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An Emerging Infectious Disease Perspective, Inter Alia

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By Raad Fadaak

As the saying goes, ‘there are no good models, only useful ones’. Tell a disease modeler that, and they might shake their head, interrupting to correct you – “only elegant ones”. And Hufnagel et al’s (2004) influential disease simulation, now ten years old, is quite elegant indeed. Published following the emergence and spread of severe acute respiratory syndrome (SARS) in 2003, their mathematical model uses SARS as a prototypical disease, deploying “almost the entire civil aviation network...[to] focus on the mechanisms of the worldwide spread of infectious diseases” (15124). The simulation—unusual for its emphasis on the spatial rather than temporal dimension of disease transmission—generated a remarkably verisimilar scenario to the actual SARS epidemic.

For this reason, Hufnagel and colleagues conclude that “in a globalized world, with millions of passengers traveling around the world...infectious diseases may spread rapidly around the world” (15128). In this, the study has persisted as a cornerstone of the narrative of dangers and drivers of disease emergence, linking “threats anywhere” to “threats everywhere” (Sebelius 2014). Of course, modelers have been some of the first epidemiologists to explode the taken-for-granted connection between ‘anywhere’ and ‘everywhere’, revealing the kinds of topographical complexity in coming to grips with ‘global flows’. Hufnagel’s model, for instance, has spawned a number of more recent influential disease modeling “packages”—bundled algorithms and equations that simulate human and pathogenic mobility—such as the ‘Global Epidemic and Mobility’ platform (Balcan et al. 2010), most recently used to estimate the likelihood of Ebola’s international spread (Gomes et al. 2014).^[1] All of these authors recognize, to quote the modelers directly, that “human mobility represents a crucial challenge both on the theoretical side and in view of the limited availability of empirical data” (Balcan et al. 2009: 21484). The following reflections do not propose a solution to the problems of human, animal, or disease mobility, but rather take up this ‘crucial challenge’ in order to illustrate just how complex it has become amidst these intersections.

Not many outside of the modeling world remember Hufnagel’s hard wrought calculus. Instead, it is their colorful graphics that survive most

intact. The aviation density map is ubiquitously republished, taking on a curiously mobile life of its own (see e.g. Howard 2012). It has become a convincing chart for the argument that increased travel is both a ‘driver’ and a ‘threat’ of emerging infectious diseases (EIDs). Stephen Morse, the founder of this ‘emerging disease’ discourse, originally called this globalized disease dissemination “microbial traffic” (Morse 1995: 9). If Morse originally labeled the idea, it was Hufnagel and others who, after SARS, insisted that it was “impossible to think about infectious disease as a local or contained problem” (van Wagner 2008: 19). It seems it was not just microbial traffic, but indeed gridlocked rush hour.

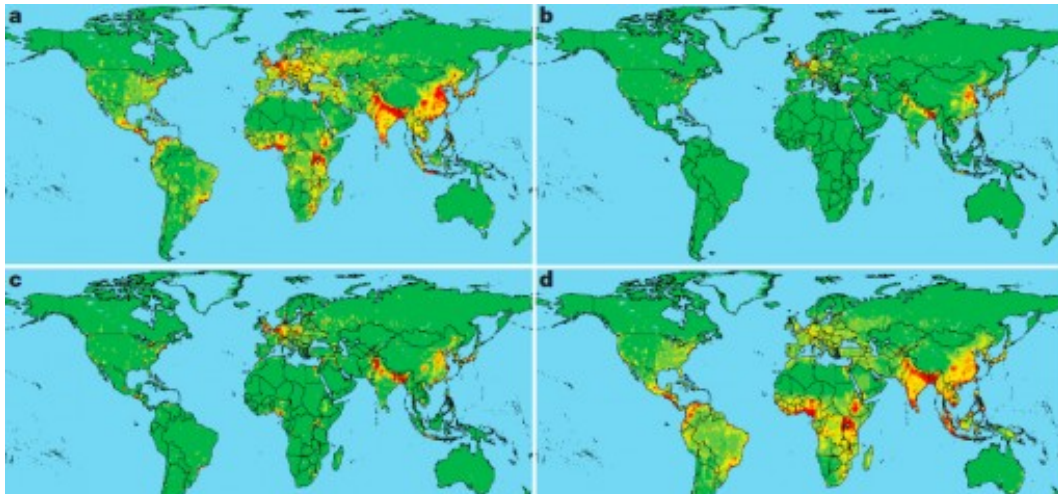


Figure 1: Global aviation network. A geographical representation of the 5000 civil aviation traffic among the 500 largest international airports, from Hufnagel et al (2004).

