this section, we offer more

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

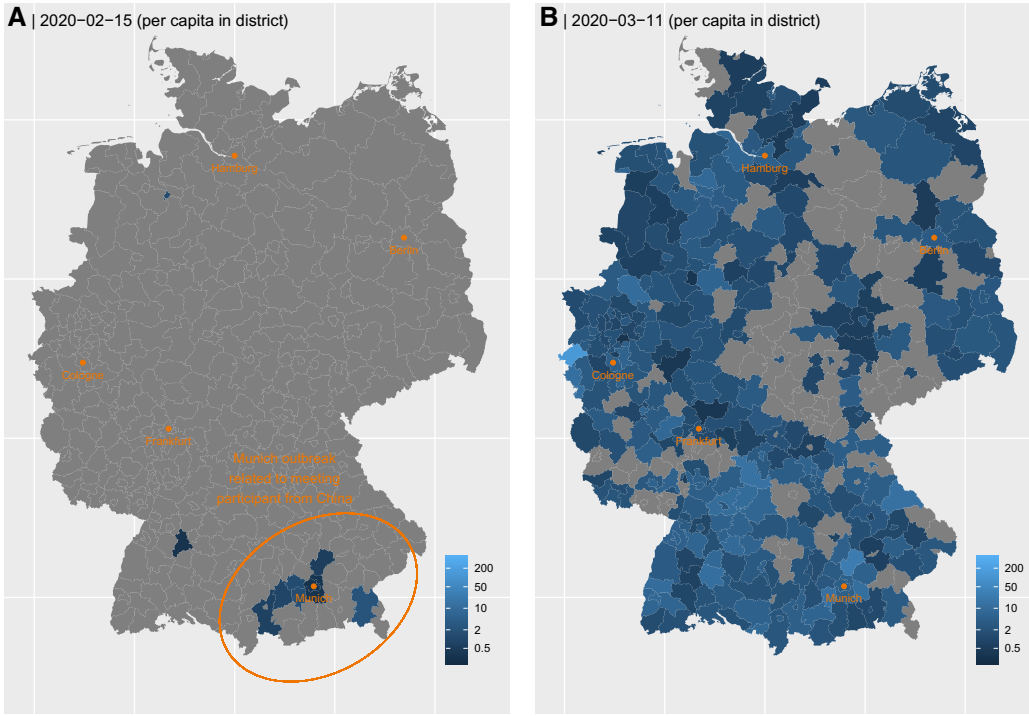


Figure 2. *Reported cases of COVID-19 per 100 000 inhabitants in German counties at the beginning (A) and end (B) of our study period. In mid February, only few cases had been reported, all of them with a direct infection chain linked to the outbreak in China. Over the following weeks, the disease spread quickly, so that on 11 March already more than half of the districts were affected. [Colour figure can be viewed at wileyonlinelibrary.com]*

detailed descriptions of these patterns before analysing these results through the lens of the TPSN approach.

Regional outbreaks through super-spreading events – The outbreak of COVID-19 in Germany was first noticed on 24 February 2020 when a man and subsequently his wife tested positive for SARS-CoV2 in Heinsberg district in North Rhine-Westphalia, without having had obvious contact with another infected individual. The number of cases increased rapidly since the index patients had participated in social activities in the previous weeks, notably a carnival celebration on 15 February 2020, which caused several infections. Aside from this event, the ongoing Rhenish carnival season facilitated the spread of the disease, since SARS-CoV2 circulated unnoticed during the week of the highly frequented 'crazy days' of the street carnival. During this period, the Rhineland is dominated by cultural festivities and street parades. These are characterised by close personal contact, collective consumption of food and alcoholic beverages, and cultural performances of local music and dance. As an integral part of regional cultural identities, the carnival festivities are attended by thousands of participants. Also, infections could be traced to other places, such as a childcare facility in which five infections were registered due to an infected kindergarten teacher. Already on 28 February 2020, four days after the initial reports, response measures were initiated by the district authorities, including bans on public events and closing public services like schools.

