Infectious Diseases Dynamics and Complexity: Multicompartment and Multivariate State-Space Modeling

Kidane Desta Gebreyesus and Chuan-Hsiung Chang

***Abstract*—It is estimated that more than 60% of the infectious diseases in humans can be passed from animals. But, research in the past few decades had been focused on human-to-human disease transmission. Wide range of mathematical and epidemiological models have been developed. However, despite the development of these computational models in the area of infectious diseases research, modeling for understanding and controlling animal-to-human or animal-to-animal (of different species) disease transmission is lacking. Here, we propose a multicompartment model, which takes human and animal or different species of animals interactions into account. We further formulate compartment model with clustering—this can be used in a large population with diverse geographical locations—to obtain an optimal parameter estimations with less computational complexity. We also develop a multivarate state-space model, which enables us to capture features of data such as diseases variability, meteorological conditions, time variations, and measurement errors. Our approaches can be used for various types of transmitted diseases including Ebola, MERS-Coronavirus, Bird flu, tuberculosis and other zoonotic diseases.**

***Index Terms*—Animal-to-Human, multicompartment model, disease transmissions, state-space model.**

I. Introduction

IT is estimated that more than 60% of the infectious diseases in humans can be passed from animals. Recent research findings on MERS-Coronavirus and Ebola virus, for example, show that the viruses appear to pass from animal to human. The largest Ebola virus outbreak in West Africa can be transmitted through direct animal-to-human contacts (e.g., from bats, apes, monkeys, etc.). Similarly, MERS-Coronavirus can be transmitted from camel to human. The widespread of Bird flu, tuberculosis and other zoonotic diseases can be passed between animals and humans.

Worldwide effort has been done to combat the global spread of infectious diseases. To better understand the dynamics of epidemics, it is important to study potential transmission routes. Wide range of computational models, which provide analytical framework for quantifying and understanding infectious diseases outbreaks [1], have been developed. Modern and traditional computational methods, ranging from basic to advanced mathematical and epidemiological approaches[2], [12], have been used to modeling human-to-human disease transmission dynamics. Compartments for discrete Tuberculosis model have been developed [19].

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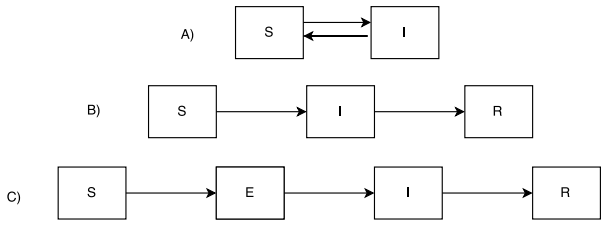

Fig. 1. Basic epidemic models

However, despite the development of these computational modeling in the area of infectious diseases research, modeling for understanding and controlling animal-to-human or animal-to-animal (of different species) disease transmissions is lacking. Here, we propose a multicompartment model, which takes human and animal or different species of animals into account [3], [9].

We formulate compartment models with clustering for parameterizing and characterizing transmission rates in a population with diverse geographical locations—to determine an optimal parameter estimations with less computational complexity.

Features of data such as behavioral processes, meteorological conditions, demographics, irregular time variation, disease variability, and measurement error variations make modeling complex and uncertain [5], [6], [7], [8], [17], [18]. We propose a multivarate state-space modeling approach to account these variations—State-space modeling is a powerful and flexible approach that incorporates and captures multi-sourced features of data [11], [12], [13].

II. BACKGROUND

We first describe the basic epidemic models and univariate state-space frameworks and their assumptions. Next we extend these approaches and formulate multicompartment and multivariate state space models.

A. Basic Epidemic Models

We describe and present the standard epidemic models, Susceptible-Infective-Susceptible (SIS), Susceptible-Infective-Recovery (SIR), and Susceptible-Expose-Infective-Recovery (SEIR), as Fig. 1.

- Susceptible: individual/host is susceptible to infection: no pathogen is present.
- Exposed: the host may or may not exhibit obvious signs of infection.