Of course, it has not just been disease modelers and epidemiologists who have labored over these issues of infectious connectivity; social scientists have also been taking up the problematic in unique ways. Medical geographers, anthropologists, and sociologists have astutely warned about the “slippery geographies” opened up by new and existing connections between “bodies, ecologies, and geopolitical realities” (Del Casino Jr et al. 2014: 546). But look at the map closely—note the clustering, the unevenly distributed density of mobilities. Rather than homogenous, flattened global connectivity (where a ‘threat anywhere is a threat everywhere’), we see that certain “alternative orderings might emerge when patterns of health and disease are considered” (Ali and Keil

2008: 19).

And indeed, these ‘orderings’ reveal themselves, at least in these chic graphical depictions, as divided among two particular axes, which I believe worth exploring. To do so, I have to superimpose another map onto Hufnagel’s. In 2008, Jones et al. published a seminal article that detailed some of the “global trends” in emerging infectious diseases, arguing that a constellation of “socio-economic, environmental and ecological factors” particularly favor EID appearance; they call these “emerging disease ‘hotspots’” (990).^[2] The ‘hotspots’ are largely rural, agricultural regions, and – in most cases – precisely do *not* overlap with Hufnagel’s map, which overrepresents a selection of hyper- or emerging “global cities”. What I am pointing out is fairly obvious: that these discourses are primarily articulated with reference to two counterpoints — ‘emergence’ is a *rural* (or *rural-to-urban*) issue, and ‘spread’ or ‘transmission’ is primarily an *urban* (or *urban-to-urban*) one.



“Global Distribution of Relative Risk of EID Event”, upper left quadrant (a) shows relative risk from zoonotic transmission from animals. Reprinted from Jones et al (2008).

On a case-to-case basis, it doesn’t work out quite as neatly as the truisms suggest. In the 2004 outbreak of Nipah encephalitis in Bangladesh, for instance, the disease emerged originally in the moderately populous district of Faridpur, and then spread, through the close ties made by trade, family, and fruit bats, to surrounding satellite villages (Stone 2011; Blum et al. 2009). Perhaps one might push the emergence argument further back to the disease’s ‘source’—that famous index farm in Malaysia where ‘the wrong bat met the wrong pig’.^[3] Yet, nobody knows exactly where these

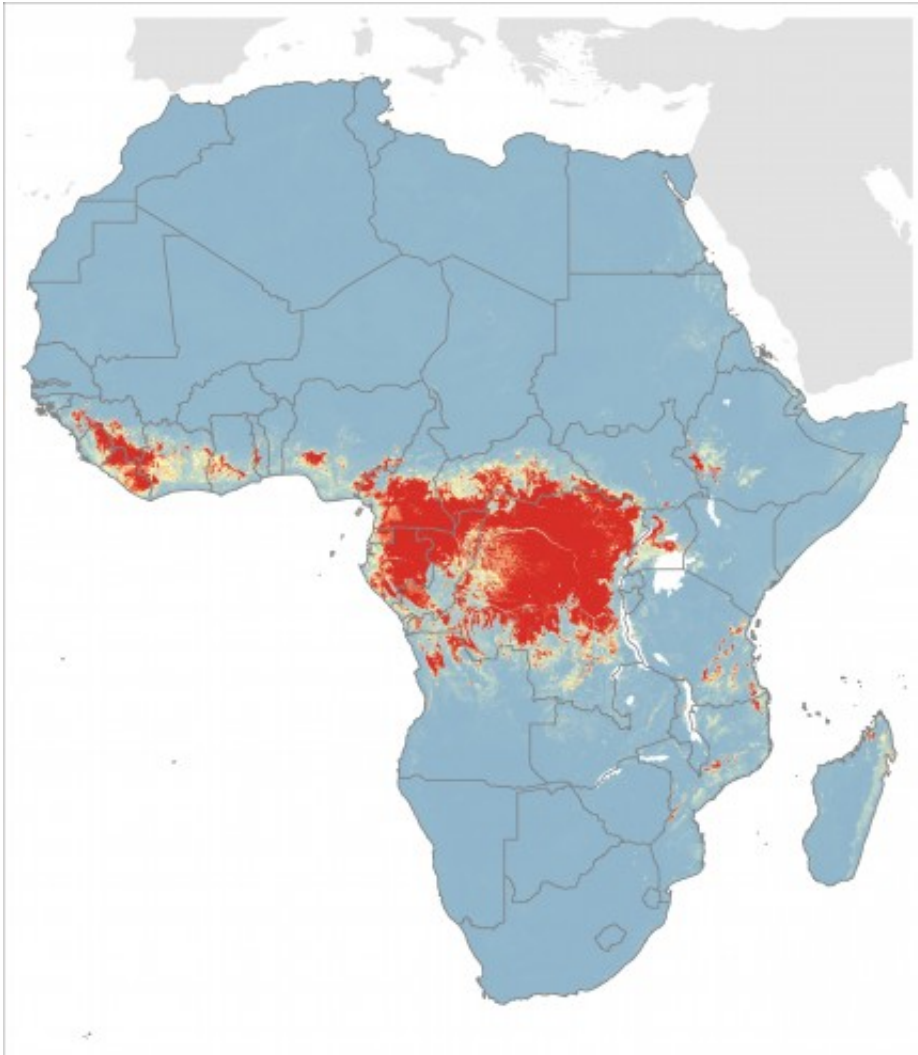
migratory carrier bats, “flying foxes”, that transferred it to the pigs—call “home”. They seem to ‘range’ across quite a large area in southeast Asia.