The unfortunate coincidence of the COVID-19 outbreak in Heinsberg district with the carnival festivities is arguably the most important reason for the rapid spread of COVID-19 there. Besides the initial super-spreading event on 15 February 2020, several others followed, causing a large number of infections. While Heinsberg

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

district itself was by far most dramatically hit by the outbreak, with 390 cases in Heinsberg in our sample attributed to local infections, several infections were registered in adjacent districts as well. But although about forty cases can be directly attributed to commuting patterns within the Rhineland metropolitan area, neither other Rhenish districts nor the Dutch districts close by were strikingly affected during our period of analysis and beyond, aside from neighbouring Aachen district.[5] Spatially contagious diffusion thus occurred only within Heinsberg district, especially accelerated through the open infection paths enabled through the festivities. In contrast, scaling to the regional level was avoided and infections in neighbouring districts were mostly limited to direct network ties to Heinsberg. The prompt measures initiated by the district authorities might, therefore, represent a relatively successful example of territorialising the outbreak. However, the Heinsberg outbreak caused at least 15 infections in regions far beyond the immediate vicinity, because visitors from other German districts caught infections while participating in carnival festivities (see Figure 3). Accounts of such relocation diffusion, also based on direct ties, were documented in other regions of North Rhine-Westphalia, as well as in districts of five other German states.

Numerous other infections can be traced to being present at a specific location at the same time with an individual carrying SARS-CoV2. A second, less prominent outbreak related to local super-spreading events occurred in Berlin. On Saturday 29 February 2020, an individual infected with COVID-19 spent some hours in a nightclub in Berlin's Mitte district as part of a group celebrating a birthday. This resulted in at least 53 infections (LAGeSo 2020), 17 of which are included in our dataset. Since Berlin had no reported cases of COVID-19 until 3 March 2020, it took about a week until the first infection was reported. From a spatial perspective, the incident led to a distribution of COVID-19 within Berlin and beyond. While the index patient was an inhabitant of Berlin Reinickendorf, the additional infections came from nine of Berlin's 12 districts. Only one instance of relocation diffusion was attributed to this incident with a visitor from Hamburg. Arguably, since this nightclub is one of the smaller ones in Berlin, the outbreak related to the incident, therefore, remained mostly on the regional scale. Similar dynamics, albeit with fewer infections, unfolded in two other nightclubs in Berlin's Mitte borough on 27 February 2020 and 27 March 2020 respectively. Probably because these incidents were recognised relatively quickly and happened at a time when the COVID-19 outbreak in Germany was already considered a major concern, an outbreak of the scale of Heinsberg was avoided in Berlin so that infection levels stayed around the German average.

