



Commuter Pathways and Epidemic Disease: A Brief Report

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Abstract

This brief report describes the potential utility of federally collected, commuter survey data to an understanding of disease propagation at varying scales. It argues this data provides a unique resource for identifying, and then quantifying, the potential for bacterial or viral passage in a city and more importantly between cities. Its focus extends the work of others on air travel and primarily international disease diffusion to finer scales of address of potential concern to local and regional public health officials and researchers. In one sentence: A consideration of commuter data promises a better way to both predict disease incidence at various scales and to effectively promote programs for its concern.

Keywords: Commuter pathways; Diffusion; Epidemiology; Public health; Viral diffusion

Introduction

From the fourteenth century introduction of quarantine protocols during plague episodes [1] to the mapped progress of cholera in the 1830's, public health experts have long recognized that infectious diseases are spread by human travel patterns. While much of this work traditionally focused on international pathways it has included the disease diffusion at the national level [2]. In recent years, the revolution in digital information has provided an unprecedented wealth of data potentially applicable to the means by which human trade and travel act as engines of infectious promotion. Khan and associates, for example, innovatively used international airline passenger data to describe the rapid global diffusion of H5N1 influenza in 2009 [3] and later, of other diseases including Chikungunya from the Caribbean to other American nations [4]. Here we introduce a US database of commuter travel as a resource that describes potential pathways of disease promotion at national, regional and local levels. This brief report presents the database and its organization in a format permitting both cartographic and statistical analysis. It then suggests its potential utility to epidemiologists and public health officials at local and regional as well as national scales of concern. A fuller description of its applicability is reserved for later and longer presentations. In the interim, we hope this brief statement will interest other researchers in its potential.

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Methods

The United States Census Bureau's American Community Survey (ACS) annually surveys more than 143 million citizens living at 3.5 million addresses, asking where each worked "last week" [5]. Respondent data is available in one, three or five year collections in which 4,156,426 vectors, each joining one origin and one destination, are documented between respondents living in 74,002 U.S. census tracts. Each vector documents origin-destination (o-d) data for one or more residents with the same commuting profile. The sheer size of the database will strain even the most powerful of contemporary desk top computers. Recently, however, researchers have translated the raw ACS dataset into a more flexible, spatially grounded, mappable, database (.dbf) [6]. It includes for each spatially-ground vector a measure of "flow," the number of persons traveling between any two specific points, and the distance between those locations [7]. The resulting dataset can be analyzed (and projected) in most GIS programs including ArcGIS and QGIS, the program in which it was constructed, as well as a range of statistical packages.

Results

As a first step, the total database was then divided into a series of separate databases, and maps, based on the distance people report traveling to work and the number of people traveling that distance. The result presents a detailed portrait of work-related travel paths along which infected persons and goods may travel. The travel-by-distance breakdown is summarized in Table 1. In it the number of origin-destination paths (vectors) and the average number of persons (flow) traveling a specific distance (both total and mean numbers) are calculated (Table 1) presents a coarse

Table 1: Summary Data US ACS Commuter survey.

Commute range (in kilometers)	total trips (flow)	% total flow	Number of vectors (O-D)	Mean dist. of vectors	Flow range ¹ each vector	mean flow per vector (O-D)
0-0 Kilometers.	15,090,980	12.3	75,564	0	4 to 20,950	199.71
0.1-5	21,771,587	17.74	495,525	3.136	4 to 3,955	43.94
5.1-26.259	68,956,614	56.19	2,240,743	14.14	4 to 2,640	30.78
26-55.9	11,080,745	9.03	528,632	31.26	4 to 1,105	21.36
56-104.6	3,768,626	3.07	251,993	72.3	4 to 1,045	14.95
104.7-169	679,502	0.55	51,047	127.23	4-480	13.31
169.1-700.0	857,147	0.7	65,697	329.4	4-205	13.04
700.1-2099.5	384,740	0.31	28,215	1,256.09	4-195	13.63
2099.5-4398.21	133,335	0.11	9,815	3,035.51	4-105	13.58
4400-8271.65	5,575	0.0045	443	6,247.89	4-55.	12.58
Totals:	122,728,851	100	4,155,548	44.07	4 to 20,950	31.32

¹Flow is a measure of the number of persons traveling a single origin-destination route.

breakdown of American Community Survey commuter travel data origin-destination routes categorized by travel distance. The number of persons who report no travel between home and work include those with home offices as well as those who live and work in a single building, for example above a local store. For epidemiologists, they present a dense, static reservoir in which diseases may evolve and from which they may spread among commuters. At the other end of the scale the relatively small but still significant number of those traveling more than 3,000 kilometers include persons commuting from Alaska and Hawaii to the Continental US and, not insignificantly, military personnel traveling between different bases. Others traveling more than 800 but less than 3,000 kilometers include national travel between major cities: New York to Los Angeles, Atlanta to Los Angeles, etc.