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TABLE I
SUMMARY OF NOTATIONS

Parameter	Description
β	Transmission rate between susceptible and infectious
γ	Recovery rate
$S_A(0)$	Initial number of susceptible animals
$I_A(0)$	Initial number of infectious animal
$S_H(0)$	Initial number of infectious human

- Infectious: Host encounters infectious individual and becomes infected.
- Recovered: The host is either no longer infectious or removed/ dead. [14]

SIS, SIR, and SEIR models, which are commonly used to model human-to-human diseases transmission, have similar differential equation expressions. In this paper we use the SIR model as a background to our approaches. The basic equations of SIR models are as follows:

$$\frac{dS}{dt} = -\beta\frac{IS}{N} \quad (1)$$

$$\frac{dI}{dt} = \beta\frac{IS}{N} - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

here $S_t = S$, $I_t = I$, and $R_t = R$ represent for the numbers of susceptible, infection, and recovery. The SIR model can also be used for modeling animal-to-animal of a single-species.

We introduce some assumptions: We assume that the human-to-human transmission and contact rates change with time in large population size. Weekly or monthly time dependent rate in small communities is assumed (i.e. daily contact rate in small areas such regions, cities, rural and urban may not change).

B. Dynamical Systems and Univarate State-Space Models

Dynamical systems are systems that change over time such that their current states are some how dependent upon their previous states. The term state-space model corresponds to a general way of representing dynamic relations of unobserved/latent state processes and observations of these relations, which are often made at different points in time. Hidden markov model, State-space model with discrete state variable, has been used to detect prospective diseases outbreaks [15].

State-space models help to estimate and predict optimal control strategies with flexible frameworks. It can be used to model univariate or multivariate dynamic systems.

- x_t Measurements or unobserved/latent state process, which can incorporate measurement errors (w_t) in a model.
- y_t: Observations, which is conditionally independent of the past given x_t. It assumes Gaussian noise, v_t

The standard equations of univarate state-space models are described as follows:

$$x_t = f(x_{t-1}, w_t) \quad (4)$$

$$y_t = g(x_t, v_t) \quad (5)$$

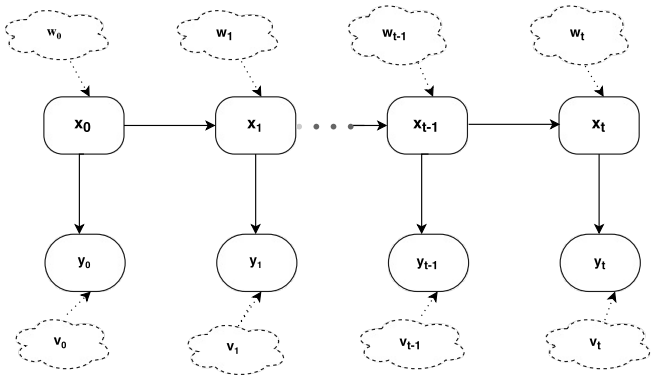

Fig. 2. Hidden Markov Chain: State-space model with discrete state variable framework

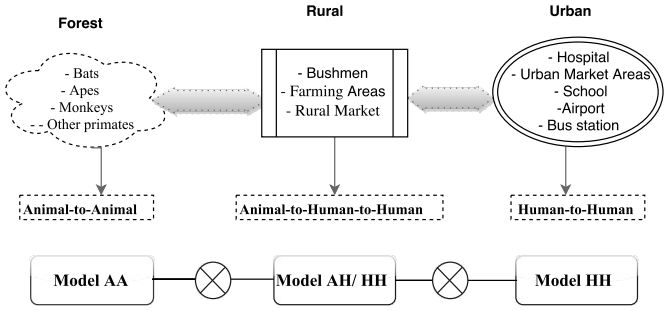

Fig. 3. Possible population interactions and transmission routes.

where $f(.)$ and $g(.)$ can be linear or nonlinear functions. w_t and v_t follow Gaussian univarate normal(N) distribution, with mean zero and constant variance,

$$w_t \approx N(0, d)$$

$$v_t \approx N(0, r)$$

$$x_0 \approx N(\lambda, \theta).$$

x_0 is the univarate initial state distribution. d, r, λ, and θ are parameters. Three sub-models of a univariate state-space models have been proposed, namely:

- Gauss-linear forward and observation model: when both f(.) and g(.) are linear.
- Nonlinear forward and Gausslinear observation model: when f(.) is nonlinear and $g(.)$ is linear.
- Nonlinear forward and observation model: when both $f(.)$ and $g(.)$ are nonlinear [16].

III. MULTICOMPARTMENT MODELING

The SIR models can be redefine to implement animal-to-human and animal-to-animal of different species.