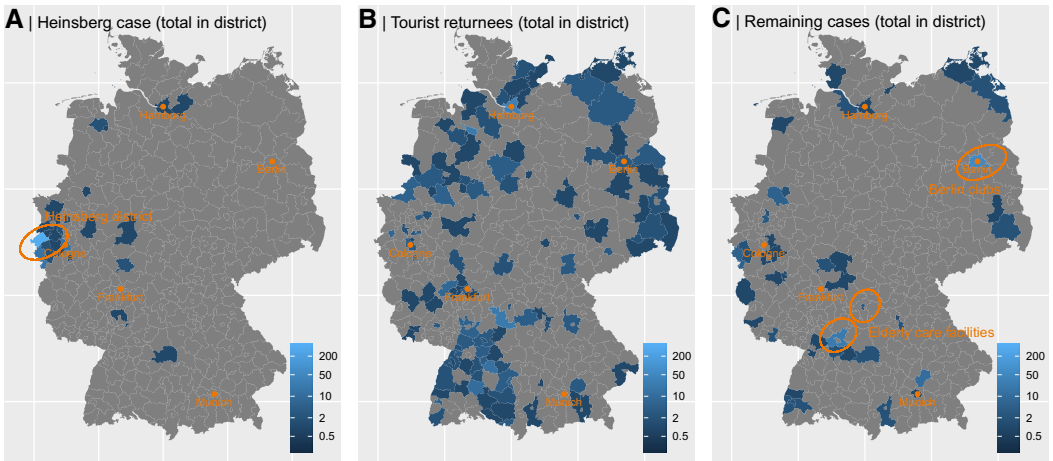


Figure 3. *Cases in German counties attributed to three patterns of epidemic spread. While the outbreak in Heinsberg district had mostly regional implications, widespread relocation distribution of COVID-19 can be connected to ski tourist retournees. [Colour figure can be viewed at wileyonlinelibrary.com]*

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

These two cases imply that the characteristics of places have high relevance for super-spreading events. Close personal contact on crowded dance floors and practices such as shouting, singing, and consuming beverages, create situations perfectly suited for respiratory transmission. In the case of Heinsberg district, characteristics of the place impact the transmission process both on a micro-level (crowded venues) and on a macro level (multiple festivities in the region). However, the spatial reach of the cases differs significantly: while the Berlin nightclub in question attracted a relatively small and mostly local audience, the carnival festivities in Heinsberg are an important element of social and cultural life in the region. Both a larger share of the population is involved in one of the carnival celebrations and participants are attracted from much farther away regarding the embodiment of infectious disease.[6]

Widespread relocation diffusion through tourist mobility – About a third of the COVID-19 cases in our sample reportedly 'imported' their infection while returning from touristic or business trips abroad. This pattern of wide-spread relocation diffusion emerged early, since already the third case in our sample was a returnee from Italy, tested positive for SARS-CoV2 in Göppingen district in the state of Baden-Würtemberg on 25 February 2020. Among the countries named as the site of infection, Italy dominated with 225 of the 320 returnee cases in our sample. Two other notable countries in the dataset were Austria with 46 and Iran with 14 infections among returnees, with 32 further infections related to eight other countries.

The dominance of Italy as a source for infections is not surprising since (Northern) Italy faced a drastic COVID-19 outbreak beginning in mid-February and is one of the most popular destinations for German tourists. Most infections of German tourists did not occur in the most affected Italian regions of Lombardia (14) and Veneto (2), but in Trentino-Alto Adige/Südtirol region (169), which is a major hotspot for ski tourism. A closer look reveals the overall relevance of ski tourism in this pattern: with 206 out of 320 returnee infections, ski tourists represent a clear majority. While for most returnee infections only the destination region could be tracked, we were able to narrow down several of these to specific touristic destinations, such as Ischgl (28) in Tyrol, Austria and Selva/Wolkenstein (16) in Trentino-Alto Adige/Südtirol region.

This implies that specific ski resorts were hotspots for the transmission of COVID-19 during late February and early March. Since ski tourism is concentrated on a relatively small number of resorts due to its reliance on infrastructures such as chairlifts or gondolas, these places are densely populated during the season and thus places with high potential of transmission. Furthermore, aside from winter sports activities, ski resorts based in touristic villages, such as those identified here, also offer nightlife amenities such as bars and parties. For the example of Ischgl, numerous infections occurring in the first two weeks of March were later traced to super-spreading events in a specific nightlife venue. From a network perspective, this pattern is interesting, because the disease transmission in relatively isolated ski resorts can resemble closed infection paths within the venue up until the moment when the tourists return home. Then, the network opens up, which implies a massive scaling potential.

In spatial terms, the impact of returnee infections is extremely widespread according to our sample. The 320 cases are scattered among 119 districts in all sixteen states (see Figure 3). The significant impact of returnee infections of ski tourists on the German COVID-19 outbreak is also pronounced by numbers published by RKI on 22 March 2020 – about 10 days after our period of analysis – when more than 20 per cent of infections were reported to originate in Austria (RKI 2020b). Although the spread of diseases through networks of tourist mobility is not a new phenomenon per se (Hall 2017), this seems to be a rather drastic example of relocation diffusion of infectious diseases through tourist mobility.