And, I might add, only very rarely do we see such detailed aviation networks for animals like the *Pteropus vampyrus* (notable exceptions include Epstein et al. 2009; Gilbert et al. 2011).^[4] Recent events have prompted an intersection of multispecies geographies, using demographic and migration data in intriguing new ways. The ongoing Ebola outbreak has reaffirmed and reinvigorated the popularity of geospatial mapping as a tool to visualize risk for both primary (animal-to-human) and secondary (human-to-human) transmission, i.e., using both Hufnagel-style aviation networks and Jones-style zoonotic ‘hotspots’. There has been a torrent of analyses that have emerged using reservoir mapping (e.g. fruit bats and chimpanzees) and population mobility measures to generate more precise ‘hotspot’ maps than those seen in Jones’ study. The work, nevertheless, remains largely confined to the ecologists and the modeling community, who must use ‘low resolution’ census data and satellite imagery to calculate rural settlement structures, population densities, and human-animal mobility patterns (Piggott et al. 2014; Linard et al. 2012).

Take another example: live-animal (so-called ‘wet’) markets, which are presumed to be both source and amplifier of zoonotic disease (Webster 2004; Woo, Lau, and Yuen 2006). Evidence has indeed shown them to have played a central role in the SARS outbreak in China in 2002 and 2003 (Peiris and Guan 2004). Although one might assume these to be rather direct conduits from rural-urban, the rise of supermarkets, food processors, and changes in food supply chains suggest a more complex, evolving story of production, consumption, and distribution linkages (Chowdhury et al. 2005). Indeed, such food-market integration has been more of an ideal (‘farm-to-fork’) than an obvious reality in many places, and the material and symbolic linkages, when closely examined, often extend beyond simply ‘rural-urban’, involving intermediate cities and market towns along the way (Songster et al. 2006). Recent ethnographic work on health and biosecurity interventions in the poultry domain, particularly in Indonesia in the middle 2000s following the H5N1 outbreaks, illustrate some of the profoundly complicated networks, associations, and transfers happening here (Hinchliffe forthcoming; Forster 2012). At the very least, we can complicate the ‘urban-rural’ divide, or at least add a few more transitory linkages in the chain.

Although we know quite well that SARS’ global mobility patterns followed Hufnagel’s map quite closely (albeit somewhat unpredictably), its emergence seems to ‘thicken’ the story—moving us in spaces between urban-rural, human-animal, animal-animal (i.e., civets to bats; domestic poultry to wild birds), and of course, ‘local-global’. The congeries of avian

flyways and aviation byways mean that morbidity and mortality implicate mobility in ways we are just beginning to understand.



Map of Ebola niche ‘hotspots’ following the 2014 outbreak. Areas where Ebola virus infection in animals is likely (color scale ranging from red for most likely, through yellow to blue for least likely). Reproduced from Piggott et al. 2014, under Creative Commons License

In that sense, *hotspots* should help us draw new kinds of maps and associations, maybe ones closer to an expansive ecological imaginary. Hannah Brown and Anne Kelly (2014) have recently and persuasively argued for just such a perspective, one that accounts for temporary and enduring “convergence[s] of rainfall, political designs, [animal] populations, armed conflict, economic strategies, agricultural techniques, built environments, and practices of care that create the conditions for disease communicability” (281). Adding this litany of things together into our perspectives means that the object of our preoccupations—“flows”, “mobilities”, “travel”—gets rather viscous. It is an infectious disease

perspective, quite literally *inter alia*—one as much about context as contact.