A. Epidemic models for Animal-to-Human: Eboal as cases study

Consider a susceptible bushmen who travel regularly to a particular forest, which are widely available in West Afirca. Assume there are a large number of Ebola infected animals such as bats or apes or monkey or others living in the forest. Then the possible transmission model for single-specie animals (A) to the bushmen (H) (S_H, S_A and I_A labeled as the number of susceptible bushmen, number of

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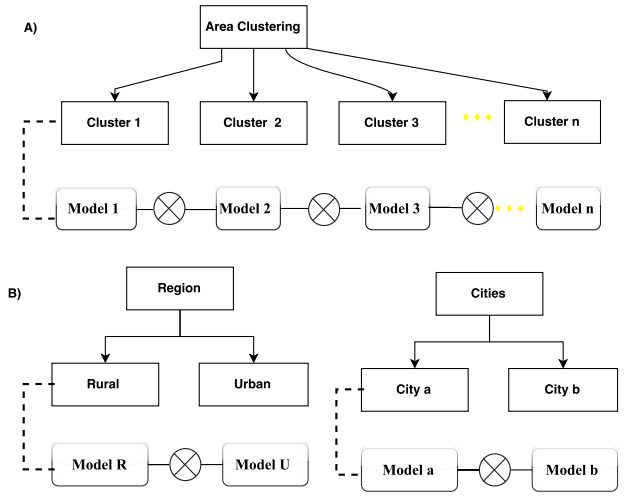

Fig. 4. Possible population interactions and transmission routes.

Fig. 5. Highlight of selected terms and features of infectious diseases

single-specie susceptible and infected animals respectively) would be as follows

$$\frac{d(S_H + S_A)}{dt} = -\beta \frac{(S_H + S_A)I_A}{N_A + N_H} \quad (6)$$

$$\frac{dI_A}{dt} = \beta \frac{(S_H + S_A)I_A}{N_A + N_H} - \gamma I_A. \quad (7)$$

The SIR models can be redefine to implement animal-to-animal of multiple species (E.g., for transmission from bats-to-apes or from apes-to-monkeys or from bates-to-monkeys or multiple interactions etc.).

B. Epidemic Models with Clustering

$$\frac{dS_i}{dt} = -\sum \beta_i \frac{S_i I_i}{N_i} \quad (8)$$

$$\frac{dI_i}{dt} = \sum \beta_i \frac{S_i I_i}{N_i} - \gamma_i I_i \quad (9)$$

$$\frac{dR_i}{dt} = \gamma_i I_i \quad (10)$$

Where the notations are similar with that of in equations (1)-(3). We simple split one large population into subpopulation/ clusters, labeled as cluster i. The clustering approach enables us to find an optimal transmission and recovery parameters.

Our approach can be also used to estimate parameters in case of transmission variations (e.g., during school period and summer breaks, during some events such weeding, church days, shopping days, when a large group of people meet).

IV. Multivariate State-Space Modeling

We formulate a multivariate state-space model of SIR, which takes the form

$$X_t = (S, I, R)^t \quad (11)$$

$$X_t = f(X_{t-1}, W_t) \quad (12)$$

$$Y_t = g(X_t, V_t). \quad (13)$$

Where $f(.)$ and $g(.)$ can be linear or nonlinear forms. W_t and V_t are measurement and observation errors, which follow multivarate normal (MVN) distribution,

$$W_t \approx MVN(0, D)$$

$$V_t \approx MVN(0, R)$$

$$X_0 \approx MVN(\Lambda, \Theta).$$

X_0 is the multivarate initial state distribution. D, R, Λ, and Θ are matrix/ vector parameters.

V. Conclusion and Discussions

We proposed a multicompartment modeling with clustering of diverse geographical locations, such as cities, rural, and urban areas, which helps to obtain an optimal parameter estimation of the transmissions dynamics. The methods can also be used to characterize the transmission rates in places where a large number of people meet, such as hospitals, schools, bus-station, churches, rural and urban markets, and related. We showed how the basic epidemic model can be extended in animal-to-human, animal-to-animal of different species, and the compartment model with clustering.

We proposed a multivarate state-space model to estimate and predict an optimal control measure strategies. We consider various major model uncertainty factors in our model. We also highlight some basic factors that could help to improve the estimations of transmission and contact rates [11] (e.g., vary during school period and summer breaks, during some events such weeding, churches, shopping days, where a large group of people meet, can bring a significant variation in estimating transmission and contact rates).

Our approach can be implemented for various transmission diseases, including Ebola, foot-and-mouth disease, MERS, West Nile virus, and influenza, and Malaria. Needless to say, there is always room to improve in the algebraic, approaches, formulations and assumptions.

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