Several other, much smaller cases of relocation diffusion were caused by gatherings of specific communities: During the annual meeting of members of a religious community in late February, several infections occurred on 27 February 2020. The event with several hundred participants was held in a conference centre in

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

the city of Karlsruhe in Baden-Württemberg. Although a small number of infections occurred, inhabitants of four different districts in four German states were affected. In contrast, neither the index patient nor one of the infected individuals were from Karlsruhe, and no infections related to the event were reported by the city of Karlsruhe itself, where the site of transmission was located. A similar incident occurred when a participant from Northern Italy infected several other participants from three districts in three different German states during a scientific workshop in Munich on 20 February 2020.

These instances of relocation diffusion prove the relevance of network spaces for the development of the outbreak. They prove that outbreak processes in mobile network societies do not diffuse in the steady, horizontal manner of SCD. Instead, the pathogen can 'jump' in space over large distances. In the case of the religious conference, the population of the place of infection is not even affected directly. Instead, the characteristics of the place itself have limited relevance for the process of infection, while seemingly random patterns of spread (see Figure 3) can be explained through the embeddedness of individuals in far-reaching networks, in this case, ski-tourism. Diffusion via these networks can cause extreme scaling of the outbreak process, due to the reach of the network.

Local outbreaks in closed environments – A comparably rare but relevant feature of the outbreak process in Germany were local outbreaks in closed or rather semi-closed networks as the following two examples show: after an employee returned infected with COVID-19 from a tourist visit to Milan in late February, several infections emerged in an elderly care facility in Heilbronn district in the state of Baden-Württemberg. The 18 infections documented in our dataset include 13 patients and five employees of the facility, with two patients subsequently succumbing to the disease. Although the first infection was documented relatively quickly and measures were taken to limit the outbreak, further cases occurred over several days. A similar outbreak in an elderly care facility occurred in Würzburg, Bavaria, in the middle of March, resulting in 32 infections among the staff, 44 infected patients, and 16 casualties, while several other similar incidents were reported later. Unfortunately, this pattern was not limited to the early days of the outbreak, but reappeared multiple times later, even after access to care facilities had been restricted.

These cases imply individuals in dense and enclosed environments to be at risk of being 'trapped' within a closed or semi-closed network space, in which the pathogen spreads. After the pathogen has entered the network, it is transmitted further inside even after being detected since isolation is only a limited possibility in a closed community. While this process is especially dangerous for vulnerable individuals like residents of care facilities, it also applies to places with similar restrictions in terms of the limited possibility of evasion. A prominent example would be large ships, such as the several cruise liners featured in news reports. In any of these examples, the place, in which the transmission is contained structures the scaling of the outbreak. While this process is arguably similar to how the disease spreads in villages or dense city quarters, the characteristics of a closed environment heavily impact the outbreak.

DISCUSSION AND CONCLUSION

Through analysing the German outbreak of COVID-19 through the lens of the TPSN, we were able to identify three socio-spatial processes that played a relevant role in the diffusion of COVID-19 in Germany.

First, we found, somewhat surprising, relocation diffusion as extremely relevant based on tourist returnees, mostly from ski resorts. In contrast, hierarchical diffusion was completely absent, and spatially contagious diffusion was only relevant in the Heinsberg case in this stage of the outbreak, and even there only locally. This is surprising since it contradicts the general models of disease diffusion (Meade & Emch 2010) as well as the findings from the SARS epidemic in 2002 (Litaker *et al.* 2003). The far-reaching spatial 'jumping' was facilitated through individuals being

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

embedded in trans-local networks, including ski tourism, and others, as the example of the religious meeting shows. We consider this process a network-based scaling process, since embeddedness in the network structures the scaling process, while the place of infection is secondary.

