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Physica A

journal homepage: www.elsevier.com/locate/physa

Q1 Effects of human dynamics on epidemic spreading in Côte d'Ivoire

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HIGHLIGHTS

- We prove that the local BRN is to be greater than unity is neither necessary nor sufficient for outbreaks of epidemics.
- By abandoning the well-mixed assumption and considering the heterogeneity of human interaction intensity, we observe more realistic spatiotemporal patterns of epidemic spreading.
- We can identify critical paths for preventing nationwide epidemic outbreaks in the future.
- By defining proper distance according to human mobility, we can map the observed levy-flight-like spreading process back to classical diffusion process and qualitatively predict the spreading paths.

ARTICLE INFO

Article history:

Received 18 September 2015

Received in revised form 1 September 2016

Available online xxxx

Keywords:

Epidemic spreading dynamics

Human mobility

Human interaction intensity

Mobility distance

ABSTRACT

Understanding and predicting outbreaks of contagious diseases are crucial to the development of society and public health, especially for underdeveloped countries. However, challenging problems are encountered because of complex epidemic spreading dynamics influenced by spatial structure and human dynamics (including both human mobility and human interaction intensity). We propose a systematical model to depict nationwide epidemic spreading in Côte d'Ivoire, which integrates multiple factors, such as human mobility, human interaction intensity, and demographic features. We provide insights to aid in modeling and predicting the epidemic spreading process by data-driven simulation and theoretical analysis, which is otherwise beyond the scope of local evaluation and geometrical views. We show that the requirement that the average local basic reproductive number to be greater than unity is not necessary for outbreaks of epidemics. The observed spreading phenomenon can be roughly explained as a heterogeneous diffusion–reaction process by redefining mobility distance according to the human mobility volume between nodes, which is beyond the geometrical viewpoint. However, the heterogeneity of human dynamics still poses challenges to precise prediction.

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1. Introduction

Understanding and predicting outbreaks of contagious diseases are crucial to the development of society and public health. The degree of risk of outbreaks of some epidemics is quite high in underdeveloped countries, such as bacterial diarrhea (e.g., cholera), SARS, avian flu, H1N1/9, yellow fever and influenza, among others [1]. Apart from some severe diseases (such as SARS, Ebola), even cholera is a leading cause of death and affects infants and children in low-income countries, in

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<http://dx.doi.org/10.1016/j.physa.2016.09.059>

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particular [2]. Unfortunately, epidemic spreading is becoming increasingly more complex. Hundreds of years ago, epidemic spreading was modeled as a diffusion process with a speed of 300–600 km/year [3], for which it was quite easy to make precise predictions. However, at present, epidemics spread much faster and can spread around the world in about 6 months [4], presenting a much more complex phenomenon—contagious diseases may suddenly appear in a region spatially distant from the original outbreak area, and its path has become difficult to predict.

Evidences increasingly show that epidemic spreading dynamics are influenced by spatial structure and human dynamics (including both human mobility and human interaction intensity) [5–13]. With rapid transportation, human mobility has already changed the 2D geometrical space to a higher-dimensional manifold. A place spatially far away can be “drawn” much closer by a variety of rapid transit methods (such as airlines, high-speed rails, etc., for inter-city; or light rails, subways, Bus Rapid Transits (BRTs), etc., for intra-city), which means that people living far way geometrically may not be really distant. In this perspective, the world we perceive is not how the real world ought to look. This change will strongly affect epidemic spreading dynamics. Additionally, there is a super-linear relationship between the total human interactions and city size [11], which indicates that epidemics have more opportunity to spread in larger cities and with different infection durations. The temporal aspect of human dynamics, especially the bursty nature of human contacts, is also very important. Great efforts have been devoted to determine the impact of the temporal aspect of human dynamics on epidemic spreading [14–18]. These factors all pose great challenges to epidemic modeling and prediction.

Therefore, it is of great importance to develop a realistic dynamic model that incorporates the effects of spatial structure and human dynamics (both human mobility and human interaction intensity) to understand and predict the spreading patterns and provide insights into the course of past and ongoing epidemics (especially in low-income countries), which can be helpful in assisting in emergency management and allocating health-care resources via an assessment of intervention strategies [19–24].

In this paper, we mainly focus on the effects of human mobility and human interaction intensity on contagious diseases spreading in Côte d'Ivoire at sub-prefecture spatial resolution based on call detailed record (CDR) data provided by the Orange Group and organizers of the D4D Challenge [25,26]. More specifically, we concentrate on modeling and predicting the epidemic spreading process once cases appear in one sub-prefecture and providing a systematic analysis of the conditions under which an epidemic can start and along what kind of path it spreads. Interestingly, the spreading process is not a classical diffusion process but is a kind of lévy flight [9], which consists of local diffusion and long-range jumps. Furthermore, we determine the underlying mechanism behind such kinds of lévy flight. By defining a proper distance, beyond the geometrical distance, according to the human mobility matrix at sub-prefectures resolution, we can recover the diffusion process from the lévy flight. Apart from the “effective distance” proposed in Ref. [10], the inverse of the human mobility volume is also a proper distance for predicting the spreading process. The effects of heterogeneous human interaction intensity, which can lead to some repetitive infected nodes, should also be considered when defining a proper distance.

The remainder of this paper will be organized as follows. Section 2 will introduce our model and the associated improvements compared with former models and the results. Section 3 presents the conclusion and discussion. Appendix will mainly describe the details of the CDR dataset [26], how we extract human mobility and interaction intensity from it, and other related empirical results which support our model.

2. Model and results

The basis of our analysis is a spatially explicit nonlinear differential model that incorporates mainly human mobility networks and human interaction intensity. The epidemic spreading dynamic is a classical susceptible-infected-recovered (SIR) contagion process in metapopulation networks [5–7,27,12,13]. There are 255 nodes in our model, corresponding to 255 sub-prefectures in Côte d'Ivoire, and 21,952,093 individuals (the total estimated population by CIA [1] in 2013) are allocated within these nodes, according to the population distribution (see Appendix for details). In the i th sub-prefecture, with a population of N_i ($i = 1, 2, \dots, 255$), the state variables at time t are the local abundances of susceptible individuals, $S_i(t)$, infected individuals, $I_i(t)$, and recovered people, $R_i(t)$. The population distribution (i.e., N_i) is estimated based on the census in 1989 (see Appendix for details). Connections between sub-prefectures are characterized by the human mobility volume, which can be denoted as a matrix $A = [A_{ij}]$, where A_{ij} is the number of people moving from sub-prefecture i to j , extracted from the CDR data (see Fig. 1 and Appendix for details). The CDR data provide us the anonymous user-id, timestamp, subpref-id (and its position) when the user makes a call. Once the user makes a call in a new place, we can identify a movement (since the resolution is at sub-prefecture, this movement extraction is little affected by the signal noise (i.e., the people does not move but due to tower traffic balancing, the signal might be assigned to another tower) [28], see Appendix for more details of movement extraction). Using real human mobility data is an advantage compared with previous models, where the mobility volume between cities was estimated by gravity or a gravity-like model [7,8,19–23,29].

In order to quantitatively depict the effects of interaction intensity upon the infectivity of an infectious disease, we introduce the local basic reproductive number (BRN) R_0 , which is the number of infected cases that one case generates on average over the course of his infectious period. When $R_0 < 1$, the infection will die out in the long run in that region; if $R_0 > 1$, the infection will be able to spread among the population. The local BRN of sub-prefecture i is

$$R_{0i} = \frac{S_i \eta_i \beta_i}{\mu_i}, \quad (1)$$

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