A more detailed analysis reveals a densely connected network in which local commuters traveling less than sixty kilometers may create broadly regional pathways for disease diffusion along densely populated corridors, for example between Boston, New York City and Washington, DC. Effectively, the density of travel makes of that "mega-region" a single entity within which infectious may be spread by commuters from place to place over time (Figure 1). The means by which short-distance, high volume commuting pathways create pathways for disease expansion is illustrated in these two maps of central and southern California from Sacramento to San Diego. Figure 1 presents two maps of dense commuting corridors in California. In the first map local, high volume commuting vectors (under 5.1 km.), shown in red, reflect local urban boundaries. Commutes under 26.1 km., illustrated in blue, quickly enlarge the local area of potential infection to include suburban and exurban areas. A capillary-like network is created that expands the potential for microbial transmission beyond the city. In the right-hand map, all commutes under 109 km. are presented in grey. At this distance, slightly less than sixty miles, the density of commuter vectors, origin-destination, creates a complete field across which infectious disease might progress. Obviously, there will be a time lag if microbial expansion occurs site-to-site across five, ten or even 20 km. distances. And while commuter volumes decline at greater distances, the volumes are still sufficient to assure microbial expansion of several evolving epidemic scenarios. The results even at this general level of presentation are fundamental. First, they for the first time illuminate local pathways for disease diffusion which have previously gone unreported. To date, attention has focused primarily on larger scale pathways for disease introduction into major cities rather than the avenues for local and

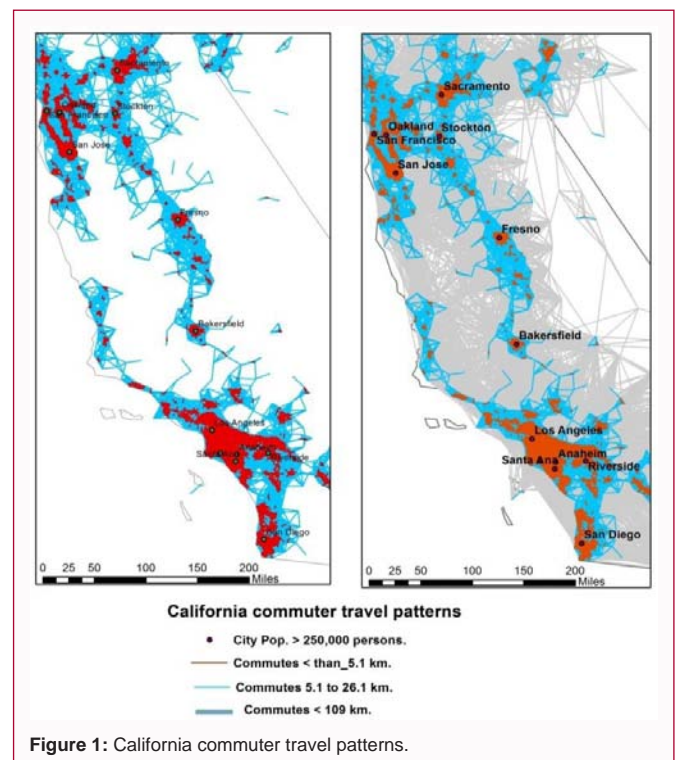


Figure 1: California commuter travel patterns.

regional expansion. That said, attention to multiple scales of spatial analysis are critical for an understand of and planning for epidemic events [8]. Second, the rapidity with which even relatively local commuter pathways create extra-urban "megaregions" extending beyond traditional jurisdictional boundaries questions the potential effectiveness of traditional public health jurisdictions to plan for and then respond to epidemic events. Finally, the dataset provides a medium in which the potential for epidemic progress may be better analyzed through a combinatorial approach combining sequential travel vectors following the introduction of a pathogen or its vector (mosquitoes, ticks, etc.).

Discussion

The applicability of this data to any specific event will depend on the precise nature of the infection and its principal means of transmission. Whether the bacterium or virus is transmitted interpersonally (for example, influenza) or is vector born (for example, by mosquitoes)

will affect the incubation times and transmission rates of a specific infectious disease. At present, research has begun to apply commuter data to an analysis of the 2003 H3N2 influenza outbreak in 2009. The goal is to demonstrate through that manner in which an infectious disease will spread, over time, through local as well as regional, national, and international pathways in a predictable manner. More generally, when fully analyzed and localized, commuter survey data will provide local and regional public health officials tools for a fairly precise estimation of the potential for a disease event to travel into and from their jurisdictions. It may also serve as a predictive tool with which the report of incidence elsewhere may be used to calculate the likelihood and timing of its introduction to a seemingly distant jurisdiction. Because the data is bidirectional (vectors being "from" and separately "to" different census tracts) the potential for not only infection but re-infection can be described by local health researchers. One obvious limit of this data is that it deals only with commuter data. Cities that are vacation destinations obviously will host significant numbers of travelers not included in this survey. Another limit is the lack of cross-border data for commuters traveling for work between the United States and its neighbors, Canada and Mexico. Limitations aside, an exploration of the data by public health officials in different jurisdictions presents the opportunity for the calculation of disease risk and potential based on commuter travel in a manner that hopefully will permit greater preparedness and more response to evolving disease events.

References

1. Tom K. Disease Maps: Epidemics on the Ground; 2011.
2. Koch T. Cartographies of Disease: Maps, Mapping and Medicine, Second Edition; 2018.
3. Khan K, Arino J, Hu W, Raposo P, Sears J, Calderon F, et al. Spread of a novel Influenza A (H1N1) virus via global airline transportation. *N Engl J Med.* 2009;361(2):212-14.
4. Khan K, Bogoch I, Brownstein JS, Miniota J, Nicolucci A, Hu W, et al. Assessing the origin of and potential for international spread of chikungunya virus from the Caribbean. *PLoS Curr.* 2014;6.
5. US Census Bureau. American Community Survey (Economic Characteristics); 2017.
6. Dash Nelson G, Rae A. An economic geography of the united states: from commutes to megaregions. *PLoS One.* 2016;11(11):e0166083.
7. Alasdair R, Garrett GD, Nelson. United States Commutes and Megaregions data for GIS; 2017.
8. Pigott DM, Deshpande A, Letourneau I, Morozoff C, Reiner RC, Kraemer MUG, et al. Local, national, and regional viral haemorrhagic fever pandemic potential in Africa: A multistage analysis. *Lancet.* 2017.