Second, superspreading events in festival venues functioned as an accelerator for the outbreak. These events were decisive both for the local outbreaks in Heinsberg and Berlin and likely also for the proliferation of the pathogen within the ski resorts. Interestingly, we are not aware of superspreading events due to nosocomial infection during our study period, which was typical for both the SARS and MERS outbreaks (Lloyd-Smith *et al.* 2005, Cho *et al.* 2016). We consider superspreading events in festival venues to be place-based scaling processes because the characteristics of the place strongly affect the scale of transmission. Since these represent an example of extremely open infection paths, the network dimension is less relevant.

Third, outbreaks in closed environments such as care facilities are less relevant for the spatial diffusion, but an important feature of the geography of the outbreak process. Here, place-based networking occurs, because the place structures the shape of the infection network and due to the closed environment scaling is limited to its size. All three patterns underline how pathogen transmission is shaped by the inter-relatedness of place characteristics with relational dynamics.

To sum up, the three socio-spatial processes of networked-based scaling, place-based scaling, and place-based networking can explain much of the COVID-19 outbreak in Germany as found in our sample. However, these processes should not be looked at separately but as overlapping. While they were artificially separated for analytical reasons in this study, they must be thought of intertwined elements of the COVID-19 outbreak. This is especially evident in the example of ski tourist returnees. In this case, COVID-19 was able to circulate within the ski resorts through local superspreading events during nighttime activities or other situations of close personal contact and then diffused through their network when they returned home. This example shows, how the pathogen travels with existing socio-spatial processes such as tourism as a 'blind passenger'. The patterns of diffusion are thus not random but depend on which network is affected. However, the networks through which these instances of relocation diffusion occur need to be characterised through temporal co-presence of their members, during which the pathogen can be transmitted. Therefore, we assume that the spread of epidemic space of infectious diseases such as COVID-19 is determined by the interaction between several social-spatial processes.

The rapid speed of the outbreak undermines most efforts to contain the outbreak through territorialising. However, locally occurring spatially contagious diffusion can be curbed through territorialising, as the Heinsberg example shows. From a process perspective, we can subsume that the effects of territorialising seem both more relevant upstream (previously established conditions like the health system) and downstream (public health measures like isolation) from the period of rapid proliferation analysed here. In hindsight, it seems possible that the outbreak in Germany was less deadly than in other countries not because of successful territorialising on the national level, as the large share of infections 'imported' from ski resorts suggests. Instead, the uncommon diffusion pattern and the luck of most super-spreading events occurring relatively late in the outbreak helped. In the light of the processes analysed here, the rationale of measures targeting specific places, such as closing certain types of venues or targeting networks such as social distancing seems to be far more sensible compared to measures purely targeting territories, such as closing borders.

Looking forward and despite these insights, several issues remain open at this early stage of investigating the global COVID-19. Especially the interconnectedness of the peripheries proves for us, that disease outbreaks in contemporary societies do not follow simple or repetitive patterns. Therefore, a balanced geographical analysis is valuable to understand these processes. Undoubtedly, the nexus of topological diffusion of epidemic outbreaks will need further analysis, conducted hopefully under less concerning circumstances.

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

Acknowledgements

We would like to thank the editor, two anonymous reviewers for their rapid and very helpful remarks as well as our colleagues Lukas Vogelgsang, Verena Brinks and Oliver Ibert for their support while drafting the manuscript.

Notes

1. Description is based on a dataset obtained by RKI on 10 April.
2. Numbers are based on the ongoing investigation of RKI (Schilling 2020) and are often updated retrospectively, which explains the different dimensions.
3. Since in the German federal system the local district authorities (*Kreise/ Kreisfreie Städte*) are responsible for civil protection, they were the dominant source of information.
4. For the document analysis we relied on public sources only. Since these were often very explicit about personal details, we tried to anonymise the information where necessary by not naming specific venues.
5. Data published in late April suggest that in fact not even all of Heinsberg district was affected disproportionately, but just four out of ten municipalities had very high infection rates.
6. While highly susceptible to the spread of COVID-19, this process is not limited to nightlife activities. For example, in Hohenlohe district, a regional outbreak similar to that in Heinsberg but several weeks later, was attributed to a local choir in a village church.