Such an understanding, undoubtedly, should not be a singular burden on the spatial ecologists, disease modelers, or geographers. Those social scientists I mentioned earlier have, for some time now, also been pushing for something along these lines. This would include expanding work on tracing contact and community networks, and causal or contextualizing assemblages of behavior (Janes et al. 2012). Dr. S. Harris Ali and Roger Keil, both professors in the Faculty of Environment at York University, ask us to “conceptualize infectious disease as a phenomenon arising from the convergence of various social and material processes that are linked together in rather nuanced, complicated, and unanticipated ways” (Ali and Keil 2008: 230). But I think the effort should go further. As Alex Nading’s recent work (2011; 2014) has shown, these intimate, ‘unexpected’ ecologies often produce new forms of citizenship, new forms of knowledge production, and disputes over what should make up the ecological space and its connections—in short, what he terms an “ethics of connectivity” (2011: 17). In this manner, a focus on *hotspots*—beyond an exercise in detailed ethnographic landscape painting—might take up ‘connectivity’ as the subject and object of anthropological inquiry. It should indeed remain a possibility to think of infectious disease as a ‘local’ problem, if by that we mean locating concrete problematizations, configurations, and connectivities of animals, people, pathogens, and politics (see e.g. Collier and Lakoff 2008; Hinchliffe 2014; Caduff 2014).

Thus, on the one hand, unraveling the complexities of these ‘trading zones’ of humans, animals, and diseases remains a critical task, one to be shared in collaborative research. It is perhaps one way to encourage continued interdisciplinary study into the “complex adaptive systems” that drive disease emergence (Janes et al. 2012; see also Wood et al. 2012). On the other hand, reflecting on what kind of knowledge this produces, how it circulates, and which connections matter might be a unique opportunity for anthropological contribution.

In any case, alongside epidemiologists, veterinarians, public health officials, and conservationists, nobody has quite figured out what this kind of collaborative conceptual-practical work will look like in the near future. Or even how to make sense of the “fluid, irregular shapes of these landscapes” today, particularly given the dramatic and acute nature of some of these epidemic events and their ability to fundamentally and rapidly *alter* existing topographies and temporalities (Appadurai 1996: 33; Lynteris 2014). This is especially true with the unprecedented challenges faced by the tragic and worsening Ebola outbreak, which should teach us that practical, conceptual, or technical shortcuts have no place in global health work.

* * *

The challenge then, one I feel most pressing for the work at the forefront of the research on emerging diseases—both epidemic and epizootic—is to “better imagine how different types of viruses, bodies, built and natural ecologies, and geopolitical realities interact to produce the present landscape of infectious disease” (Del Casino Jr et al. 2014: 546). It seems that this has been forefront on the minds of disease ecologists for some time now (see e.g. Aguirre et al. 2002; Aguirre et al. 2012). SARS may have indeed been the first “post-Westphalian” disease event for the 21st century, but nobody could have guessed that we would still be grappling with claims to ‘viral sovereignty’ or the controlled (re)patriation of Ebola patients to North America and Europe (Fidler 2004; Holbrooke and Garrett 2008). Movement, again, occurs in many directions simultaneously—and that goes for time as well as space. Hufnagel and the other spatial ecologists know that as well as anyone.

The task, then, is also to shake up the truism that ‘diseases know no borders’, which today might be—at the very least—worth closer examination. Rather than minimize the threats faced by the spread of EIDs, I hope we can more accurately and more honestly complicate them, in order to reflect better the intricacies of the multidimensional, intergovernmental, multisectoral challenges of sovereignty and accountability in today’s world of global health security and governance (Frenk and Moon 2013).

In West Africa, the damage has already been done. We will be picking up the pieces, and picking out the lessons, for years to come. And, as those working at the frontlines and in the policy offices might say, there are indeed no good solutions. Let’s hope however, that in the meantime we are able to find some elegant ones.

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[1] The Global Epidemic and Mobility Model, note Gomes et al. (2014), “is a spatial, stochastic and individual based epidemic model, in which the world is divided into geographical regions defining a subpopulation network, where connections among subpopulations represent population traffic flows due to transportation and mobility infrastructures” (11).

[2] The article was influential in providing evidentiary support for programs like USAID’s PREDICT, a ‘virus hunting’ program at hotspot sites throughout SE Asia and Africa. The second iteration of this program is currently in the process of approval and operationalization by USAID and its partners.

[3] The allusion here is to the language used by the EIS officer played by Kate Winslet in the 2011 film, *Contagion*.

[4] This is not to neglect the abundance of geospatial analyses of aviation networks and flyways that were published amidst and following the outbreaks of H5N1 avian influenza throughout the 2000s.

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