correspondence

The neglected geography of human pathogens and diseases

To the Editor — As highlighted in the Feature article 'Predicting zoonoses' in the April issue of *Nature Ecology & Evolution*[1], the emergence of new viruses presents many challenges to humanity, including predicting outbreaks of diseases we don't even know about yet. The featured PREDICT[1] project is a welcome step forward with regards to finding the world's unknown viruses. Yet, amidst the focus on newly emerging diseases such as Zika and avian influenza, an even more consequential, albeit less headline-grabbing, challenge is being missed: we know little about the geographical distribution of the vast majority of 'older' human pathogens that collectively kill millions of people each year, much less how such distributions will change given global changes in climate, land-use and economy.

Science and human society are capable of documenting the distribution of species in great detail. For birds and mammals, we know not only the global distributions of each species at relatively fine spatial resolutions[2], but often their relative abundances[3] and genetic diversity[4] as well. When it comes to the distribution of the species that live in or on us, we know far less.

The impact of the diseases caused by human pathogens has a highly uneven geographic distribution. The majority of the ~9.6 million deaths per year due to infectious diseases[5] are in the tropical regions of the world, as are most cases of parasitism, for example, due to worms and protists. Yet, despite the critical global health and economic implications of pathogens and their geography, only a handful have been explored in sufficient detail to allow insights into the global determinants and constraints of their distributions. In fact, less than 5% of the 355 clinically important human infectious diseases have been mapped reliably at a global scale[6], and studies of human disease biogeography have been at very coarse spatial grains[7,8].

Our point is illustrated by comparison of the spatial grain of the data used to map the global patterns of bird richness[9] (Fig. 1a) with maps of potential human pathogen richness based on the most-comprehensive, published global data currently available[10] (Fig. 1b,c).
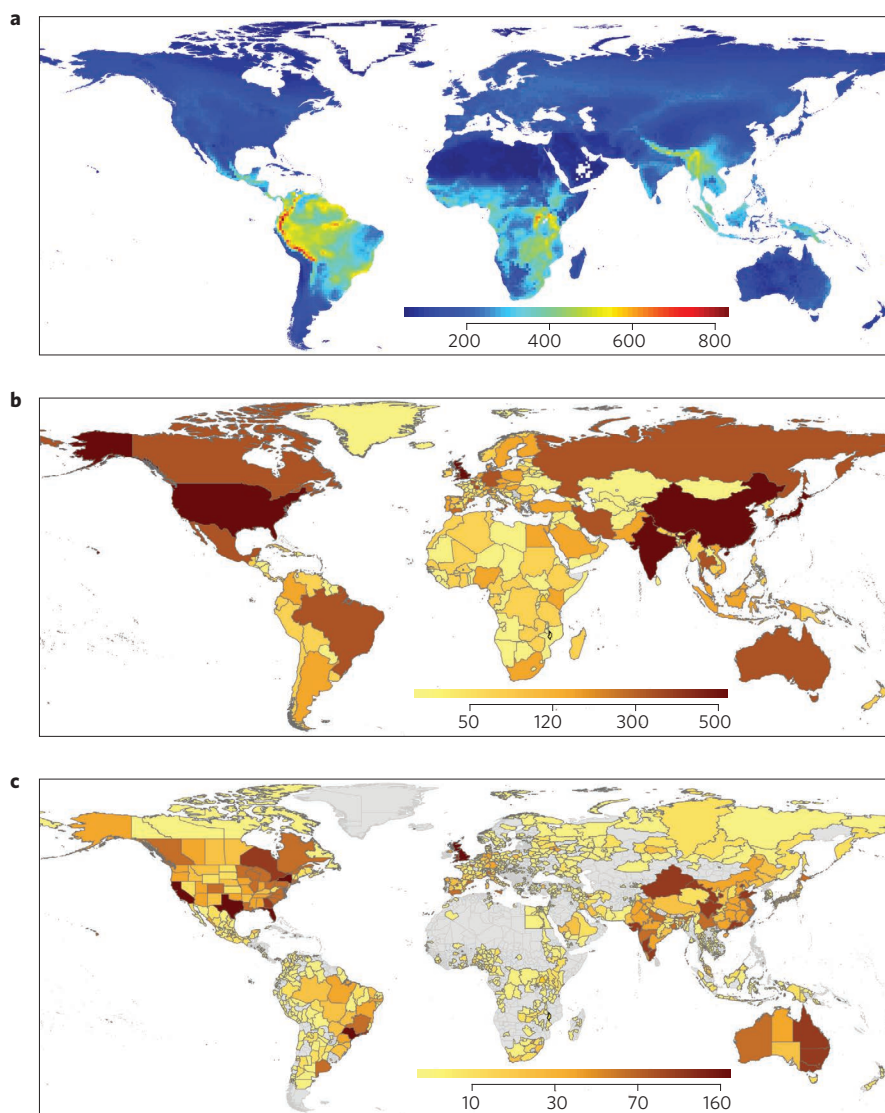
Figure 1 | Comparison of the available global data on the distribution of free-living bird and potential human pathogen species richness. **a**, Avian species richness (10,361 species) at one-degree gridded resolution[9]. **b,c**, Richness of potential human pathogens (1,611 'species' of viruses, bacteria, fungi, protozoa and helminths associated with humans) at national (**b**) and sub-national scales (**c**) for the regions in which such data are available (**b** and **c** are based on data extracted from ref. [10]). Publ. note: Springer Nature is neutral about jurisdictional claims in maps.

The good news is that ongoing initiatives have laid down successful paths to rigorous data-mining and development of high-quality open access databases and associated distribution maps of some of the worst infectious diseases, such as malaria[11] and the most-common helminth infections[12,13]. Furthermore, recent advances in bioinformatics tools have facilitated the association of geographic names

or coordinates with publicly available genetic sequences at a massive scale[4,10], and hold great potential to scale-up the extraction of fine-scale geographically referenced data from existing resources. High-resolution global data are possible for human pathogens. Such data may not be as newsworthy as those related to novel viruses, but they are necessary to understand what drives human pathogen diversity, transmission and emergence. Just as with the discovery of new pathogens, the study of old pathogens does not face intrinsic barriers, but instead simply barriers of the old-fashioned kind: money, time and collective will. ❒

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