REFERENCES

Ali, S.H. & R. Keil (2008), *Networked Disease: Emerging Infections in the Global City*. Chichester: John Wiley & Sons.

Andersen, K.G., A. Rambaut, W.I. Lipkin, E.C. Holmes & R.F. Garry (2020), The Proximal Origin of SARS-CoV-2. *Nature Medicine*, 26(4), 1–3.

Bian, L. (2004), A Conceptual Framework for an Individual-based Spatially Explicit Epidemiological Model. *Environment and Planning B: Planning and Design* 3, pp. 381–395.

Bian, L. & D. Liebner (2007), A Network Model for Dispersion of Communicable dDiseases. *Transactions in GIS* 2, pp. 155–173.

Bowen, J.T. Jr & C. Laroe (2006), Airline Networks and the International Diffusion of Severe Acute Respiratory Syndrome (SARS). *Geographical Journal* 2, pp. 130–144.

Brinks, V.& O. Ibert (2020), Zur Räumlichkeit von Krisen: Relationalität. Territorialität, Skalarität und Topologien. *In*: F. Bösch, N. Deitelhoff & S. Kroll, eds., *Handbuch Krisenforschung*, pp. 41–57. Wiesbaden: Springer.

Casey, E.S. (2008), Comments on 'Theorising Sociospatial Relations'. *Environment and Planning D: Society and Space* 3, pp. 402–404.

Castells, M. (1996), *The Information Age*. Oxford: Blackwell Publishers.

Chan, T.-C. & C.-C. King (2011), Surveillance and Epidemiology of Infectious Diseases using Spatial and Temporal Clustering Methods. *In*: C. Castillo-Chavez, H. Chen, W.B. Lober, M. Thurmond & D. Zeng, eds. *Infectious Disease Informatics and Biosurveillance*, pp. 207–234. Boston, MA: Springer US.

Cho, S.Y., J.-M. Kang, Y.E. Ha, G.E. Park, J.Y. Lee, J.-H. Ko, J.Y. Lee, J.M. Kim, C.-I. Kang, I.J. Jo, J.G. Ryu, J.R. Choi, S. Kim, H.J. Huh, C.-S. Ki, E.-S. Kang, K.R. Peck, H.-J. Dhong, J.-H. Song, D.R. Chung & Y.-J. Kim (2016), MERS-CoV Outbreak following a Single Patient Exposure in an Emergency room in South Korea: An Epidemiological Outbreak Study. *The Lancet* 388, pp. 994–1001.

Cui, J., F. Li & Z.L. Shi (2019), Origin and Evolution of Pathogenic Coronaviruses. *Nature Reviews Microbiology*, 17, 181–192.

Cummins, S., S. Curtis, A.V. Diez-Roux & S. Macintyre (2007), Understanding and Representing 'Place'in Health Research: A Relational Approach. *Social Science & Medicine* 9, pp. 1825–1838.

Dong, E., H. Du & L. Gardener (2020), An Interactive Web-based Dashboard to Track COVID-19 in Real Time. *The Lancet Infectious Diseases*, 20(5), 19–20.

Elden, S. (2010), Land, Terrain, Territory. *Progress in Human Geography* 6, pp. 799–817.

Fidler, D.P. (2003), SARS: Political Pathology of the First Post-Westphalian Pathogen. *The Journal of Law, Medicine & Ethics* 4, pp. 485–505.

Gailing, L., Bues, A., Kern K., & A. Röhring (2019) Socio-spatial dimensions in energy transitions: Applying the TPSN framework to case studies in Germany. *Environment and Planning A: Economy and Space*. http://doi.org/10.1177/0308518x19845142.

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

Hall, M. (2017), Tourism, Ddisease and Global Environmental Change: The Fourth Transition? *In*: S. Gössling & M. Hall, eds., *Tourism and Global Environmental Change*, pp. 159–180. Abingdon: Routledge.

Jessop, B. (2018), The TPSN Schema: Moving beyond Territories and Regions. *In*: A. Paasi, J. Harrison & M. Jones, eds., *Handbook on the Geographies of Regions and Territories*, pp. 89–101. Cheltenham: Edward Elgar Publishing.

Jessop, B., N. Brenner & M. Jones (2008), Theorising Sociospatial Relations. *Environment and Planning D: Society and Space* 3, pp. 389–401.

Keeler, C. & M. Emch (2018), Infectious-disease Geography: Disease Outbreaks and Outcomes through the Lens of space and place. *In*. Crooks, V.A., Andrews, G.J. & Pearce, J., eds., *Routledge Handbook of Health Geography*, pp. 67–73. London & New York: Routledge.

Koopman, J.S. (2005), Infection Transmission Science and Models. *Japanese Journal of Infectious Diseases* 6, pp. 3–8.

Kwan, M.-P. & J. Lee (2004), Geovisualisation of Human Activity Patterns using 3D GIS: A Time-geographic Approach. Spatially Integrated. *Social Science* pp. 721–744.

Kwan, M.-P., A.T. Murray, M.E. O'Kelly & M. Tiefelsdorf (2003), Recent Advances in Accessibility Research: Representation, Methodology and Applications. *Journal of Geographical Systems* 1, pp. 129–138.

LAGeSo & (2020), *EPI-Info Wochenübersicht Meldewoche 11/2020*. Landesamt für Gesundheit und Soziales Berlin. https://www.berlin.de/lageso/_assets/gesundheit/publikationen/wochenberichte-2020/ewu_11-2020-publ.pdf. Accessed on 22 April 2020.

Lee, K. (2019), Epidemiology is ecosystem science. *Synthese*, 1–29. http://doi.org/10.1007/s11229-019-02129-5

Lipsitch, M., T. Cohen, B. Cooper, J.M. Robins, S. Ma, L. James, G. Gopalakrishna, S.K. Chew, C.C. Tan & M.H. Samore (2003), Transmission Dynamics and Control of Severe Acute Respiratory Syndrome. *Science* 5627, pp. 1966–1970.

Litaker, J.R., J.Y. Chou, S. Novak & J.P. Wilson (2003), Implications of SARS: Medical Geography and Surveillance in Disease Detection. *Annals of Pharmacotherapy* 37, pp. 1841–1848.

Lloyd-Smith, J.O., S.J. Schreiber, P.E. Kopp & W.M. Getz (2005), Superspreading and the Effect of Individual Variation on Disease Emergence. *Nature*, 438, 355–359.

Massey, D. (2007), Politik und Raum/Zeit. *In*: B. Belina & B. Michel, eds., *Raumproductionen: Beiträge der Radical Geography: Eine Zwischenbilanz*, pp. 111–133. Münster: Westfälisches Dampfboot.

Mckinney, K.R., Y.Y. Gong & T.G. Lewis (2006), Environmental Transmission of SARS at Amoy Gardens. *Journal of Environmental Health* 68, pp. 26–30.

Meade, M.S. (1977), Medical Geography as Human Ecology: The Dimension of Population Movement. *Geographical Review* 4, pp. 379–393.

Meade, M. & M. Emch (2010), *Medical Geography*. New York: The Guilford Press.

Paasi, A. & J. Metzger (2017), Foregrounding the Region. *Regional Studies* 1, pp. 19–30.

Park, S. Y., Y.-M. Kim, S. Yi, S. Lee, B.-J. Na, C.B. Kim, J. Kim, H.S. Kim, Y.B. Kim, Y. Park, I.S. Huh, H.K. Kim, H.J. Yoon, H. Jang, K. Kim, Y. Chang, I. Kim, H. Lee, J. Gwack, S.S. Kim, M. Kim, S. Kweon, Y.J. Choe, O. Park, Y.J. Park & E.K. Jeong (2020), Coronavirus Disease Outbreak in Call Centre, South Korea. *Emerging Infectious Diseases* 26. https://doi.org/10.3201/eid2608.201274

Rescher, N. (2007), The Promise of Process Philosophy. *In*: C. Boundas, ed., *The Edinburgh Companion to Twentieth-Century Philosophies*, pp. 143–155. Edinburgh: Edinburgh University Press.

RKI (2020a), Täglicher Lagebericht des RKI zur Coronavirus-Krankheit-2019 (COVID-19) 05.03.2020. RKI Berlin. https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/Situationsberichte/2020-03-05-de.pdf?__blob=publicationFile. Accessed on 22 April 2020.

RKI (2020b), Täglicher Lagebericht des RKI zur Coronavirus-Krankheit-2019 (COVID-19) 22.03.2020. RKI Berlin. https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/Situationsberichte/2020-03-22-de.pdf?__blob=publicationFile. Accessed on 22 April 2020.

Schilling, J., M. Diercke, D. Altmann, W. Haas & S. Buda (2020), Vorläufige Bewertung der Krankheitsschwere von COVID-19 in Deutschland Basierend auf Übermittelten Fällen Gemäß Infektionsschtuzgesetz. *Epidemologisches Bulletin* 17, pp. 1–9.

Sack, R.D. (1983), Human Territoriality: A Theory. *Annals of the Association of American Geographers* 1, pp. 55–74.

Shannon, G.W. & J. Willoughby (2004), Severe Acute Respiratory Syndrome (SARS) in Asia:

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig

A Medical Geographic Perspective. *Eurasian Geography and Economics* 5, pp. 359–381.

Stein, R.A. (2011), Super-spreaders in Infectious Diseases. *International Journal of Infectious Diseases* 8, pp. 510–513.

Tan, S. (2016), *Space and Environment in the Industrialising Mekong Delta*. Münster: LIT Verlag.

van Wagner, E. (2008), Toward a Dialectical Understanding of Networked Disease in the Global City: Vulnerability, Connectivity, Topologies. *In*: S.H. Ali & R. Keil, eds., *Networked Disease: Emerging Infections in the Global City*. Oxford: Blackwell Publishing, pp. 13–26.

van Loon, J. (2005), Epidemic Space. *Critical Public Health* 1, pp. 39–52.

WHO (2020), Coronavirus disease 2019 (COVID-19) Situation Report - 90. https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200419-sitrep-90-covid-19.pdf?sfvrsn=551d47fd_4. Accessed on 22 April 2020.

Wilder-Smith, A., Chiew, C. J., & V. J. Lee (2020) Can we contain the COVID-19 outbreak with the same measures as for SARS? *The Lancet Infectious Diseases*, 20 (5), 102–107. http://doi.org/10.1016/s1473-3099(20)30129-8.

Wolf, M. (2016), Rethinking Urban Epidemiology: Natures, Networks and Materialities. *International Journal of Urban and Regional Research* 5, pp. 958–982.

Woolhouse, M.E., C. Dye, J.-F. Etard, T. Smith, J. Charlwood, G. Garnett, P. Hagan, J. Hii, P. Ndhlovu & R. Quinnell (1997), Heterogeneities in the Transmission of Infectious Agents: Implications for the Design of Control Programs. *Proceedings of the National Academy of Sciences* 1, pp. 338–342.

Yu, I.T., Y. Li, T.W. Wong, W. Tam, A.T. Chan, J.H. Lee, D.Y. Leung & T. Ho (2004), Evidence of Airborne Transmission of the Severe Acute Respiratory Syndrome Virus. *New England Journal of Medicine* 17, pp. 1731–1739.

© 2020 The Authors. Tijdschrift voor Economische en Sociale Geografie published by John Wiley & Sons Ltd on behalf of Royal Dutch Geographical Society / Koninklijk Nederlands Aardrijkskundig